

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

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Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

- x This is a new application for a
x Utility patent.
☐ Design patent.
x Applicants claim small entity status (See 37 CFR 1.27)

2. Application Papers Enclosed

- 1 Title Page
142 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
4 Page(s) of Claims
1 Page(s) of Abstract
0 Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal
723 Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on November 17, 2000, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EK415382545US


Sandy Fong

3. Oath or Declaration

- ☐ Enclosed
- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
- ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
- ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
- ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- x Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- x Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- x Statement Under 37 CFR § 1.821
- x Paper copy of sequence listing identical to computer copy (723 pages)
- ☐ Microfiche computer program
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- x Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$355.00		\$710.00
TOTAL	30-20	= 10	X 9 =	\$90.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 40 =	\$00.00	X 80 =	\$0.00
Γ First Presentation of Multiple Dependent Claim			+ 135 =	\$135.00	+ 270 =	\$0.00
FILING FEE:				\$580.00	OR	\$0.00

B. ☐ **Design Application (\$160.00/\$320.00)** Filing Fee: \$ _____

C. ☐ **Plant Application (\$245.00/\$490.00)** Filing Fee: \$ _____

D. **Other fees**

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ _____

☐ Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached [Fee -- \$130.00] \$ _____

☐ Other \$ _____

TOTAL FEES ENCLOSED \$ 580.00

7. Method of Payments of Fees

- ☐ Enclosed check
- x Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Leslie A. Mooi at the address below.

Respectfully submitted,

Date: November 17, 2000

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

Express Mail Label No.: EF415382545US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. BACKGROUND OF THE INVENTION

5 1.1 TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

10 1.2 BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

30 2. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 362 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 – 362 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 – 362. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 – 362 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 – 362. The sequence

information can be a segment of any one of SEQ ID NO: 1 – 362 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 – 362.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1–362; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1–362; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1–362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under

stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-362; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-362; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These

techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form

the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 1); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

3. DETAILED DESCRIPTION OF THE INVENTION

3.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules.

The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells.

PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil).

Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of

oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-362.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-362. The sequence information can be a segment of any one of SEQ ID NOs: 1-362 that uniquely identifies

or represents the sequence information of that sequence of SEQ ID NO: 1-362. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol)

and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions,

deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation.

Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of

glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted"

proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

5 Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

10 The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

15 In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

20 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences.

Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no

more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and

the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

5

3.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1 – 362; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 – 362; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1 – 362; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 362. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known

methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1 - 362 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1 - 362 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1 - 362 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1 - 362, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can

differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 362, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 362 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 362, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably

constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by

the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis

5 techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA
10 sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

15 The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate
20 polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-362, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in
25 appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor
30 Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and

the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell.

- 5 Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a
10 nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof is inserted, in a forward or reverse orientation. In the
15 case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of
20 example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an
25 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein
30 "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the

protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT

(chloramphenicol transferase) vectors or other vectors with selectable markers. Two

5 appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will

10 include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat

15 shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired

20 characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of

25 replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

30 As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived

from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

3.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous

promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7

lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed

5 primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking

10 nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion

15 chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

20 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella*

25 *typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

30 In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the

invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this

purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No.

5 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

10 3.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-362 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 362 or the corresponding full length or mature protein. Polypeptides of the
15 invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NOs: 1 – 362 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-362 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization
20 conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-362 or the corresponding full length or mature protein; and “substantial equivalents” thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least
25 about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-362.

Fragments of the proteins of the present invention which are capable of exhibiting
30 biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for

example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments

of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

5 The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level.

10 One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

15 The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded
20 polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

25 In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes,
30 *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in*

Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-362.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in

the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin

(TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

- 5 One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or
10 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces
15 fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity
20 and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be
25 fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

30 **3.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

3.5 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient

expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human

5 disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of

10 antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to

15 express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of

20 cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein

25 encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron

30 DNA may be inserted along with the heterologous promoter DNA. If linked to the desired

protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting

sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

5 The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by
10 reference herein in its entirety.

3.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed
15 or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals,
20 preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals,
25 are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using
30 homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased

protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

3.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of

5 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the
10 invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein
15 expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular
20 antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

25 3.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either
30 constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when

labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology:

Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

3.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

3.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION

ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

- 5 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 15 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- 25 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 30

6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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3.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of

specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

3.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation

of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I.

Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

5 **3.7.6 TISSUE GROWTH ACTIVITY**

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

10 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an
15 osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

20 A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

25 Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing
30 damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising

such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

3.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes

viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul et al., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected

cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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3.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

3.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

3.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assays for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

3.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases,

blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl,

Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

3.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of

such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and

5 receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of

10 receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek,

15 D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,

20 Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

25 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in

30 Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of

colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

5 **3.7.13 DRUG SCREENING**

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One
10 method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One
15 invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include
20 (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or
25 compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.
30 Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

3.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind

polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

3.7.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or

promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

3.7.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

3.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases

or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple

sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive

bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

3.7.18 OTHER ACTIVITIES

5 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue
10 pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional
15 factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case
20 of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is
25 cross-reactive with such protein.

3.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for
30 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving

inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

3.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963,

Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

3.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods.

Examples of therapeutic applications include, but are not limited to, those exemplified herein.

3.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically,

the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable

5 parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

3.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source
15 derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other
20 active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain
25 cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These
30 agents include various growth factors such as epidermal growth factor (EGF),

platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

3.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome

coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

3.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol,

propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

5 When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to
10 pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other
15 vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal
20 administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

 For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills,
25 dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including
30 lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose,

hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose,

5 concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

10 Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds
15 may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

20 For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be
25 determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit
30 dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or

aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without

destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T

cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with
5 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a
10 liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids,
15 and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and
20 severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response.

25 Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more
30 preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are

useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering

agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final

composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

3.9.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical

procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀.

5 Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of
10 administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration
15 (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should
20 be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the
25 invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the
30 subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

3.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

3.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab', F(ab')₂, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), *Antibodies A Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988),

Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell,

A.M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al., Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding, J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

3.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 362 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NOs: 1 - 362 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence

information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs)

5 within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence
10 information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present
15 invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded
20 thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which
25 match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily
30 recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based

systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

3.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

3.13 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays*:

Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

3.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

3.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NOs: 1 - 362, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives

expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspaczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a

skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA.

- 5 Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple
10 helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization
15 blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present
20 invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

3.16 USE OF NUCLEIC ACIDS AS PROBES

25 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 362. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from
30 of any of the nucleotide sequences SEQ ID NOs: 1 - 362 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes.

Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

3.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987;

Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond

joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of

Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

3.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to

the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

3.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the

density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

4.0 EXAMPLES

4.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

4.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genepet release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1- 362.

Table 1 shows the various tissue sources of SEQ ID NO: 1-362.

The homology for SEQ ID NO: 1-362 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1-362 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1-362 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren

Brunak, and Gunnar von Heijne in the publication “ Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites” Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al as reference, was obtained for the

5 polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

TABLE 1

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	4 18 39-40 83 88 98 110 112-113 136 168-169 201-203
adult brain	GIBCO	ABD003	7 15-16 31-32 39-41 45 54 58 63 70 73-75 82-84 92 98 106 110 114 116-117 126 128 130 139 144 155 164 168-169 191-192 195 198 204-215 239-240 249 252 258 272-274
adult brain	Clontech	ABR001	10-11 15 19 39-40 88 106 120 144 168 215-216 258
adult brain	Clontech	ABR006	13 17 20 23 33 39-40 50 58 62 75 82 84 88 100 104 121-122 129 149 168 208 216 223 232-233 239 256 269 277 287-288 353 360
adult brain	Clontech	ABR008	4 10-11 13 17 20 23 25 28-30 32 34-35 39-41 48 50 53-54 58 61 63 68-69 74 76 78 80 84-89 91 98 104 107 112-114 118 121-122 130 134-136 143 153-155 158-160 163-166 168 172-173 184-188 199-200 203 212-213 215-216 219-220 226-227 234 239 242 244 251-252 255-257 263 268 271-272 277-280 287 291 300-301 305-306 316 322 338 346-347 360
adult brain	Clontech	ABR011	157 306
adult brain	BioChain	ABR012	36 247
adult brain	Invitrogen	ABR013	176
adult brain	Invitrogen	ABR014	50 53 100 269
adult brain	Invitrogen	ABR015	19 38 74 161-162
brain	Invitrogen	ABR016	53 74 137 139 239
adult brain	Invitrogen	ABT004	8 15 19-20 28 30 35 75 78 100 106-107 113 134 160 179 181 184 198-199 210 216 224 227 252 254-255 288 340
adipocytes	Stratagene	ADP001	9 13 19 45 74 98 121-122 131 164 187 189-190 217 239
adrenal gland	Clontech	ADR002	9 15 18-19 24-25 31-32 46 56 77-78 112 114-115 117-119 121-122 124 139 170 182 192 209 213 218 220 225 249 276 306
adult heart	GIBCO	AHR001	2 4 7 17 19-22 26-27 34 38 45-46 50 53-54 58 60-61 63 74 76-77 86-87 91 96 98 108 112 114 121-122 131 133 136-140 144 155 160 165-168 184 188 217 226 239 241-242 251 259 265 277-278 290 306
adult kidney	GIBCO	AKD001	4 6-11 13 15-17 19-20 24 30-32

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			34 36-38 47 53-54 60-63 66 69 73-75 78 82-85 87 89-92 96 98 100 103 106 108 110 112-113 116 121-123 126 129 131 134 136 139-142 144 153 155 158- 159 169-170 176 181 207 237 239 266-267 271-272 306
adult kidney	Invitrogen	AKT002	7-8 10-11 13 15 19 25-27 32 37-38 53 55-56 66 75 86 90 92 108 123 144 165-166 172 182 199 218 225 233 236 238 260 266-267 332
adult lung	GIBCO	ALG001	8 22 26-28 38-40 47 54 78 91 98 104 110 112 117 139 148 168 189 196 225 239 248 351-352
lymph node	Clontech	ALN001	7 26-27 32 35 38-40 79 82 120 127 152 158-159 169 171 219 239 244
young liver	GIBCO	ALV001	7 14 16-17 19 33 37 53 72 77 107 113 116 118 134 152 168 212 249
adult liver	Invitrogen	ALV002	12 14 17 24 28 32-33 36 58 73 75-76 84 101 116 131 138 140 158-160 182 194 212 238 275 284 323 342-343
adult liver	Clontech	ALV003	271 284 358
ovary	Invitrogen	AOV001	4 6-11 13 15-16 18-21 25-27 31-32 34 36 38-40 46 48 50 53- 54 56 58 60 65 70 73-78 80 83- 84 86 91-92 95 98 100-101 103- 106 108 110-112 115 117-118 124 126-127 129-131 136 139- 142 144 148 155 157-161 163- 167 169 173-174 178 180-186 188-189 191-193 196 199-200 204-208 210-211 220-223 233 236 239 249-252 260-263 266- 270 287-288 306 315 351-352
placenta	Clontech	APL001	30 50 74 82 230
placenta	Invitrogen	APL002	45 50 59 70 75 103 163 223
adult spleen	GIBCO	ASP001	7 19 30 38 45 54 58 62 74 81 83 91 106 110 112-113 116 131 144 151 155 162 165-166 172 176 189 191 215 230 236 239 249 329
testis	GIBCO	ATS001	4 15 19-20 30 48 53 74 89 94 110 126 140 158-159 173 214- 215 220 239 245 306
bladder	Invitrogen	BLD001	30 35 59 61 74-75 123 164 221 241 318
bone marrow	Clontech	BMD001	3 6-7 9 13 17 20 26-27 30-31 34 38-40 42 46 53-54 63-79 82- 83 85 91 93-98 101 105 110 115 121-122 126 128-129 133-134

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			143 145 154 161-162 176 192 205-206 234 236 239 243 264 289 306 322
bone marrow	Clontech	BMD002	3-4 7 9 13 16-17 19-20 23 30 32 34 36 38-40 47-48 54-56 58 61 68-69 74-75 79 84 108 118- 119 121-122 125 128-129 131 133 140 144 147 149 153-154 158-159 161 163 167 171 174 176 185-187 200 211 218 232 239 241 247 252 277-278 285 296 303 310 320 324 329 339 341 353 356 359
bone marrow	Clontech	BMD004	64
colon	Invitrogen	CLN001	18 32 100 106 110 143 153 163- 164 178 213 247 266-267 284
cervix	BioChain	CVX001	4 6 8-9 19 22 24-25 28 32 45- 46 53 55-56 63 74-75 77-78 83 87 91-92 95 102 105 108 110 123 127 136-137 140 169 172 182 184-186 189-191 199 211 238 249 266-267 274 283 306- 308 317 354
endothelial cells	Stratagene	EDT001	2 4 6-7 9 15 17-21 25-28 30 32 36 39-40 45 47-48 53 55-57 60 62-63 69-70 74-76 78 83 85-87 98 101-104 106 108 112-113 119 121-123 130-131 136-137 139- 142 155-156 158-159 161 174 189-192 204 208 218 220 223 230 239 251 280 306
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM001	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM003	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM004	223
fetal brain	Clontech	FBR001	32 227
fetal brain	Clontech	FBR004	319
fetal brain	Clontech	FBR006	7 10-11 13 17 20 23-25 28-29 32 35 41-42 48 50 53 63 75 80 89 91 104 112 121-122 125 130 154 163 165-166 168 171 173 191 199 210 215-216 218 226 232 239 256 272 277 290 300 306 309 319-320 333 353 360
fetal brain	Invitrogen	FBT002	15 17 19 35 69 75 87 104 109 140 163 174 192-193 198-199

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			207 220 228 239 252 256-258
fetal heart	Invitrogen	FHR001	3 8 19 32 41 48 77-79 91 114 119 126 163 165-166 172 174 176 200 218 232 244 263 331 351-352 360-361
fetal kidney	Clontech	FKD001	16-17 36 46 53 74 82 95 104 111 117 169 189
fetal kidney	Clontech	FKD002	26-27 165-166 218 220 232 238 263 306
fetal kidney	Invitrogen	FKD007	38 74
fetal lung	Clontech	FLG001	32 48 139 173 217
fetal lung	Invitrogen	FLG003	10-11 19 36 58 61 69 74 134 163 168 178 194 249 263 266- 267 351-352
fetal liver- spleen	Columbia University	FLS001	1-19 21-38 41-62 68 70 72 74- 78 87 90-91 93 100-104 106-121 123-125 127 130-131 133-134 141-142 144 149 155-156 161 163 165-167 169 176 194-196 200 207 210 221 224-225 227 231-233 236 238 263 303 306 313 324 336 342
fetal liver- spleen	Columbia University	FLS002	2 5 7-9 12 14 16-18 22-24 30- 33 35-40 43-46 48-50 52-53 57 70 72 76-78 84-85 87 90 92 101-102 106-108 110 112 114 116-120 124 127-128 130-131 134-135 140-142 144 155 163 172 174 187 189-190 192 195- 196 199 205-207 210 220-221 223-224 230-234 244 251 258 260-261 263 265 275 296 313- 315 331 337-338 345 362
fetal liver- spleen	Columbia University	FLS003	19 30 33 139 174 265 313 339 355
fetal liver	Invitrogen	FLV001	10-11 14 17 19 21 37 46 50 61 63 156 163 165-166 172 200 210 238 253
fetal liver	Clontech	FLV002	19 32 74 163 356
fetal liver	Clontech	FLV004	3 14 19 32-33 37 42 47-48 50 58 60 82 85 121-122 129 131 152 171 193 272 353
fetal muscle	Invitrogen	FMS001	28 32 39-40 45 48 50 57 74 107 121-122 131 137 139-140 147 173 204 230 281
fetal muscle	Invitrogen	FMS002	19 23 32 34 55-56 80-81 98 121-122 124 131-132 158-159 199 212 230 280-281 353 357 360
fetal skin	Invitrogen	FSK001	2 4 14-15 17-19 22 41 46 50 53 59 72 75-76 81-82 84 94 103 106 113 128 135 140 144 156 164 167 170 174 188 209-210 220 227 230 238-239 254 306

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			321-322 333-335
fetal skin	Invitrogen	FSK002	4 34 47 54 79 84 113 126-127 129 134 156 192-193 208 223 230 241 277 285 333
fetal spleen	BioChain	FSP001	32 104
umbilical cord	BioChain	FUC001	4 19 22-23 32 38-40 46 55-56 58 61 73-75 91 98-99 103 106 110 112 116 120 123 129-130 139 160 165-166 175 182 230 234 249 251 302
fetal brain	GIBCO	HFB001	6 9 16 19-20 25 32 35-36 39-41 45 48 53-54 56 60 73 80-81 83- 92 98 107 112 114 157-159 163 165-166 172 191 197-198 211 226-227 239 350
infant brain	Columbia University	IB2002	6-8 13 15-17 19 21 32 35 41-42 48 50 60-61 77 81 84-85 88 92 104-106 112-113 116 119 134 139 144 160 165-166 168-169 173 176 191 196 199-201 215 223 225 227-228 239 261 285 290 329 339-340 348
infant brain	Columbia University	IB2003	7-9 13 32 39-41 58 92 103 105- 106 144 160 162 199 205-206 219 227-228 271 357
infant brain	Columbia University	IBM002	32 88 340
infant brain	Columbia University	IBS001	6 26-27 32 164 199 340
lung, fibroblast	Stratagene	LFB001	2 4 18-19 25 39-40 46 53 55-56 106 112 124 129 136 139 146 150 164 169 189-190 215 230 239 260 349
adult lung	Invitrogen	LGT002	2 6 8-11 15-16 19 26-28 30 32 39-40 46 48 50 53-56 60-61 66 72 74-75 85 87 92 94 96 98 103-104 108 110 112-113 117 119-120 124 130-131 139-140 149 152-153 155 158-159 167 169 174 176 178 184 189-190 195-196 217 220 229-230 234- 239 248-250 263 265-267 280 286 310 329-330 351-352
lymphocyte	ATCC	LPC001	7 13 16 19 32 39-40 54 63 74 82 96 113 120 126 130-131 133 144 150 178 184-186 223 239 241 260 262 294 305 339
leukocytes	GIBCO	LUC001	1 3-4 7-9 13 16-20 26-27 30 32 34-35 38-40 46 48 51 53-56 63 66 70 72-76 78 82 84-85 87 89 91-92 95-96 101 106 108 110- 112 114 116 120-122 126-127 129-133 136 139 144 146-152 164 175-179 187 192 232 236

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			239 241 266-267 292-294 306 325-327 329 339 359
leukocytes	Clontech	LUC003	7-8 17 55-56 76 84 112 129 131 161-162 176 180 185-186 329
melanoma	Clontech	MEL004	4 13 17 28 30-31 39-40 83 85 92 113 126 129 139 160 162 182 198 232 239 303 324
mammary gland	Invitrogen	MMG001	8-11 16-21 28 30 32 35 41 45 58-59 61 72 74-75 78 84 87 92 103-104 106-107 110 113 115- 116 123 128 131 134-135 144 152 163 176 181 183 210 212 220-221 230 234 236 238-239 248 251 260 272-273 275-276 306 331 351-352 360
neuron	Stratagene	NTD001	18-19 39-40 45 74 78 85 91
neuron	Stratagene	NTR001	19 21 57 246 265
neuronal cells	Stratagene	NTU001	8-9 18-19 21 32 81 85 87 128 164 174 184
pituitary gland	Clontech	PIT004	13 47 82 87 98 112 288 354
placenta	Clontech	PLA003	13 48 50 58 77 100 106 112 126 129 152 178 232
prostate	Clontech	PRT001	16 19 22 26-27 32 34 46-47 76- 77 92 98 106 112 124 172 214 239 260 280 294
rectum	Invitrogen	REC001	8 10-11 18 30 54 74-76 106 113 123-124 143 163 172 213 220 232 237 260 322-323 340
salivary gland	Clontech	SAL001	8 19 36 74 83 104 118 124 150 176 260 295 304
skin fibroblast	ATCC	SFB002	239
small intestine	Clontech	SIN001	9 17 19 22 32 34 54 57 59-60 73 75 84-85 96 99 107 113 118 134 139 144 149 151 185-187 189 197 199 217 219 221 230- 231 248 250 253-254 260 266- 267 295 304 356
skeletal muscle	Clontech	SKM001	17 19 39-40 48 89 104 116 131 281
spinal cord	Clontech	SPC001	8 19 32 34 38-40 47 58 61 74 80 83-84 89 104 108 131 139- 140 168 187 213 226 236 239 300 350
adult spleen	Clontech	SPLc01	1 46 54 134 236
stomach	Clontech	STO001	7 32 38-40 51 66 74 76 89 117 124 128 169 229 239 253 280 294 296
thalamus	Clontech	THA002	24 30 50 87 124 127 143 163 201 207 220 223 230 266-267 269 279
thymus	Clontech	THM001	7 13 19 25 32 36 39-40 54-56 72 74 82 96 108 113 119 127

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			137 139 141-142 146 169 184 192 260 276 296
thymus	Clontech	THMc02	9 17 28 30 32 39-40 48 53 61 72 74-75 77 79 82 91 107 112 119-122 125-126 131 139-142 153 171 175-176 178 184 187 205-206 222-223 227 235-236 269 278 289 297 305 310-311 325 327-329 336
thyroid gland	Clontech	THR001	7-11 15 17 19-20 25-27 32 34 36 46 48 53 59 72 82-87 89 91 96 98-99 104 106 110 118-119 121-122 127 130 136 139 144 151-152 158-159 165-167 179 187 204 208 220 239 249 281 283 295 298-299 312 316 344
trachea	Clontech	TRC001	62-63 73 75 86-87 89 101 147 192 239 266-267 282-283
uterus	Clontech	UTR001	4 8 17 19 22 26-27 32 39-40 46 63 82 98 110 130 151

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	L29075	Dictyostelium discoideum G-box binding factor	173	21
2	AL359215	Streptomyces coelicolor A3(2) putative phosphoglycerate mutase.	133	28
3	AF228713	Homo sapiens EDAG-1	1671	100
4	AC007130	Homo sapiens similar to 3-hydroxyisobutyrate dehydrogenase ; similar to P29266 (PID:g416873)	1557	100
5	AB040926	Homo sapiens KIAA1493 protein	1973	98
6	AF193016	Homo sapiens methyltransferase COQ3	1609	99
7	U95825	Homo sapiens androgen-induced prostate proliferative shutoff associated protein	2968	63
8	AL390081	Homo sapiens SEMA4B, Semaphorin 4B	3560	99
9	AC002130	Arabidopsis thaliana F1N21.9	258	50
10	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	323	27
11	D88733	Equine herpesvirus 1 membrane glycoprotein	284	24
13	M80783	Homo sapiens B12 protein	1144	70
14	U72678	Mus musculus EF-9	792	92
15	AK026486	Homo sapiens unnamed protein product	427	83
16	AK025813	Homo sapiens unnamed protein product	1010	100
17	AF151036	Homo sapiens HSPC202	722	84
18	AY007148	Homo sapiens similar to Homo sapiens HSPC197 mRNA with GenBank Accession Number AF151031.1	984	100
19	X57432	Rattus rattus ribosomal protein S2	956	97
20	AF164793	Homo sapiens protein x 013	386	100
21	J02642	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	1639	95
22	M34573	Homo sapiens alpha-2 collagen type VI-a	515	100
23	AL109928	Homo sapiens dJ551D2.5 (novel protein)	1999	100
24	AF111858	Homo sapiens dimethylglycine dehydrogenase precursor	3918	99
25	U64854	Caenorhabditis elegans partial CDS	184	25
26	AF151072	Homo sapiens HSPC238	838	99
27	AF151072	Homo sapiens HSPC238	393	96
28	AK024825	Homo sapiens unnamed protein product	1794	99
29	AF285631	Rattus norvegicus secretory carrier membrane protein 4	894	75
30	AK024113	Homo sapiens unnamed protein	3672	99

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
31	AL161515	Arabidopsis thaliana putative protein	146	52
32	AJ007798	Homo sapiens stromal antigen 3, (STAG3)	6320	99
33	D31856	Bacillus subtilis HutI protein, imidazolone-5-propionate hydrolase	667	39
34	AL391145	Arabidopsis thaliana putative protein	423	24
35	AF134726	Homo sapiens G7A	1591	46
36	AJ276485	Homo sapiens integral membrane transporter protein	1502	100
37	J05158	Homo sapiens carboxypeptidase N (EC 3.4.17.3)	2274	88
38	X57351	Homo sapiens l-8D	673	97
39	AF230904	Homo sapiens c-Cbl-interacting protein	3437	100
40	AF230904	Homo sapiens c-Cbl-interacting protein	2615	99
41	AF276893	Homo sapiens p21-activated protein kinase 6	3550	100
42	AF269255	Homo sapiens lysosomal apyrase-like protein 1	3198	100
43	S85655	Homo sapiens prohibitin	742	84
44	AB040926	Homo sapiens KIAA1493 protein	1973	98
45	AF151063	Homo sapiens HSPC229	1012	100
46	X68277	Homo sapiens protein-tyrosine phosphatase	1886	100
47	Z98745	Homo sapiens dJ29K1.2	889	51
48	AF032668	Rattus norvegicus rsec15	3738	92
50	AF195534	Rattus norvegicus GERp95	4513	99
51	AF161368	Homo sapiens HSPC105	513	98
52	W73147	Amino acid sequence of the soluble complement receptor 1	651	81
53	AF271212	Homo sapiens disrupter of silencing SAS10	2431	100
54	AF116646	Homo sapiens PRO0082	598	100
55	AF145613	Drosophila melanogaster BcDNA.GH03108	817	46
56	AF145613	Drosophila melanogaster BcDNA.GH03108	884	38
57	AL023803	Homo sapiens dJ616B8.3 (novel gene)	2287	100
59	AC024877	Caenorhabditis elegans contains similarity to Pfam families PF00621 (Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases, score=58.2, E=1.7e-13, N=10 and PF00169 (PH (pleckstrin homology) domain, score=17.0, E=0.00071, N=1)	296	31
60	AL390114	Leishmania major probable proteophosphoglycan	154	30
61	AL031427	Homo sapiens dJ167A19.1 (novel	732	51

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein)		
62	AL390935	Leishmania major possible CG17807 protein	151	43
63	J04067	Canis familiaris microsomal signal peptidase	930	99
64	AF062378	Mus musculus calmodulin-binding protein SHA1	1782	60
65	AE001002	Archaeoglobus fulgidus ATP-dependent RNA helicase, putative	195	29
66	X69065	Erythroid ankyrin [Mus musculus]	181	30
68	AF017807	Homo sapiens Arp2/3 complex 16kDa subunit	371	100
69	AC007660	Arabidopsis thaliana putative translation initiation factor	173	29
70	AJ243177	Xenopus laevis Xenopus RPA interacting protein alpha	447	42
71	AF226055	Homo sapiens HTGN29	1367	100
72	AF090930	Homo sapiens PRO0478	180	89
73	AF118084	Homo sapiens PRO1914	350	98
74	AB028893	Homo sapiens ribosomal protein S11	824	100
75	AK024500	Homo sapiens FLJ00109 protein	1514	100
76	AF238866	Mus musculus LNR42	1041	99
77	AC026875	Arabidopsis thaliana T6D22.6	129	30
78	U42436	Caenorhabditis elegans Hypothetical protein C49H3.3	130	32
79	M80902	Homo sapiens AHNAK nucleoprotein	8529	99
80	W90962	Human CSGP-2 protein [homo sapiens]	2346	99
81	AF206661	Gallus gallus neuronal tetraspanin	1066	81
82	S73591	Homo sapiens brain-expressed HHCPA78 homolog VDUP1	800	42
83	AF116650	Homo sapiens PRO0786	302	100
84	L26335	Cavia porcellus zinc finger protein	1493	99
85	AF209198	Homo sapiens zinc finger protein 277	2357	100
86	AE001399	Plasmodium falciparum GAF domain protein (cyclic nt signal transduct.)	178	35
87	Y48226	Human prostate cancer-associated protein 12 [Homo sapiens]	1204	96
88	M94389	Loligo pealei neurofilament protein	165	23
89	AF121775	Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16	903	58
90	AF116675	Homo sapiens PRO1942	257	100
91	AE002760	Drosophila melanogaster CG14464 gene product	195	43
92	AK000100	Homo sapiens unnamed protein product	841	100
93	AB020236	Homo sapiens ribosomal protein L27A	754	99
94	AF119865	Homo sapiens PRO2176	470	97
96	AF138863	Homo sapiens PRO1677	868	99
97	X14361	Homo sapiens CR-1 receptor SCR9 (or	135	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		16) C-term. (21 is 3rd base in codon) (106 is 1st base in codon)		
98	Z24725	Homo sapiens mitogen inducible gene mig-2	3576	99
99	U64598	Caenorhabditis elegans weakly similar to S. cerevisiae PTM1 precursor (SP:P32857)	398	45
100	AC004770	Homo sapiens BC269730 4	1527	84
101	AL139075	Campylobacter jejuni NOL1\NOP2\sun family protein	312	35
102	AF113694	Homo sapiens PRO1359	416	100
103	U15158	Homo sapiens ESP-2	564	41
104	AL020996	Homo sapiens dJ317E23.3 (novel protein)	1818	99
105	AF161370	Homo sapiens HSPC107	824	100
106	AK000161	Homo sapiens unnamed protein product	284	100
107	AK001784	Homo sapiens unnamed protein product	684	100
108	AE000913	Methanobacterium thermoautotrophicum conserved protein	221	25
109	AF165527	Homo sapiens DGCR8	859	100
110	AF230200	Homo sapiens OVN6-2	358	95
111	Z72516	Caenorhabditis elegans T25G3.1	180	36
112	AF201940	Homo sapiens DC6	505	100
113	AK001301	Homo sapiens unnamed protein product	2040	98
114	U23515	Caenorhabditis elegans weakly similar to gastrula zinc finger protein	205	47
115	AF228021	Bos taurus cyclophilin I	345	91
116	AF166124	Homo sapiens selenoprotein X	527	100
117	AF079445	Dictyostelium discoideum TipC	529	30
118	AB032179	Homo sapiens similar to mouse Ehm2	2255	100
119	U89867	Homo sapiens nuclear matrix protein 55	2449	98
120	U29056	Mus musculus Src-like adapter protein	352	47
121	U22015	Mus musculus retinoid X receptor interacting protein	2190	73
122	AF113538	Homo sapiens retinoid x receptor interacting protein	1800	100
123	AK000158	Homo sapiens unnamed protein product	740	100
124	AF260924	Mus musculus UFD2/D4COLE1E fusion protein	1222	82
125	U12465	Homo sapiens ribosomal protein L35	591	97
126	AJ277591	Homo sapiens p15-2a protein	749	100
127	AF205599	Mus musculus transposase-like protein	2406	74
128	U58975	Homo sapiens proto-oncogene	659	90

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
129	X98374	Rattus norvegicus KIS	2193	99
130	AF151049	Homo sapiens HSPC215	627	100
131	M59807	Homo sapiens putative	907	99
132	U12979	Homo sapiens PC4	563	99
133	AF076642	Homo sapiens regulator of G-protein signaling 13	1218	100
134	AF116718	Homo sapiens PRO2900	396	100
135	AC018758	Homo sapiens GPI-anchored metastasis-associated protein homolog	213	31
136	AC025416	Arabidopsis thaliana F5011.12	135	36
137	M83186	Homo sapiens cytochrome c oxidase subunit VIIa	247	100
138	AF232937	Mus musculus thymic stroma derived lymphopoietin	247	41
139	M15841	Homo sapiens U2 small nuclear ribonucleoprotein B''	638	100
140	AK026916	Homo sapiens unnamed protein product	2612	99
141	Y05317	Human secreted protein bn97_1 [Homo sapiens]	1508	100
142	Y05317	Human secreted protein bn97_1 [Homo sapiens]	851	99
143	AF041083	Rattus norvegicus RoBo-1	139	25
144	AC024260	Arabidopsis thaliana cell division control protein, putative; 15914-18846	194	25
146	AL022398	Homo sapiens dJ434014.3.2 (putative protein) (isoform 2)	575	100
147	AF212842	Homo sapiens immunoglobulin-like transcript 11 protein	1280	99
148	AB042827	Rattus norvegicus Nadrin	477	66
149	AK001841	Homo sapiens unnamed protein product	1916	100
150	AJ278120	Homo sapiens putative ankyrin-repeat containing protein	540	98
151	AL135959	Homo sapiens dJ233G16.1 (novel protein)	770	100
152	Y58196	[Homo sapiens] Human STRAP-3 protein, encoded by testis EST AI139607	671	100
153	U41060	Homo sapiens LIV-1 protein	373	50
154	AJ007590	Homo sapiens XRP2 protein	1766	100
155	AB046868	Xenopus laevis beta-catenin-interacting protein	125	46
156	AB027258	Homo sapiens basal transcriptional activator hABT1	1408	100
157	AF039656	Homo sapiens neuronal tissue-enriched acidic protein	1109	96
158	AK001425	Homo sapiens unnamed protein product	1695	99
159	AK001425	Homo sapiens unnamed protein	858	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
		product		
160	AK002030	Homo sapiens unnamed protein product	1029	100
161	X79417	Sus scrofa 40S ribosomal protein S12	510	83
162	X12597	Homo sapiens HMG-1 protein (AA 1-215)	1140	99
163	AK001159	Homo sapiens unnamed protein product	764	100
164	AK000020	Homo sapiens unnamed protein product	1613	100
165	AK001322	Homo sapiens unnamed protein product	1207	100
166	AK001322	Homo sapiens unnamed protein product	892	98
167	AE003822	Drosophila melanogaster CG8493 gene product	357	36
168	AF023451	Bos taurus guanine nucleotide-exchange protein	187	21
169	AK000154	Homo sapiens unnamed protein product	673	100
170	AJ132702	Mus musculus ATFa-associated factor	435	64
172	AL022311	Homo sapiens dJ1014D13.3 (novel protein)	405	38
174	AB017634	Mus musculus ENP	770	65
175	U40407	synthetic construct T cell receptor alpha chain	1119	80
176	AF043179	Homo sapiens T cell receptor beta chain	681	73
177	AF116678	Homo sapiens PRO1995	587	100
178	AF217522	Homo sapiens uncharacterized bone marrow protein BM046	262	42
179	AB046074	Macaca fascicularis unnamed protein product	515	83
180	X79417	Sus scrofa 40S ribosomal protein S12	429	84
181	AF002668	Homo sapiens MLD	1235	65
182	AB036422	Bos taurus molybdopterin cofactor sulfurase	3509	79
184	AF036696	Caenorhabditis elegans contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632)	662	42
185	AJ277276	Homo sapiens rapa-2	5155	99
186	AJ277275	Homo sapiens rapa-1	5086	100
187	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform	1444	93
188	AE003750	Drosophila melanogaster CG9996 gene product	468	44
189	Z97056	Homo sapiens dJ434P1.2 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum	1103	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein retention receptor 3)		
190	AF081126	Drosophila melanogaster ER lumen protein retaining receptor	409	75
192	AF226047	Homo sapiens GL002	863	100
193	AF269167	Homo sapiens arsenite related gene 1	906	60
195	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor	162	26
197	AL357374	Homo sapiens bA353C18.2 (novel protein)	404	97
199	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	964	42
202	AF230201	Homo sapiens OVC10-2	396	100
203	AK001984	Homo sapiens unnamed protein product	658	100
204	AK000530	Homo sapiens unnamed protein product	691	100
205	U37134	Drosophila melanogaster inturnd protein	248	23
206	U37134	Drosophila melanogaster inturnd protein	244	23
208	AB033130	Mus musculus testis-specific gene	871	85
209	AK000464	Homo sapiens unnamed protein product	221	100
210	AJ277557	Homo sapiens mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2)	617	100
211	AF127564	Arabidopsis thaliana ubiquitin-protein ligase 1	854	42
213	Y17108	Homo sapiens rhomboid-related protein	485	39
214	AL132776	Homo sapiens dJ393D12.2 (novel LIM domain protein)	1660	99
215	U73819	Mus musculus polypeptide GalNAc transferase-T4	1039	42
216	AL035406	Homo sapiens dJ233K16.1 (KIAA0444, a putative chromodomain helicase DNA binding protein 3 (CHD3))	3844	100
217	M15800	Homo sapiens MAL protein	308	42
218	L29554	Rattus norvegicus alpha 2,6-sialyltransferase	942	80
219	AL137315	Homo sapiens hypothetical protein	983	100
220	AK026027	Homo sapiens unnamed protein product	647	100
221	AL137584	Homo sapiens hypothetical protein	246	97
223	AC005498	Homo sapiens R31665 1	1752	78
225	AC010155	Arabidopsis thaliana F3M18.5	171	34
226	AL080276	Homo sapiens dJ101K10.2 (regulator of G-protein signaling 17 (RGS17) (RGSZ2))	1126	100
227	AF042345	Homo sapiens truncated EVI5	1815	64
228	J04214	Bos taurus retinaldehyde-binding protein precursor	504	39

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
230	AF181263	Homo sapiens EH domain containing 2	2816	99
231	AP001660	Homo sapiens putative gene, multidrug resistance associated protein like	1424	100
232	AB000910	Sus scrofa ribosomal protein	542	100
233	AL133404	Homo sapiens dJ238023.9 (novel protein similar to rat SAC (soluble adenylyl cyclase))	298	100
234	X51397	Mus musculus MyD88 protein (AA 1-243)	136	25
235	X01403	Homo sapiens T-cell receptor alpha-chain	840	90
236	X14254	Rattus rattus invariant chain (AA 1-280)	745	77
238	U23084	Saccharomyces cerevisiae Ynl0470p	344	35
239	X03342	Homo sapiens rpL32 (aa 1-135)	152	96
240	AF116669	Homo sapiens PRO1828	237	100
241	U23181	Caenorhabditis elegans final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein	135	25
242	AF263913	Mus musculus fidgetin	3864	97
243	AF090892	Homo sapiens PRO0106	290	100
244	U21310	Caenorhabditis elegans F40H6.3 gene product	153	27
246	AK001673	Homo sapiens unnamed protein product	3661	100
247	AL022603	Arabidopsis thaliana putative protein	166	43
248	AL023803	Homo sapiens dJ616B8.3 (novel gene)	339	42
249	X52140	Rattus norvegicus precursor polypeptide (AA -28 to 1152)	5429	87
250	AB020755	Arabidopsis thaliana gene id:MZN1.18~unknown protein	139	46
251	AE003619	Drosophila melanogaster CG7224 gene product	186	43
252	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), and C01164 (NID:g1433394); alternatively spliced form of H_DJ130H16.1a (C-terminal truncation confirmed by C01164)	388	67
254	AE003588	Drosophila melanogaster CG13947 gene product	115	42
256	Y50934	Human fetal brain cDNA clone vc30_1 derived protein #1 [Homo sapiens]	498	100
257	AF242768	Homo sapiens mesenchymal stem cell protein DSC43	1554	100
259	M95779	Bos taurus G protein gamma-5 subunit	333	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
260	AL035521	Arabidopsis thaliana putative protein	145	28
261	AF247501	Drosophila melanogaster PINEAPPLE EYE	333	36
263	AL034548	Homo sapiens dJ1103G7.2 (novel protein)	262	100
264	AF119851	Homo sapiens PRO1722	143	63
265	L41834	Ensis minor nuclear protein	173	26
266	X97966	Homo sapiens calcyphosine	963	100
267	X97966	Homo sapiens calcyphosine	660	95
269	AF022383	Homo sapiens complexin I	668	99
271	Y10054	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase	224	67
274	AF153201	Homo sapiens zinc finger protein dp	179	36
275	X85738	Bos taurus novel brain-specific protein	326	55
277	AF250342	Arabidopsis thaliana SMC-related protein MSS2	266	39
278	AL080242	Homo sapiens bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	131	100
279	Z83760	Ciona intestinalis COS41.4	1162	62
280	U41534	Caenorhabditis elegans similar to yeast MAK16 protein (SP:MK16 YEAST,P10962)	721	54
281	AF272975	Gallus gallus smoothelin-C	543	37
282	AL035414	Homo sapiens dJ667H12.2.2 (novel protein (isoform 2))	588	100
283	AF116661	Homo sapiens PRO1438	145	62
285	AK001757	Homo sapiens unnamed protein product	1300	100
287	U20897	Homo sapiens melanoma ubiquitous mutated protein	2133	100
289	U09847	Homo sapiens zinc finger protein	880	100
290	AJ000079	Trypanosoma cruzi glycosylphosphatidylinositol-specific phospholipase C	225	26
291	AF156549	Mus musculus putative E1-E2 ATPase	2108	49
293	AF161345	Homo sapiens HSPC082	439	100
294	AF116694	Homo sapiens PRO2219	351	88
295	M74027	Homo sapiens mucin	461	39
298	AL133640	Homo sapiens hypothetical protein	2149	100
299	M17886	Homo sapiens acidic ribosomal phosphoprotein (P1)	161	76
300	Y99368	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100 [Homo sapiens]	300	32
303	AE003708	Drosophila melanogaster CG6171 gene product	144	27
304	M32639	Homo sapiens statherin precursor	276	87
305	Z83844	Homo sapiens dJ37E16.2 (SH3-domain binding protein 1)	897	96

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
306	AE003791	Drosophila melanogaster CG18065 gene product	120	32
307	AF135026	Homo sapiens kallikrein-like protein 3 splice variant 1	1392	100
310	AF198257	Felis catus immunoglobulin kappa light chain	678	76
311	X57725	Homo sapiens TCR Vbeta 22a	626	100
312	AC018513	Homo sapiens unknown	818	100
313	X03249	Bos taurus epsilon-4 beta-globin	321	79
314	AB046099	Macaca fascicularis unnamed protein product	395	88
315	AC006033	Homo sapiens T cell receptor gamma chain; match to S08328 (PID:g106470)	1017	95
316	AB046103	Macaca fascicularis unnamed protein product	801	94
317	U88895	Homo sapiens ORF2	399	81
318	U09848	Homo sapiens zinc finger protein	242	49
319	AB003184	Homo sapiens ISLR	880	59
320	AB036921	Chrysophrys major maturation-inducing protein	797	69
322	AF284422	Homo sapiens cation-chloride cotransporter-interacting protein	4694	100
325	AE000659	Homo sapiens TCRAV8S2	577	100
327	R59748	T cell receptor Valpha2.3 chain [homo sapiens]	636	100
328	AJ004871	Homo sapiens TCR alpha chain	1328	94
329	AF043179	Homo sapiens T cell receptor beta chain	1286	92
330	AF090930	Homo sapiens PRO0478	140	50
332	AF077043	Homo sapiens 60S ribosomal protein L36	275	87
333	AL121988	Homo sapiens dJ34M23.3 (gap junction protein, beta 4 (connexin 30.3))	1457	100
334	D86424	Mus musculus high-sulfur keratin protein	521	87
335	AF090434	Fundulus heteroclitus cytochrome P450 2N1	760	40
336	AF116688	Homo sapiens PRO2133	370	98
337	X85372	Homo sapiens Sm protein F	222	84
338	D87009	Homo sapiens putative	1822	99
339	AE000860	Methanobacterium thermoautotrophicum conserved protein	631	35
340	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	1305	98
341	AE000004	Mycoplasma pneumonia MG207 homolog, from M. genitalium	141	27
342	AF151076	Homo sapiens HSPC242	135	100
343	AB037902	Homo sapiens truncated aldo-keto reductase	670	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
345	M33014	Drosophila melanogaster ubiquitin	153	62
346	AF053356	Homo sapiens leucin rich neuronal protein	580	46
348	AL137512	Homo sapiens hypothetical protein	751	100
349	S68015	Homo sapiens c6.1A	1664	100
350	AF151037	Homo sapiens HSPC203	318	100
351	AB036432	Homo sapiens advanced glycation endproducts receptor	2133	100
352	AB036432	Homo sapiens advanced glycation endproducts receptor	2094	96
353	AC006942	Homo sapiens R31181_2, partial protein	547	100
354	AF125535	Homo sapiens pp21 homolog	502	95
355	AF227130	Homo sapiens candidate taste receptor T2R3	1629	100
357	AB046626	Macaca fascicularis hypothetical protein	291	93
358	Z69597	Canis familiaris Rod transducin alpha subunit	1145	100
359	AE000659	Homo sapiens TCRAV16S1	565	100
360	Y99368	Human PRO1326 (UNQ686) Amino acid sequence SEQ ID NO:100. [Homo sapiens]	2034	100
362	L06499	Homo sapiens ribosomal protein L37a	187	55

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 4.025e-06 60-80
2	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 7.750e-06 208-220
3	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.438e-07 285-319
4	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 7.061e-22 151-190 BL00895C 20.10 8.071e-22 200-236 BL00895A 12.61 1.973e-18 42-63
5	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
7	PF00598	Influenza Matrix protein (M1).	PF00598C 19.35 3.333e-07 531-563
9	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 3.250e-06 287-297
10	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
11	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
12	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775G 10.64 3.487e-07 8-27
13	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 1.000e-05 176-200
14	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.127e-07 159-171 PR00875D 5.00 1.000e-05 158-169
15	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 9.200e-07 181-191 DM01803A 10.51 1.000e-06 178-199 DM01803C 7.00 7.337e-06 214-224
16	PF00803	3A movement protein.	PF00803D 14.15 2.622e-06 41-71
17	PR00170	SODIUM CHANNEL SIGNATURE	PR00170G 7.74 1.000e-05 24-53
18	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 5.684e-06 117-133
20	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 6.063e-06 55-68
21	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 7.731e-06 64-112
22	BL00616	Histidine acid phosphatases phosphohistidine proteins.	BL00616D 15.83 7.268e-06 117-133

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611A 7.73 5.826e-06 173-181
24	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832D 21.81 5.017e-06 425-449
25	PR00354	7FE FERREDOXIN SIGNATURE	PR00354C 5.72 8.590e-09 543-561
26	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 3.851e-07 89-105
27	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 1.439e-06 168-180
28	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552A 11.97 1.000e-05 130-152
29	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 3.088e-06 102-126
30	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.	DM00060 6.92 3.284e-07 680-690
34	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 6.971e-07 484-496
35	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 4.183e-06 722-744
37	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513C 10.79 8.927e-07 287-304
38	PR00166	AROMATIC AMINO ACID PERMEASE SIGNATURE	PR00166I 11.06 1.000e-05 98-118
39	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
40	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
41	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 8.788e-07 2-14
42	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701F 14.45 7.750e-06 25-46
43	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895B 8.85 4.185e-06 157-167
44	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
45	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519A 8.06 8.984e-06 137-154
46	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 1.828e-07 151-168
47	DM00892	3 RETROVIRAL PROTEINASE.	DM00892B 9.78 2.047e-06 21-27
48	BL00832	2'-5'-oligoadenylate synthetases	BL00832B 15.45 6.836e-07 375-416

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	
49	DM00588	8 kw CHO2 ALPHA ANTIGEN PARAMYOSIN.	DM00588A 10.87 7.128e-06 20-31
50	DM00604	2 SHIGA/RICIN RIBOSOMAL INACTIVATING TOXINS.	DM00604D 13.26 8.250e-06 263-273
51	BL01193	Ribosomal protein S8e proteins.	BL01193A 13.21 1.000e-05 19-50
52	PR00172	GLUCOSE TRANSPORTER SIGNATURE	PR00172F 8.47 9.901e-06 69-90
53	PR00297	10 KD CHAPERONIN SIGNATURE	PR00297A 13.91 4.740e-06 379-395
54	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.710e-06 81-96
55	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
56	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
57	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547E 13.94 4.656e-06 229-252
58	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 3.723e-06 32-68
60	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 7.338e-07 171-185
61	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 3.187e-06 205-244
62	PR00439	11-S SEED STORAGE PROTEIN FAMILY SIGNATURE	PR00439G 17.85 9.239e-07 82-100
63	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652F 11.66 4.767e-06 100-122
64	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785A 14.90 2.196e-06 218-261
65	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 5.104e-06 315-336
67	BL00405	43 Kd postsynaptic protein.	BL00405F 8.07 9.920e-06 13-44
68	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 9.043e-06 44-66
69	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683D 15.87 9.571e-06 46-65
70	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753C 13.93 7.330e-06 192-213
71	PF00602	Influenza RNA- dependant RNA	PF00602J 9.52 9.727e-06 47-102

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polymerase subunit PB1.	
72	DM01855	PROTEIN-GLUTAMATE O-METHYLTRANSFERASE.	DM01855A 11.54 7.594e-06 27-44
74	BL01277	Ribonuclease PH proteins.	BL01277A 17.39 1.000e-05 50-88
75	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517G 16.45 6.919e-06 755-771
77	PF01073	3-beta hydroxysteriod dehydrogenase/isomerase family.	PF01073B 12.26 9.767e-07 102-147
78	PR00351	MAS20 PROTEIN IMPORT RECEPTOR SIGNATURE	PR00351C 7.03 6.182e-06 99-112 PR00351C 7.03 1.000e-05 5-18
79	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 4.549e-06 1489-1501
80	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111C 9.35 2.800e-06 44-73
82	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 1.000e-06 94-111
83	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 9.850e-06 14-44
84	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517F 11.48 7.250e-06 45-62
87	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 3.535e-07 223-237
88	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 8.034e-08 270-320
91	DM01242	3 THREONINE--TRNA LIGASE.	DM01242B 23.57 4.672e-06 71-120
92	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388E 6.66 3.797e-06 124-136
93	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 9.676e-06 15-32
94	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 4.555e-06 16-52
95	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551H 11.29 8.740e-06 21-39
96	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756E 11.91 9.338e-06 68-81
97	PR00547	X OPIOID RECEPTOR SIGNATURE	PR00547B 6.96 3.268e-06 17-36
98	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR	PR00651A 16.53 4.000e-06 653-674

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
99	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208C 11.51 9.775e-06 54-71
101	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 1.000e-05 152-161
102	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832B 15.45 7.569e-06 1-42
103	BL00405	43 Kd postsynaptic protein.	BL00405J 13.28 6.952e-06 142-176
104	DM01242	3 THREONINE--TRNA LIGASE.	DM01242F 10.61 5.500e-07 187-201
105	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834A 4.96 7.097e-06 53-60
107	PR00101	ASPARTATE CARBAMOYLTRANSFERASE SIGNATURE	PR00101E 5.52 1.000e-05 111-117
109	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 9.922e-06 91-115
110	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259A 9.27 9.716e-06 9-33
111	BL00785	5'-nucleotidase proteins.	BL00785B 10.65 6.507e-06 53-67
112	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652G 10.94 5.429e-06 14-32
113	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 3.661e-06 372-384
114	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637D 7.09 9.449e-07 32-44
115	DM01235	5 kw T4 55.10 METHYLCYTOSINE TRANSCRIPTASE.	DM01235 20.29 9.832e-06 77-108
116	PR00873	ECHINOIDEA (SEA URCHIN) METALLOTHIONEIN SIGNATURE	PR00873C 6.16 9.906e-06 70-81
117	PR00387	3'5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE SIGNATURE	PR00387D 10.81 4.889e-06 155-172
118	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 7.158e-06 211-254
119	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 8.036e-06 428-467
120	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419D 10.62 9.430e-06 18-33
121	DM00396	5 kw INTRON COI ND4L	DM00396B 7.85 3.739e-07 381-389

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		ND5.	
122	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 5.500e-06 135-147
123	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 4.208e-06 93-110
124	BL00405	43 Kd postsynaptic protein.	BL00405G 7.78 6.294e-06 130-167
125	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298D 10.23 3.847e-06 14-40
126	PR00317	EPENDYMIN SIGNATURE	PR00317A 13.39 9.897e-06 79-99
127	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 3.971e-06 277-290
130	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516G 15.11 8.811e-06 18-35
131	PR00828	FORMIN SIGNATURE	PR00828F 8.56 1.000e-05 61-81
132	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.279e-06 28-56
133	PR00586	PROSTANOID EP4 RECEPTOR SIGNATURE	PR00586B 14.97 7.322e-06 10-28 PR00586H 8.65 9.791e-06 16-40
134	PF00954	S-locus glycoprotein family.	PF00954D 18.68 9.843e-06 9-44
135	PR00018	KRINGLE DOMAIN SIGNATURE	PR00018A 14.52 1.000e-05 120-136
136	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115E 14.13 9.921e-06 40-69
137	PR00521	ANDROGEN RECEPTOR SIGNATURE	PR00521A 17.02 9.729e-06 5-25
138	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 5.267e-07 16-40
139	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.085e-08 93-121
140	PR00915	LUTEOVIRUS GROUP 1 COAT PROTEIN SIGNATURE	PR00915D 16.14 1.000e-05 374-392
143	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 4.441e-06 94-104
144	PF00598	Influenza Matrix protein (M1).	PF00598B 13.10 1.623e-06 89-133
145	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 6.250e-06 24-40
147	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 6.049e-06 266-288
148	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513D 11.06 9.920e-06 103-121
149	PF00603	Influenza RNA- dependant RNA polymerase subunit	PF00603D 8.49 9.319e-07 30-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PA.	
150	DM01688	2 POLY-IG RECEPTOR.	DM01688N 11.93 9.920e-08 72-100
151	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637B 10.68 6.906e-06 186-195
152	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461A 15.90 1.764e-08 21-57
153	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554A 6.07 2.565e-06 589-599
154	BL00405	43 Kd postsynaptic protein.	BL00405E 8.84 8.125e-06 109-135
155	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637A 15.49 5.179e-06 42-65
156	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 7.339e-06 85-97
157	DM01688	2 POLY-IG RECEPTOR.	DM01688P 13.54 1.925e-07 44-89 DM01688L 4.36 2.367e-07 123-133
159	PR00933	B-LYTIC METALLOENDOPEPTIDASE (M23) SIGNATURE	PR00933D 13.92 1.000e-05 85-106
161	PR00352	3FE-4S FERREDOXIN SIGNATURE	PR00352A 11.15 6.162e-06 94-106
163	BL00785	5'-nucleotidase proteins.	BL00785E 15.85 4.000e-06 95-111
164	PR00916	2C ENDOPEPTIDASE (C24) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00916C 8.02 2.655e-06 121-133
165	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 154-164
166	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 123-133
167	DM01023	2 GLYCOSYL HYDROLASES FAMILY 5.	DM01023C 13.51 6.486e-06 149-175
168	PF00803	3A movement protein.	PF00803A 15.38 8.088e-06 255-290
169	PR00282	SNAKE CYTOTOXIN SIGNATURE	PR00282D 11.82 9.882e-06 74-85
170	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 5.787e-06 83-100
172	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.804e-06 136-157
173	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 9.724e-06 14-30
174	BL00118	Phospholipase A2 histidine proteins.	BL00118A 16.00 9.842e-06 132-145
175	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 1.825e-06 89-121
176	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 146-159

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
177	PR00510	NEBULIN SIGNATURE	PR00510F 9.88 8.552e-06 34-51
179	PF00432	Prenyltransferase and squalene oxidase repeat proteins.	PF00432A 11.90 1.000e-05 27-39
180	PR00537	MU OPIOID RECEPTOR SIGNATURE	PR00537A 8.17 1.000e-05 27-41
183	PR00536	MELANOCYTE STIMULATING HORMONE RECEPTOR SIGNATURE	PR00536C 8.58 8.833e-06 64-82
184	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973B 17.81 8.261e-06 158-184
185	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
186	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
187	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651A 16.53 6.447e-06 144-165
188	BL01017	Ergosterol biosynthesis ERG4/ERG24 family proteins.	BL01017D 20.82 9.737e-06 21-67
191	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315B 6.84 7.459e-06 95-107
192	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE	PR00930E 5.98 9.740e-06 285-298
193	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794B 22.12 8.967e-06 150-191
194	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 5.853e-06 115-128
196	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.031e-07 11-32
197	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171B 14.73 1.000e-05 15-35
198	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407J 10.55 6.610e-06 69-81
199	PF00604	Influenza RNA-dependant RNA polymerase subunit PB2.	PF00604F 10.21 2.417e-06 276-331
201	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409D 13.02 9.900e-06 43-58
202	BL00660	Band 4.1 family	BL00660A 31.50 9.595e-06 1-54

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		domain proteins.	
203	PR00745	GLYCOSYL HYDROLASE FAMILY 39 SIGNATURE	PR00745D 15.85 9.700e-06 68-83
204	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364A 6.18 9.667e-06 9-16
205	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
206	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
207	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 3.170e-06 241-266
208	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 4.835e-06 59-71
209	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 9.719e-06 20-50
210	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551E 10.27 9.432e-06 19-34
211	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418B 22.51 3.289e-06 527-569
213	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785E 12.98 6.400e-06 165-216
214	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834B 15.29 3.382e-06 64-90
215	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 4.583e-06 407-423
216	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 6.538e-36 628-675 DM00547E 13.94 2.400e-18 387-410 DM00547C 17.30 9.486e-16 266-288 DM00547B 11.28 9.217e-15 237-251 DM00547D 11.60 4.951e-12 357-371 DM00547A 12.38 6.455e-11 216-228
217	BL00407	Connexins proteins.	BL00407D 17.61 1.000e-05 57-87
218	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.481e-06 74-86
219	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 15.47 3.550e-06 90-102
220	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519E 3.58 2.404e-07 184-199
221	PD01313	INTRON PROBABLE MATURASE CHLOROPLAST MR.	PD01313B 23.27 1.000e-05 10-45
222	PR00047	C4-TYPE STEROID	PR00047A 15.70 9.878e-06 99-116

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		RECEPTOR ZINC FINGER SIGNATURE	
223	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554C 11.76 3.571e-06 255-271
224	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 5.206e-06 28-67
226	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 8.630e-07 28-40
227	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 5.173e-06 185-224
229	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 9.794e-06 13-40
230	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651B 9.95 6.416e-06 62-77
231	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 9.113e-06 214-226
232	PR00582	PROSTANOID EP3 RECEPTOR SIGNATURE	PR00582B 9.74 1.000e-05 76-95
233	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407E 13.51 9.438e-06 176-192
234	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.913e-06 6-40
235	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 4.450e-06 94-126 DM01688J 14.69 6.000e-06 34-71
236	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 1.000e-05 80-106
237	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076B 11.24 6.418e-07 14-44
239	PR00243	MUSCARINIC ACETYLCHOLINE RECEPTOR SIGNATURE	PR00243F 16.45 9.182e-06 7-18
240	BL00854	Proteasome B-type subunits proteins.	BL00854B 10.97 1.000e-05 1-9
241	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 5.263e-07 876-889
242	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111I 15.32 2.473e-07 522-552
243	BL00415	Synapsins proteins.	BL00415B 9.91 9.778e-06 53-89
244	BL00514	Fibrinogen beta and gamma chains C- terminal domain proteins.	BL00514E 14.28 1.000e-05 221-238
245	PR00187	ARTHROPOD HAEMOCYANIN SIGNATURE	PR00187B 15.70 1.000e-05 37-55

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
246	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637C 27.33 1.184e-06 368-415
247	BL00785	5'-nucleotidase proteins.	BL00785A 9.73 7.557e-06 57-68
248	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651D 12.56 2.615e-06 228-249
249	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 1.811e-06 310-325
250	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461C 18.34 9.495e-06 30-58
251	BL00888	Cyclic nucleotide- binding domain proteins.	BL00888A 18.03 9.667e-06 20-37
252	DM01242	3 THREONINE--TRNA LIGASE.	DM01242E 23.00 6.215e-07 119-161
253	DM00250	kw ANNEXIN ANTIGEN PROLINE TUMOR.	DM00250A 10.52 6.488e-06 16-32
254	BL00291	Prion protein.	BL00291A 4.49 2.469e-07 51-86 BL00291A 4.49 6.878e-07 40-75 BL00291A 4.49 5.330e-06 22-57 BL00291A 4.49 1.000e-05 30-65
255	PF00506	Influenza virus nucleoprotein.	PF00506F 9.40 5.459e-08 17-55
256	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126A 27.56 6.026e-06 25-62
257	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003D 8.10 5.131e-06 291-300
258	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 7.061e-06 10-20
259	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 8.071e-06 3-13
260	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775D 8.91 3.831e-06 147-165
261	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 1.167e-06 75-91
262	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388D 14.87 8.079e-06 69-83
263	PR00023	ZONA PELLUCIDA SPERM-BINDING PROTEIN SIGNATURE	PR00023A 17.17 9.036e-06 24-39
264	BL00024	Hemopexin domain proteins.	BL00024F 11.30 9.894e-06 3-24
265	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 6.294e-06 177-227
266	PR00652	5-HYDROXYTRYPTAMINE	PR00652A 8.92 9.224e-07 69-90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		7 RECEPTOR SIGNATURE	
267	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 9.224e-07 69-90
268	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 1.673e-06 14-35
270	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875C 8.64 9.550e-06 65-77
271	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.308e-06 21-42
272	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 4.383e-06 46-89
273	PR00113	ALKALINE PHOSPHATASE SIGNATURE	PR00113D 6.87 9.260e-06 8-19
274	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841E 18.60 9.446e-06 80-118
275	PF00600	Influenza non- structural protein (NS1).	PF00600A 20.40 1.563e-06 40-67
276	PR00877	PLANT PEC FAMILY METALLOTHIONEIN SIGNATURE	PR00877B 4.74 9.878e-06 31-38
277	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076E 12.73 6.417e-06 71-99
279	BL00101	Hexapeptide-repeat containing- transferases proteins.	BL00101A 10.95 1.000e-05 71-78
280	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111M 10.67 2.629e-06 163-187
282	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.934e-06 35-50
283	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519C 9.73 1.227e-06 22-37
284	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304E 7.79 1.000e-05 54-67
285	BL00197	2Fe-2S ferredoxins, iron-sulfur binding region proteins.	BL00197A 18.23 9.866e-07 49-79
286	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753D 6.85 8.636e-06 61-83
287	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003B 7.64 1.300e-06 166-174
288	BL00940	Gamma-thionins family proteins.	BL00940A 20.51 9.671e-06 16-40
289	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.609e-11 122-135 PD00066 13.92 1.900e-09 94-107 PD00066 13.92 2.703e-07 66-79

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD00066 13.92 1.000e-05 38-51
291	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516F 10.18 9.609e-07 761-779
293	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 8.487e-06 51-71
296	PR00635	AT1 ANGIOTENSIN II RECEPTOR SIGNATURE	PR00635C 7.44 8.602e-06 28-45
297	PF00915	Calicivirus coat protein.	PF00915E 5.71 1.000e-05 102-112
298	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 3.968e-06 495-512
299	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 9.730e-06 22-40
300	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.273e-06 7-44
301	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.752e-06 42-57
302	BL00283	Soybean trypsin inhibitor (Kunitz) protease inhibitors family.	BL00283B 16.55 1.000e-05 15-30
303	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.	DM01753A 21.93 9.830e-06 59-94
304	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516E 14.87 6.516e-06 20-38
305	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 5.452e-07 20-37
306	PR00331	HAEMAGGLUTININ HA2 CHAIN SIGNATURE	PR00331E 18.67 1.000e-05 75-93
307	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651H 5.59 8.858e-06 152-175
308	BL00208	Plant hemoglobins proteins.	BL00208A 18.41 1.000e-05 5-47
309	PR00240	ALPHA-1A ADRENERGIC RECEPTOR SIGNATURE	PR00240E 9.25 9.391e-06 36-56
310	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701C 10.53 8.255e-06 55-76
311	PR00423	CELL DIVISION PROTEIN FTSZ SIGNATURE	PR00423B 7.15 1.000e-05 5-26
312	PF00602	Influenza RNA-dependant RNA polymerase subunit PB1.	PF00602C 12.16 2.068e-07 26-66
313	PR00246	SOMATOSTATIN RECEPTOR SIGNATURE	PR00246D 7.36 1.000e-05 4-14

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
314	BL00216	Sugar transport proteins.	BL00216A 13.29 9.526e-06 26-38
316	PF00721	Tobacco mosaic virus coat.	PF00721A 14.59 9.845e-06 131-167
317	PD00489	PROTEIN TRANSMEMBRANE TRANSPORT C.	PD00489A 15.57 1.000e-05 55-71
318	PR00163	RUBREDOXIN SIGNATURE	PR00163A 10.47 9.888e-06 59-76
319	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 9.149e-07 205-217
320	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418C 20.48 5.142e-06 377-419
321	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067D 21.49 7.441e-06 9-42
322	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 7.821e-08 52-80
323	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 5.133e-06 43-53
324	PD01672	+ TRANSPORT EXCHANGER NA H TRANS.	PD01672B 15.16 1.000e-05 6-55
325	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 5.538e-06 31-68
327	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372A 19.18 1.000e-05 9-54
328	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 4.308e-06 31-68
329	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 144-157
330	PF00685	Sulfotransferase proteins.	PF00685A 19.12 9.370e-06 49-82
331	PR00347	PATHOGENESIS-RELATED PROTEIN SIGNATURE	PR00347A 13.98 9.649e-06 55-68
332	PR00538	MUSCARINIC M1 RECEPTOR SIGNATURE	PR00538F 10.59 8.667e-06 30-48
334	PR00159	2FE-2S FERREDOXIN SIGNATURE	PR00159A 9.58 1.153e-06 23-32
336	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554B 12.52 9.778e-06 41-50
337	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111G 10.39 7.250e-06 3-44
338	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 7.649e-06 214-229
340	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 5.050e-06 141-160
342	DM01664	kw.	DM01664D 16.63 1.000e-05 22-47

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
343	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841K 14.81 1.000e-05 65-95
344	PR00416	EUKARYOTIC DNA TOPOISOMERASE I SIGNATURE	PR00416D 12.12 9.772e-06 23-40
345	BL00726	AP endonucleases family 1 proteins.	BL00726C 19.90 1.000e-05 7-33
346	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.566e-06 465-507
347	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332A 10.15 9.890e-06 16-33
348	PR00518	5-HYDROXYTRYPTAMINE 5A RECEPTOR SIGNATURE	PR00518A 8.62 7.807e-06 19-36
349	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.736e-06 276-318
350	PR00503	BROMODOMAIN SIGNATURE	PR00503C 19.84 9.731e-06 28-47
351	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
352	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
353	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 5.273e-06 99-147
354	PR00216	OSTEOPONTIN SIGNATURE	PR00216F 11.79 9.913e-06 50-69
356	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895G 3.62 9.913e-06 62-72
357	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 6.329e-06 35-47
358	PR00512	5-HYDROXYTRYPTAMINE 1A RECEPTOR SIGNATURE	PR00512G 6.54 3.139e-06 3-19
359	PD02455	ELEMENT TRANSPOSABLE INSERTION PROTEIN TRANSPOSITION DNA.	PD02455D 18.65 1.000e-05 58-77
360	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 3.250e-07 16-29
361	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 9.702e-06 27-65
362	PR00866	RNA-DEPENDENT DNA-POLYMERASE (MSDNA) SIGNATURE	PR00866B 9.86 9.786e-06 60-73

* Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TABLE 4

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
2	PGAM	Phosphoglycerate mutase family	2.5e-05	23.4
6	Ubie_methyltran	ubiE/COQ5 methyltransferase family	0.035	-133.9
8	Plexin repeat	Plexin repeat	0.03	18.4
13	K_tetra	K ⁺ channel tetramerisation domain	2.3e-31	117.6
14	EGF	EGF-like domain	7.8e-14	59.4
16	Armadillo_seg	Armadillo/beta-catenin-like repeats	1.3e-05	32.1
19	Ribosomal S5	Ribosomal protein S5	1.7e-46	167.9
21	gpdh	glyceraldehyde 3-phosphate dehydrogenases	1.3e-230	773.2
24	GCV_T	Glycine cleavage T-protein (aminomethyl tran	9.3e-156	530.9
25	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.015	12.5
26	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	38.4
33	urease	Urease	0.014	11.0
35	tRNA-synt_1e	tRNA synthetases class I (C)	0.0091	12.1
37	LRRNT	Leucine rich repeat N-terminal domain	0.00049	26.8
39	SH3	SH3 domain	3.4e-60	213.4
40	SH3	SH3 domain	3.4e-60	213.4
41	PBD	P21-Rho-binding domain	1e-08	42.4
42	GDA1_CD39	GDA1/CD39 (nucleoside phosphatase) family	9e-94	324.9
43	Band 7	SPFH domain / Band 7 family	1.7e-21	84.9
46	Rhodanese	Rhodanese-like domain	2.9e-24	94.0
47	zf-C2H2	Zinc finger, C2H2 type	6.2e-32	119.5
50	ZAP	ZAP domain	1.6e-50	181.3
52	sushi	Sushi domain (SCR repeat)	9.5e-27	102.3
55	zf-C2H2	Zinc finger, C2H2 type	0.047	20.3
56	zf-C2H2	Zinc finger, C2H2 type	0.00021	28.1
59	PH	PH domain	2.6e-06	27.6
60	PHD	PHD-finger	2e-09	44.8
64	IQ	IQ calmodulin-binding motif	6.4e-42	152.7
66	ank	Ank repeat	2.7e-23	90.8
69	eIF-1a	Eukaryotic initiation factor 1A	0.0047	-2.4
74	Ribosomal S17	Ribosomal protein S17	6e-43	148.6
75	LIM	LIM domain containing proteins	0.00067	19.0
80	Phosphodiester	Type I phosphodiesterase / nucleotide py	2.7e-49	177.2
81	transmembrane4	Transmembrane 4 family	6.6e-61	197.7
84	zf-C2H2	Zinc finger, C2H2 type	1.6e-64	227.8
85	zf-C2H2	Zinc finger, C2H2 type	1.4e-07	38.6
89	ank	Ank repeat	4e-31	116.8
93	L15	Ribosomal protein L15	3.5e-21	61.9

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
98	Band 41	FERM domain (Band 4.1 family)	0.00015	16.7
101	Nol1 Nop2 Sun	NOL1/NOP2/sun family	4.5e-19	68.6
103	LIM	LIM domain containing proteins	1.3e-30	113.2
113	WD40	WD domain, G-beta repeat	0.00018	28.3
115	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	5.3e-34	120.4
116	DUF25	Domain of unknown function DUF25	1.1e-11	46.9
118	Band 41	FERM domain (Band 4.1 family)	3.2e-77	242.4
119	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	1.1e-33	125.4
120	SH3	SH3 domain	3e-05	30.9
125	Ribosomal L29	Ribosomal L29 protein	1.6e-15	65.0
126	NTF2	Nuclear transport factor 2 (NTF2) domain	7.6e-06	32.2
129	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	0.0016	25.2
130	Fork head	Fork head domain	1e-28	108.8
132	PC4	Transcriptional Coactivator p15 (PC4)	2.1e-38	141.0
133	RGS	Regulator of G protein signaling domain	2.6e-45	164.0
137	COX7a	Cytochrome c oxidase subunit VIIa	2.3e-40	147.5
139	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	3.2e-15	64.0
141	lectin_c	Lectin C-type domain	5.1e-05	30.0
142	lectin_c	Lectin C-type domain	5.1e-05	30.0
147	ig	Immunoglobulin domain	9.1e-07	26.9
150	ank	Ank repeat	8.6e-09	42.6
161	Ribosomal L7Ae	Ribosomal protein L7Ae	0.03	0.8
162	HMG box	HMG (high mobility group) box	8e-53	188.9
163	PH	PH domain	3e-13	52.4
168	Peptidase C6	Helper component proteinase	0.0056	7.9
175	ig	Immunoglobulin domain	2.3e-09	35.2
176	ig	Immunoglobulin domain	9.2e-09	33.3
178	WW	WW domain	0.054	17.2
180	Ribosomal S12e	Ribosomal protein S12e	1.9e-38	141.1
185	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
186	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
187	pkinase	Eukaryotic protein kinase domain	3.4e-26	98.4
189	ER_lumen_recept	ER lumen protein retaining receptor	3.9e-144	492.2
190	ER_lumen_recept	ER lumen protein retaining receptor	2.1e-88	307.1
195	EMP24 GP25L	emp24/gp25L/p24 family	6.9e-06	28.1
199	zf-B box	B-box zinc finger.	5.2e-07	36.7
211	HECT	HECT-domain (ubiquitin-transferase).	1.1e-115	397.8
213	Rhomboid	Rhomboid family	4.2e-42	153.3
214	LIM	LIM domain containing	8.8e-35	127.8

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
		proteins		
215	Ricin_B_lectin	Similarity to lectin domain of ricin	0.0015	19.2
216	chromo	'chromo' (CHRromatin Organization Modifier	2.1e-09	37.1
218	Sialyltransf	Sialyltransferase family	7.3e-20	79.4
219	PG_binding_2	Putative peptidoglycan binding domain	5e-06	33.5
223	zf-C2H2	Zinc finger, C2H2 type	1.5e-104	360.7
226	RGS	Regulator of G protein signaling domain	5.1e-52	186.2
227	TBC	TBC domain	7.2e-35	129.3
228	CRAL TRIO	CRAL/TRIO domain.	4.5e-47	158.6
232	Ribosomal L44	Ribosomal protein L44	1e-48	175.3
235	ig	Immunoglobulin domain	3.5e-08	31.4
236	thyroglobulin 1	Thyroglobulin type-1 repeat	3.9e-24	93.6
238	TBC	TBC domain	1.2e-54	195.0
241	zf-C2H2	Zinc finger, C2H2 type	3.8e-08	40.5
242	AAA	ATPases associated with various cellular act	2.1e-43	157.6
249	integrin_A	Integrin alpha cytoplasmic region	0.091	18.0
256	PAP2	PAP2 superfamily	0.00084	22.8
257	zf-C2H2	Zinc finger, C2H2 type	1.2e-60	214.9
259	G-gamma	GGL domain	5.5e-30	108.3
266	efhand	EF hand	3.4e-07	37.4
267	efhand	EF hand	3.4e-07	37.4
274	zf-C2H2	Zinc finger, C2H2 type	0.00014	28.6
277	RecF	RecF protein	0.036	11.1
281	CH	Calponin homology (CH) domain	7.9e-22	86.0
285	cyclin	Cyclin	3.9e-07	28.5
289	zf-C2H2	Zinc finger, C2H2 type	1.9e-21	84.7
290	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.073	10.8
299	60s ribosomal	60s Acidic ribosomal protein	4.1e-07	25.8
307	trypsin	Trypsin	6.9e-81	257.3
310	ig	Immunoglobulin domain	1.3e-10	39.3
311	ig	Immunoglobulin domain	6.1e-07	27.4
313	globin	Globin	3.8e-21	78.2
315	ig	Immunoglobulin domain	1.6e-05	22.8
318	zf-C2H2	Zinc finger, C2H2 type	9e-19	75.8
319	ig	Immunoglobulin domain	0.01	13.8
320	BTB	BTB/POZ domain	5e-17	70.0
322	aa permeases	Amino acid permease	0.0058	-262.2
325	ig	Immunoglobulin domain	1.6e-10	38.9
327	ig	Immunoglobulin domain	1.9e-09	35.5
328	ig	Immunoglobulin domain	2.9e-09	34.9
329	ig	Immunoglobulin domain	7.4e-14	49.7
332	Ribosomal L36e	Ribosomal protein L36e	6.3e-17	69.7
333	connexin	Connexin	7.6e-148	504.6
335	p450	Cytochrome P450	2.1e-100	347.0
337	Sm	Sm protein	0.00012	28.8
338	zf-C2H2	Zinc finger, C2H2 type	0.0025	24.5

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
343	aldo ket red	Aldo/keto reductase family	2.4e-53	190.7
345	ubiquitin	Ubiquitin family	3.1e-13	45.5
346	CH	Calponin homology (CH) domain	0.0017	23.8
351	ig	Immunoglobulin domain	4.8e-18	63.2
352	ig	Immunoglobulin domain	4.8e-18	63.2
358	G-alpha	G-protein alpha subunit	4.5e-148	505.3
359	ig	Immunoglobulin domain	8.9e-09	33.3
362	Ribosomal_L37ae	Ribosomal L37ae protein family	0.00083	-3.0

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
2	1-29	0.942	0.664
12	1-15	0.909	0.589
14	1-17	0.974	0.943
20	1-22	0.932	0.802
25	1-16	0.988	0.881
28	1-13	0.896	0.771
37	1-21	0.992	0.929
42	1-46	0.978	0.754
52	1-34	0.954	0.756
63	1-31	0.960	0.773
71	1-45	0.981	0.652
80	1-22	0.982	0.882
81	1-42	0.993	0.715
83	1-30	0.966	0.767
95	1-18	0.997	0.971
102	1-13	0.981	0.764
107	1-45	0.890	0.631
110	1-27	0.992	0.969
138	1-33	0.961	0.864
144	1-45	0.987	0.658
145	1-20	0.992	0.967
175	1-20	0.957	0.874
176	1-21	0.989	0.945
179	1-42	0.980	0.577
184	1-20	0.972	0.771
189	1-28	0.941	0.755
190	1-28	0.941	0.755
191	1-12	0.907	0.779
195	1-21	0.958	0.779
200	1-15	0.970	0.875
211	1-20	0.895	0.595
215	1-31	0.987	0.895
218	1-30	0.971	0.889
225	1-17	0.884	0.588
235	1-23	0.965	0.817
237	1-29	0.933	0.725
249	1-28	0.972	0.870
251	1-17	0.966	0.905
260	1-26	0.921	0.587
270	1-20	0.938	0.631
283	1-18	0.901	0.763
288	1-20	0.940	0.693
293	1-26	0.937	0.784
295	1-22	0.972	0.745
296	1-15	0.930	0.748
297	1-35	0.906	0.600
300	1-29	0.981	0.864
307	1-19	0.976	0.916
308	1-27	0.973	0.931

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
309	1-29	0.950	0.629
310	1-19	0.969	0.913
311	1-21	0.956	0.823
315	1-17	0.976	0.938
317	1-19	0.943	0.837
319	1-18	0.991	0.978
324	1-26	0.968	0.806
325	1-20	0.972	0.828
326	1-27	0.893	0.567
327	1-21	0.994	0.959
328	1-20	0.945	0.891
329	1-21	0.984	0.858
330	1-27	0.891	0.593
333	1-40	0.955	0.703
347	1-22	0.968	0.806
351	1-23	0.982	0.945
352	1-23	0.982	0.945
355	1-32	0.955	0.617
356	1-23	0.936	0.677
359	1-20	0.937	0.859
360	1-29	0.956	0.765
361	1-23	0.968	0.819

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 362, a mature protein coding portion of SEQ ID NO: 1 – 362, an active domain of SEQ ID NO: 1 – 362, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 – 362.

5 11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

10 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

15 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

20 b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

25 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

30 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 5 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

10 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- 15 b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-362, a mature protein coding portion of SEQ ID NO: 1-362, an active domain of SEQ ID NO: 1-362, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-362, under conditions sufficient to express the polypeptide in said cell; and
- 20 b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

30

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 362.

5 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

10 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

15 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

20 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

ABSTRACT OF THE INVENTION

The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

COPIES OF THE INVENTION

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

**Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi, Feiyan Ren,
Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman,
Radoje T. Drmanac**

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

 X is attached hereto.

 was filed on [date] as Application Serial Number []
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Leslie A. Mooi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

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U.S. Patent & Trademark Office

Express Mail No.: EF415382545US

Docket No.: 797

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Tang, et al.

Serial No: Not Yet Assigned

Filed: Herewith

For: NOVEL NUCLEIC ACIDS
AND POLYPEPTIDES

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BY "EXPRESS MAIL" UNDER 37 CFR § 1.10

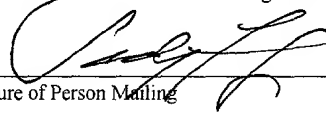
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Date of Deposit November 17, 2000

I hereby certify that this paper and all enclosures are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 CFR § 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231

Type or Print Name of Person Mailing. Sandy Fong

Signature of Person Mailing



STATEMENT REGARDING SEQUENCE LISTING UNDER 37 CFR §1.821(f)

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Dated: November 17, 2000

By:



Leslie A. Mooi
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Registration No.: 37,047
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Sunnyvale, CA 94085

SEQUENCE LISTING

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 Asundi, Vinod
 Ren, Feiyan
 Zhang, Jie
 Zhao, Qing A.
 Xue, Aidong J.
 Yang, Yonghong
 Wehrman, Tom
 Drmanac, Radoje T.

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Leu Glu Glu His His His Tyr Pro Asn Gln Ser Asn Thr Thr Leu Leu	
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Arg Glu Val Lys Ile Glu Gly Lys Pro Glu Ala Pro Pro Ser Gln Ser	
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Pro Asn Pro Ser Thr His Val Cys Ser Pro Ser Pro Met Leu Ser Glu	
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His	Leu	Lys	His	Asn	Pro	Pro	Ile	Phe	Gly	Ser	Ser	Gly	Glu	Leu	Gln		
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Asp	Asn	Cys	Gln	Gln	Leu	Met	Arg	Asn	Lys	Glu	Gln	Glu	Ile	Leu	Lys		
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Gln	Tyr	Gln	Pro	Asn	Leu	Ser	Asn	Gln	Met	Thr	Ser	Lys	Gln	Tyr	Thr		
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Lys	Thr	Thr	Gln	Leu	Glu	His	Lys	Ser	Gln	Met	Tyr	Gln	Val	Glu	Met		
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Ala	Asp	Ser	Gln	Thr	Glu	Lys	Leu	Met	Ser	Pro	Val	Leu	Lys	Gln	His		
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Leu	Asn	Gln	Gln	Ala	Ser	Glu	Thr	Glu	Pro	Phe	Ser	Asn	Ser	His	Leu		

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agt tca cat ctc cct caa aac cag caa cag cag caa aaa tta caa ata Ser Ser His Leu Pro Gln Asn Gln Gln Gln Gln Gln Lys Leu Gln Ile 360 365 370 375			2297
aag aat aaa gag gaa ata ctc cag act ttt cct cac ccc caa agc aac Lys Asn Lys Glu Glu Ile Leu Gln Thr Phe Pro His Pro Gln Ser Asn 380 385 390			2345
aat gat cag caa aga gaa gga tca ttc ttt ggc cag act aaa gtg gaa Asn Asp Gln Gln Arg Glu Gly Ser Phe Phe Gly Gln Thr Lys Val Glu 395 400 405			2393
gaa tgt ttt cat ggt gaa aat cag tat tca aaa tca agc gag ttc gag Glu Cys Phe His Gly Glu Asn Gln Tyr Ser Lys Ser Ser Glu Phe Glu 410 415 420			2441
act cat aat gtc caa atg gga ctg gag gaa gta cag aat ata aat cgt Thr His Asn Val Gln Met Gly Leu Glu Glu Val Gln Asn Ile Asn Arg 425 430 435			2489
aga aat tcc cct tat agt cag acc atg aaa tca agt gca tgc aaa ata Arg Asn Ser Pro Tyr Ser Gln Thr Met Lys Ser Ser Ala Cys Lys Ile 440 445 450 455			2537
cag gtt tct tgt tca aac aat aca cac cta gtt tca gag aat aaa gaa Gln Val Ser Cys Ser Asn Asn Thr His Leu Val Ser Glu Asn Lys Glu 460 465 470			2585
cag act aca cat cct gaa ctt ttt gca gga aac aag acc caa aac ttg Gln Thr Thr His Pro Glu Leu Phe Ala Gly Asn Lys Thr Gln Asn Leu 475 480 485			2633
cat cac atg caa tat ttt cca aat aat gtg atc cca aag caa gat ctt His His Met Gln Tyr Phe Pro Asn Asn Val Ile Pro Lys Gln Asp Leu 490 495 500			2681
ctt cac agg tgc ttt caa gaa cag gag cag aag tca caa caa gct tca Leu His Arg Cys Phe Gln Glu Gln Glu Gln Lys Ser Gln Gln Ala Ser 505 510 515			2729
gtt cta cag gga tat aaa aat aga aac caa gat atg tct ggt caa caa Val Leu Gln Gly Tyr Lys Asn Arg Asn Gln Asp Met Ser Gly Gln Gln 520 525 530 535			2777
gct gcg caa ctt gct cag caa agg tac ttg ata cat aac cat gca aat Ala Ala Gln Leu Ala Gln Gln Arg Tyr Leu Ile His Asn His Ala Asn 540 545 550			2825
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agt cag atg cac agg cca att aag gtg gaa cct gga tgc aag cca cat Ser Gln Met His Arg Pro Ile Lys Val Glu Pro Gly Cys Lys Pro His 600 605 610 615	3017
gcc tgt atg cac aca gca cca cca gaa aac aaa aca tgg aaa aag gta Ala Cys Met His Thr Ala Pro Pro Glu Asn Lys Thr Trp Lys Lys Val 620 625 630	3065
act aag caa gag aat cca cct gca agc tgt gat aat gtg cag caa aag Thr Lys Gln Glu Asn Pro Pro Ala Ser Cys Asp Asn Val Gln Gln Lys 635 640 645	3113
agc atc att gag acc atg gag cag cat ctg aag cag ttt cac gcc aag Ser Ile Ile Glu Thr Met Glu Gln His Leu Lys Gln Phe His Ala Lys 650 655 660	3161
tcg tta ttt gac cat aag gct ctt act ctc aaa tca cag aag caa gta Ser Leu Phe Asp His Lys Ala Leu Thr Leu Lys Ser Gln Lys Gln Val 665 670 675	3209
aaa gtt gaa atg tca ggg cca gtc aca gtt ttg act aga caa acc act Lys Val Glu Met Ser Gly Pro Val Thr Val Leu Thr Arg Gln Thr Thr 680 685 690 695	3257
gct gca gaa ctt gat agc cac acc cca gct tta gag cag caa aca act Ala Ala Glu Leu Asp Ser His Thr Pro Ala Leu Glu Gln Gln Thr Thr 700 705 710	3305
tct tca gaa aag aca cca acc aaa aga aca gct gct tct gtt ctc aat Ser Ser Glu Lys Thr Pro Thr Lys Arg Thr Ala Ala Ser Val Leu Asn 715 720 725	3353
aat ttt ata gag tca cct tcc aaa tta cta gat act cct ata aaa aat Asn Phe Ile Glu Ser Pro Ser Lys Leu Leu Asp Thr Pro Ile Lys Asn 730 735 740	3401
tta ttg gat aca cct gtc aag act caa tat gat ttc cca tct tgc aga Leu Leu Asp Thr Pro Val Lys Thr Gln Tyr Asp Phe Pro Ser Cys Arg 745 750 755	3449
tgt gta gat cct gta aaa ttt gaa tgt atc tgt ttt aga tca att cgc Cys Val Asp Pro Val Lys Phe Glu Cys Ile Cys Phe Arg Ser Ile Arg 760 765 770 775	3497
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gcg gcc tgc ggg ctg gcc ggg ggc tgc gcc gcc gtg ctc ttc tcg gcc	99	
Ala Ala Cys Gly Leu Ala Gly Gly Ser Ala Ala Val Leu Phe Ser Ala		
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gtg gcg gta ggg aag ccg cgc gca ggc ggg gac gcg gag cca cgc ccg	147	
Val Ala Val Gly Lys Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro		
30 35 40		
gct gag ccg ccg gcc tgg gcg ggg ggc gcg ccg ccg gcc ccc ggt gtc	195	
Ala Glu Pro Pro Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val		
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Trp Asp Pro Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val		
60 65 70		
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Arg Lys Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu		
75 80 85		
gac cac tac aaa gcc aag gcc acg ccg cac atc ttc ctc atc agg cat	339	
Asp His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His		
90 95 100 105		
tcc cag tac cac gtg gat ggc tcc ctg gag aag gac cgc act ctg acc	387	
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu Thr		
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Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu Ala Ser		
125 130 135		
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ata gag acc acc gat atc atc agc ccg cac ctg cca ggc gtc tgc aaa	531	
Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro Gly Val Cys Lys		
155 160 165		

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Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro Ile Glu Pro Asp Pro	
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ccc gtg tct cat tgg aag ccg gaa gct gtg cag tat tac gaa gac gga	627
Pro Val Ser His Trp Lys Pro Glu Ala Val Gln Tyr Tyr Glu Asp Gly	
190 195 200	
gcc cgg atc gag gcc gcc ttc cgg aac tac atc cac cgc gca gat gcc	675
Ala Arg Ile Glu Ala Ala Phe Arg Asn Tyr Ile His Arg Ala Asp Ala	
205 210 215	
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Arg Gln Glu Glu Asp Ser Tyr Glu Ile Phe Ile Cys His Ala Asn Val	
220 225 230	
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Ile Arg Tyr Ile Val Cys Arg Ala Leu Gln Phe Pro Pro Glu Gly Trp	
235 240 245	
ctc cgg ctc tcc ctc aat aat ggc agc atc acc cac ctg gtg atc cga	819
Leu Arg Leu Ser Leu Asn Asn Gly Ser Ile Thr His Leu Val Ile Arg	
250 255 260 265	
ccc aac ggc cga gtt gcg ctc agg acc ctc ggg gac acg ggg ttc atg	867
Pro Asn Gly Arg Val Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met	
270 275 280	
cct ccc gac aag atc act cga tcc tga gggct ccggcctctc cttccctctg	919
Pro Pro Asp Lys Ile Thr Arg Ser *	
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aaggatttgc agcaag atg gat ttg gga aag gac caa tct cat ttg aag	169
Met Asp Leu Gly Lys Asp Gln Ser His Leu Lys	
1 5 10	
cac cat cag aca cct gac cct cat caa gaa gag aac cat tct cca gaa	217
His His Gln Thr Pro Asp Pro His Gln Glu Glu Asn His Ser Pro Glu	
15 20 25	
gtc att gga acc tgg agt ttg aga aac aga gaa cta ctt aga aaa aga	265
Val Ile Gly Thr Trp Ser Leu Arg Asn Arg Glu Leu Leu Arg Lys Arg	
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aaa gct gaa gtg cat gaa aag gaa aca tca caa tgg cta ttt gga gaa	313
Lys Ala Glu Val His Glu Lys Glu Thr Ser Gln Trp Leu Phe Gly Glu	
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cag aaa aaa cgc aag cag cag aga aca gga aaa gga aat cga aga ggc	361
Gln Lys Lys Arg Lys Gln Gln Arg Thr Gly Lys Gly Asn Arg Arg Gly	
60 65 70 75	
aga aag aga caa caa aac aca gaa ttg aag gtg gag cct cag cca cag	409
Arg Lys Arg Gln Gln Asn Thr Glu Leu Lys Val Glu Pro Gln Pro Gln	
80 85 90	
ata gaa aag gaa ata gtg gag aaa gca ctg gca cct ata gag aaa aaa	457
Ile Glu Lys Glu Ile Val Glu Lys Ala Leu Ala Pro Ile Glu Lys Lys	
95 100 105	
act gag cca cct ggg agc ata acc aaa gta ttt cct tca gta gcc tcc	505
Thr Glu Pro Pro Gly Ser Ile Thr Lys Val Phe Pro Ser Val Ala Ser	
110 115 120	
ccg caa aaa gtt gtg cct gag gaa cac ttt tct gaa ata tgt caa gaa	553
Pro Gln Lys Val Val Pro Glu Glu His Phe Ser Glu Ile Cys Gln Glu	
125 130 135	
agt aac ata tat cag gag aat ttt tct gag tac caa gaa ata gca gta	601
Ser Asn Ile Tyr Gln Glu Asn Phe Ser Glu Tyr Gln Glu Ile Ala Val	
140 145 150 155	
caa aac cat tct tct gaa aca tgc caa cat gtg tct gaa cct gaa gac	649
Gln Asn His Ser Ser Glu Thr Cys Gln His Val Ser Glu Pro Glu Asp	
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Leu Ser Pro Lys Met Tyr Gln Glu Ile Ser Val Leu Gln Asp Asn Ser	
175 180 185	

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Ser Lys Ile Cys Gln Asp Met Lys Glu Pro Glu Asp Asn Ser Pro Asn	
190 195 200	
aca tgc caa gta ata tct gta att caa gac cat cct ttc aaa atg tac	793
Thr Cys Gln Val Ile Ser Val Ile Gln Asp His Pro Phe Lys Met Tyr	
205 210 215	
caa gat atg gct aaa cga gaa gat ctg gct cct aaa atg tgc caa gaa	841
Gln Asp Met Ala Lys Arg Glu Asp Leu Ala Pro Lys Met Cys Gln Glu	
220 225 230 235	
gct gct gta ccc aaa atc ctt cct tgt cca aca tct gaa gac aca gct	889
Ala Ala Val Pro Lys Ile Leu Pro Cys Pro Thr Ser Glu Asp Thr Ala	
240 245 250	
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Asp Leu Ala Gly Cys Ser Leu Gln Ala Tyr Pro Lys Pro Asp Val Pro	
255 260 265	
aaa ggc tat att ctt gac aca gac caa aat cca gca gaa cca gag gaa	985
Lys Gly Tyr Ile Leu Asp Thr Asp Gln Asn Pro Ala Glu Pro Glu Glu	
270 275 280	
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Tyr Asn Glu Thr Asp Gln Gly Ile Ala Glu Thr Glu Gly Leu Phe Pro	
285 290 295	
aaa ata caa gaa ata gct gag cct aaa gac ctt tct aca aaa aca cac	1081
Lys Ile Gln Glu Ile Ala Glu Pro Lys Asp Leu Ser Thr Lys Thr His	
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caa gaa tca gct gaa cct aaa tac ctt cct cat aaa aca tgt aac gaa	1129
Gln Glu Ser Ala Glu Pro Lys Tyr Leu Pro His Lys Thr Cys Asn Glu	
320 325 330	
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Ile Ile Val Pro Lys Ala Pro Ser His Lys Thr Ile Gln Glu Thr Pro	
335 340 345	
cat tct gaa gac tat tca att gaa ata aac caa gaa act cct ggg tct	1225
His Ser Glu Asp Tyr Ser Ile Glu Ile Asn Gln Glu Thr Pro Gly Ser	
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gaa aaa tat tca cct gaa acg tat caa gaa ata cct ggg ctt gaa gaa	1273
Glu Lys Tyr Ser Pro Glu Thr Tyr Gln Glu Ile Pro Gly Leu Glu Glu	
365 370 375	
tat tca cct gaa ata tac caa gaa aca tcc cag ctt gaa gaa tat tca	1321
Tyr Ser Pro Glu Ile Tyr Gln Glu Thr Ser Gln Leu Glu Glu Tyr Ser	
380 385 390 395	
cct gaa ata tac caa gaa aca ccg ggg cct gaa gac ctc tct act gag	1369
Pro Glu Ile Tyr Gln Glu Thr Pro Gly Pro Glu Asp Leu Ser Thr Glu	
400 405 410	
aca tat aaa aat aag gat gtg cct aaa gaa tgc ttt cca gaa cca cac	1417

Thr	Tyr	Lys	Asn	Lys	Asp	Val	Pro	Lys	Glu	Cys	Phe	Pro	Glu	Pro	His	
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Gln	Glu	Thr	Gly	Gly	Pro	Gln	Gly	Gln	Asp	Pro	Lys	Ala	His	Gln	Glu	
		430					435					440				
gat	gct	aaa	gat	gct	tat	act	ttt	cct	caa	gaa	atg	aaa	gaa	aaa	ccc	1513
Asp	Ala	Lys	Asp	Ala	Tyr	Thr	Phe	Pro	Gln	Glu	Met	Lys	Glu	Lys	Pro	
	445					450					455					
aaa	gaa	gag	cca	gga	ata	cca	gca	att	ctg	aat	gag	agt	cat	cca	gaa	1561
Lys	Glu	Glu	Pro	Gly	Ile	Pro	Ala	Ile	Leu	Asn	Glu	Ser	His	Pro	Glu	
460				465					470					475		
aat	gat	gtc	tat	agt	tat	gtt	ttg	ttt	taa	c	aatgctcaac	cataaagttg				1612
Asn	Asp	Val	Tyr	Ser	Tyr	Val	Leu	Phe	*							
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				Met	Ala	Ala	Ser	Leu								
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cgg	ctc	ctc	gga	gct	gcc	tcc	ggc	ctc	cgg	tac	tgg	agc	cgg	cgg	ctg	162
Arg	Leu	Leu	Gly	Ala	Ala	Ser	Gly	Leu	Arg	Tyr	Trp	Ser	Arg	Arg	Leu	
			10					15						20		
cgg	ccg	gca	gcc	ggc	agc	ttt	gca	gcg	gtg	tgt	tct	agg	tca	gtg	gct	210
Arg	Pro	Ala	Ala	Gly	Ser	Phe	Ala	Ala	Val	Cys	Ser	Arg	Ser	Val	Ala	
			25					30					35			
tca	aag	act	cca	gtt	gga	ttc	att	gga	ctg	ggc	aac	atg	ggg	aat	cca	258
Ser	Lys	Thr	Pro	Val	Gly	Phe	Ile	Gly	Leu	Gly	Asn	Met	Gly	Asn	Pro	
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atg	gca	aaa	aat	ctc	atg	aaa	cat	ggc	tat	cca	ctt	att	att	tat	gat	306
Met	Ala	Lys	Asn	Leu	Met	Lys	His	Gly	Tyr	Pro	Leu	Ile	Ile	Tyr	Asp	
		55				60					65					
gtg	ttc	cct	gat	gcc	tgc	aaa	gag	ttt	caa	gat	gca	ggg	gaa	cag	gta	354

Val	Phe	Pro	Asp	Ala	Cys	Lys	Glu	Phe	Gln	Asp	Ala	Gly	Glu	Gln	Val	
70					75					80					85	
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Val	Ser	Ser	Pro	Ala	Asp	Val	Ala	Glu	Lys	Ala	Asp	Arg	Ile	Ile	Thr	
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Met	Leu	Pro	Thr	Ser	Ile	Asn	Ala	Ile	Glu	Ala	Tyr	Ser	Gly	Ala	Asn	
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ggg att cta aaa aaa gtg aag aag ggc tca tta tta ata gat tcc agc																498
Gly	Ile	Leu	Lys	Lys	Val	Lys	Lys	Gly	Ser	Leu	Leu	Ile	Asp	Ser	Ser	
		120					125					130				
act att gat cct gca gtt tca aaa gaa ttg gcc aaa gaa gtt gag aaa																546
Thr	Ile	Asp	Pro	Ala	Val	Ser	Lys	Glu	Leu	Ala	Lys	Glu	Val	Glu	Lys	
		135				140					145					
atg gga gca gtt ttc atg gat gcc cct gtt tct ggt ggt gta gga gct																594
Met	Gly	Ala	Val	Phe	Met	Asp	Ala	Pro	Val	Ser	Gly	Gly	Val	Gly	Ala	
150					155					160					165	
gca cga tct ggg aac ctc acg ttt atg gtg gga gga gtt gaa gat gaa																642
Ala	Arg	Ser	Gly	Asn	Leu	Thr	Phe	Met	Val	Gly	Gly	Val	Glu	Asp	Glu	
				170					175					180		
ttt gct gct gcc caa gag ttg ctg ggg tgc atg ggc tcc aac gtg gtg																690
Phe	Ala	Ala	Ala	Gln	Glu	Leu	Leu	Gly	Cys	Met	Gly	Ser	Asn	Val	Val	
			185					190					195			
tac tgt gga gct gtt ggg act ggg cag gcg gca aag atc tgc aac aac																738
Tyr	Cys	Gly	Ala	Val	Gly	Thr	Gly	Gln	Ala	Ala	Lys	Ile	Cys	Asn	Asn	
		200					205					210				
atg ctg tta gct att agt atg att gga act gct gaa gct atg aat ctt																786
Met	Leu	Leu	Ala	Ile	Ser	Met	Ile	Gly	Thr	Ala	Glu	Ala	Met	Asn	Leu	
		215				220					225					
gga atc agg tta ggg ctt gac cca aaa cta ctg gct aaa atc cta aat																834
Gly	Ile	Arg	Leu	Gly	Leu	Asp	Pro	Lys	Leu	Leu	Ala	Lys	Ile	Leu	Asn	
230					235				240					245		
atg agc tca gga cgg tgt tgg tca agt gac act tat aat cct gta cct																882
Met	Ser	Ser	Gly	Arg	Cys	Trp	Ser	Ser	Asp	Thr	Tyr	Asn	Pro	Val	Pro	
				250					255					260		
gga gtg atg gat ggc gtt ccc tcg gct aat aac tat cag ggt gga ttt																930
Gly	Val	Met	Asp	Gly	Val	Pro	Ser	Ala	Asn	Asn	Tyr	Gln	Gly	Gly	Phe	
			265					270					275			
gga aca aca ctc atg gct aag gat ctg gga ttg gca caa gac tct gct																978
Gly	Thr	Thr	Leu	Met	Ala	Lys	Asp	Leu	Gly	Leu	Ala	Gln	Asp	Ser	Ala	
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acc agc aca aag agc cca atc ctt ctt ggc agt ctg gcc cat cag atc																1026
Thr	Ser	Thr	Lys	Ser	Pro	Ile	Leu	Leu	Gly	Ser	Leu	Ala	His	Gln	Ile	

295	300	305	
tac agg atg atg tgt gca aag ggc tac tca aag	aaa gac ttc tca tcc	1074	
Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys	Lys Asp Phe Ser Ser		
310	315 320 325		
gtg ttc cag ttc cta cga gag gag gag acc ttc	tga gtgt gccctttggc	1124	
Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe	*		
330	335		
cacggacact gttgggaacc aaactctgtc ttggagcctc	cttttagctc actccacaag	1184	
taaattggatt taatcaaagg tcacctatct gcttttgatt	gtctagggtca cagtaatccc	1244	
taggattttt caccgcttat tctttttgtc tttttaacaa	acatattatc cgaatttttt	1304	
ttctgcaagc cactgatagt ctctgctaac tagcttaatt	gaccttttta caaagtttga	1364	
tccccaagca tcttcaacta aatcattgaa tacttcaatc	aggatattat ctgctttact	1424	
ttacaaataa aaccaaactct tttgtcaaca ggatgaaacc	catcttaaag gaaagaaaag	1484	
gaattggtgt gaagagagaa gttagagaag ggaaatgcag	tgaattacta tctgtgtcca	1544	
tcaggaagtt tgtcctgtta accaaatggt tactgcacta	ccagggttac tggtttattt	1604	
tccagggagc tgataaagca ggagaactgt tgctgcatgt	tttctatttg gactccgtca	1664	
caatatggta ggatatccct caccaactcc cgacactcag	cagacttggt tttatatattt	1724	
tttctttctt gttcattctt actacgtatt ttttgactta	agaatgacat ctttagatgc	1784	
atttcagagc caatgatgat atttgcttta gataattatt	atattattat aaatatagcc	1844	
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<220>
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	Met
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Lys Asn Ile Lys Ala Leu Val Ala Phe His Ser	Thr Ala Leu Asp Lys
5	10 15
	105

gaa att aca tca gca aat tat gct ggt gtc tgt aca tca tct gtg att Glu Ile Thr Ser Ala Asn Tyr Ala Gly Val Cys Thr Ser Ser Val Ile 20 25 30	153
aaa gaa gaa aac att gat caa cca gga tac tgt tat ctc tca cct gat Lys Glu Glu Asn Ile Asp Gln Pro Gly Tyr Cys Tyr Leu Ser Pro Asp 35 40 45	201
gga aag aga aaa act atg ctc tgc ttg gct tgt gga caa tcc atg aga Gly Lys Arg Lys Thr Met Leu Cys Leu Ala Cys Gly Gln Ser Met Arg 50 55 60 65	249
aca gag aaa gga ctg aaa caa ttg ctt cca ggg gtt cca ttc ctc tgt Thr Glu Lys Gly Leu Lys Gln Leu Leu Pro Gly Val Pro Phe Leu Cys 70 75 80	297
att tca ggc acc aag act cag aag ccc ttc tta caa ggg ccc ttc aag Ile Ser Gly Thr Lys Thr Gln Lys Pro Phe Leu Gln Gly Pro Phe Lys 85 90 95	345
gtc atc agt gtg gct gag gtt gat ttg tgc tgt gac aag gct gaa aaa Val Ile Ser Val Ala Glu Val Asp Leu Ser Cys Asp Lys Ala Glu Lys 100 105 110	393
act cta agt tac tac caa gca cgt cta ttg tct tta cgg atg aag acc Thr Leu Ser Tyr Tyr Gln Ala Arg Leu Leu Ser Leu Arg Met Lys Thr 115 120 125	441
tgc acg caa gct gca tct cac agt ggc atg gca gcc aca cac cag aag Cys Thr Gln Ala Ala Ser His Ser Gly Met Ala Ala Thr His Gln Lys 130 135 140 145	489
gca gtg aaa ata att gca tac aaa aat ggg gat ggg tat cgt aat ggg Ala Val Lys Ile Ile Ala Tyr Lys Asn Gly Asp Gly Tyr Arg Asn Gly 150 155 160	537
aag tta att gtg gct gga aca ttc ccc atg ctt ctt aca gaa tgc acg Lys Leu Ile Val Ala Gly Thr Phe Pro Met Leu Leu Thr Glu Cys Thr 165 170 175	585
gaa caa ctt ggg ctt gcc aga gca gcc tcc aaa gta tat acc aaa gat Glu Gln Leu Gly Leu Ala Arg Ala Ala Ser Lys Val Tyr Thr Lys Asp 180 185 190	633
gga acc cca atc ttt acc ttg cgt gat ttg gtt tta tgg gct cta gat Gly Thr Pro Ile Phe Thr Leu Arg Asp Leu Val Leu Trp Ala Leu Asp 195 200 205	681
gaa tcc ttt ctc cag aga gac tct gag aaa caa aag caa gat gca gct Glu Ser Phe Leu Gln Arg Asp Ser Glu Lys Gln Lys Gln Asp Ala Ala 210 215 220 225	729
cct gtt gga aaa gaa cag ata att gtt gaa agt atg gaa gaa aat cca Pro Val Gly Lys Glu Gln Ile Ile Val Glu Ser Met Glu Glu Asn Pro 230 235 240	777
aga atg aaa gtg aaa aac aga tta ttt gca aaa tct gtg aca tcc gat	825

Arg Met Lys Val Lys Asn Arg Leu Phe Ala Lys Ser Val Thr Ser Asp	
245 250 255	
agt ttg gat ggt ata gac aag tct ttg ctt acc ctc atc ctc aga aat	873
Ser Leu Asp Gly Ile Asp Lys Ser Leu Leu Thr Leu Ile Leu Arg Asn	
260 265 270	
cct att gcc atc tgg gtg tct tgt ggt gaa cca ttt cta cct cca aat	921
Pro Ile Ala Ile Trp Val Ser Cys Gly Glu Pro Phe Leu Pro Pro Asn	
275 280 285	
gct ttg cag aaa gca gaa aaa tta gag aaa cag aac tgg cta aaa aag	969
Ala Leu Gln Lys Ala Glu Lys Leu Glu Lys Gln Asn Trp Leu Lys Lys	
290 295 300 305	
gac aga att ttg gct gat cta gat acc atg aga cac aaa atg aga cag	1017
Asp Arg Ile Leu Ala Asp Leu Asp Thr Met Arg His Lys Met Arg Gln	
310 315 320	
tta aaa ggg cgg cga gta gcg gca tgt cag cca gcc acc atg gtt cct	1065
Leu Lys Gly Arg Arg Val Ala Ala Cys Gln Pro Ala Thr Met Val Pro	
325 330 335	
acc aag agc cct gtg cag ccc gtg gtg gtt gaa gga ggc tgg acc gaa	1113
Thr Lys Ser Pro Val Gln Pro Val Val Val Glu Gly Gly Trp Thr Glu	
340 345 350	
cag act caa cag gaa att aaa ctc atg gaa ctt ata aga cat aca gag	1161
Gln Thr Gln Gln Glu Ile Lys Leu Met Glu Leu Ile Arg His Thr Glu	
355 360 365	
gca cac ctt tct gaa atc caa gaa atg gaa tcc aaa ata aat ttt cca	1209
Ala His Leu Ser Glu Ile Gln Glu Met Glu Ser Lys Ile Asn Phe Pro	
370 375 380 385	
att gca acc aaa cgt ata gca gtc aag ccg agc aac ctg tat aag cag	1257
Ile Ala Thr Lys Arg Ile Ala Val Lys Pro Ser Asn Leu Tyr Lys Gln	
390 395 400	
ccc aac aca aaa cga gtg tgg att tat cta aat gga ggc aga cct gaa	1305
Pro Asn Thr Lys Arg Val Trp Ile Tyr Leu Asn Gly Gly Arg Pro Glu	
405 410 415	
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Asp Gly Thr Tyr Ala Trp Gly Lys Thr Ile Ser Glu Leu Leu Gln Asp	
420 425 430	
tgc tcc tct cgt ctc aaa atg acc cac cca gct aga gca ctg tac acc	1401
Cys Ser Ser Arg Leu Lys Met Thr His Pro Ala Arg Ala Leu Tyr Thr	
435 440 445	
ccc agt gga gag cca att cag tcc tgg gac gac ata gag cga gat atg	1449
Pro Ser Gly Glu Pro Ile Gln Ser Trp Asp Asp Ile Glu Arg Asp Met	
450 455 460 465	
gtc atc tgt gtg tct atg gga cat ggt ttc aaa acc cca aaa gag tta	1497
Val Ile Cys Val Ser Met Gly His Gly Phe Lys Thr Pro Lys Glu Leu	

470	475	480	
aaa caa ctg atg gag atc aga gca aat tat gcc aga atc cga agg cag			1545
Lys Gln Leu Met Glu Ile Arg Ala Asn Tyr Ala Arg Ile Arg Arg Gln			
485	490	495	
cag ggc cct caa gcc aca gac att gtg gtg tca cca tcc acg aag ctg			1593
Gln Gly Pro Gln Ala Thr Asp Ile Val Val Ser Pro Ser Thr Lys Leu			
500	505	510	
ctg tct ctg gca cat ctc cac aat taa ctctc atcagaacca tcggattttc			1645
Leu Ser Leu Ala His Leu His Asn *			
515	520		
tgctgtatattt ttctggaaag aaaacttttct ttaccactt ataaacagaa gactgtgaca			1705
agaaggccaa ttattttccat cgctgaagac tctaaatttg gcaaattcttc taaataacaa			1765
tcctgcatag ttattataaaa aaaattagtc gtaaaattta tccttcaaaa atctgcattt			1825
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ctaacagact gctctgggca tcttttctct ttgccttggc caggcctctc agaattgagt			1945
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Lys Leu Gly Ser Ser Gly Gly Trp Phe Leu Arg Val Leu Gly Pro Gly			
10	15	20	
ggc tgt aat aca aaa gct gcg cgt ccc tta att tcc tcg gcg gtt tat			149
Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr			
25	30	35	
gtg aag aac cag ctc agt ggg act cta cag att aaa cca ggg gtt ttc			197
Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe			
40	45	50	

aat gaa tac aga acc ata tgg ttc aaa tcc tac agg acg atc ttt tcc	245
Asn Glu Tyr Arg Thr Ile Trp Phe Lys Ser Tyr Arg Thr Ile Phe Ser	
55 60 65	
tgt ttg aac aga ata aag agt ttc agg tac cct tgg gcg aga ctg tac	293
Cys Leu Asn Arg Ile Lys Ser Phe Arg Tyr Pro Trp Ala Arg Leu Tyr	
70 75 80 85	
agt act tcc caa acc act gtc gac agc ggt gag gta aaa acc ttc ttg	341
Ser Thr Ser Gln Thr Thr Val Asp Ser Gly Glu Val Lys Thr Phe Leu	
90 95 100	
gcc ctg gct cac aaa tgg tgg gat gaa caa gga gta tat gca cct ctt	389
Ala Leu Ala His Lys Trp Trp Asp Glu Gln Gly Val Tyr Ala Pro Leu	
105 110 115	
cat tcc atg aat gac ctg agg gtg cca ttt att agg gac aat ctt ctg	437
His Ser Met Asn Asp Leu Arg Val Pro Phe Ile Arg Asp Asn Leu Leu	
120 125 130	
aaa aca att cct aat cac cag cca gga aaa cct ttg ttg ggg atg aag	485
Lys Thr Ile Pro Asn His Gln Pro Gly Lys Pro Leu Leu Gly Met Lys	
135 140 145	
att ctt gac gtt ggc tgt ggt ggt ggg ctg tta act gaa cct cta ggg	533
Ile Leu Asp Val Gly Cys Gly Gly Gly Leu Leu Thr Glu Pro Leu Gly	
150 155 160 165	
cgg ctt ggg gct tca gtt att gga atc gac cct gtg gat gag aac att	581
Arg Leu Gly Ala Ser Val Ile Gly Ile Asp Pro Val Asp Glu Asn Ile	
170 175 180	
aaa aca gca caa tgc cat aaa tca ttt gat cca gtc cgg gat aag aga	629
Lys Thr Ala Gln Cys His Lys Ser Phe Asp Pro Val Arg Asp Lys Arg	
185 190 195	
ata gag tac aga gtg tgt tcc ctg gaa gag att gtg gaa gag act gca	677
Ile Glu Tyr Arg Val Cys Ser Leu Glu Glu Ile Val Glu Glu Thr Ala	
200 205 210	
gaa aca ttt gat gct gtt gta gct tct gaa gtt gta gaa cat gtg att	725
Glu Thr Phe Asp Ala Val Val Ala Ser Glu Val Val Glu His Val Ile	
215 220 225	
gat cta gaa aca ttt tta cag tgc tgc tgt caa gtg tta aaa ccc ggt	773
Asp Leu Glu Thr Phe Leu Gln Cys Cys Cys Gln Val Leu Lys Pro Gly	
230 235 240 245	
ggg tct tta ttc att act aca atc aac aaa aca caa ctt tcc tat gcc	821
Gly Ser Leu Phe Ile Thr Thr Ile Asn Lys Thr Gln Leu Ser Tyr Ala	
250 255 260	
ttg gga att gtt ttt tca gag caa att gca ggt att gta cca aaa ggt	869
Leu Gly Ile Val Phe Ser Glu Gln Ile Ala Gly Ile Val Pro Lys Gly	
265 270 275	
act cat aca tgg gag aag ttt gtt tca cct gaa aca cta gag agc att	917

Thr His Thr Trp Glu Lys Phe Val Ser Pro Glu Thr Leu Glu Ser Ile	
280 285 290	
ctg gaa tca aat ggt ctg tca gtt caa aca gtg gta gga atg ctc tat	965
Leu Glu Ser Asn Gly Leu Ser Val Gln Thr Val Val Gly Met Leu Tyr	
295 300 305	
aac ccc ttc tca ggt tac tgg cat tgg agt gaa aat acc agc ctt aac	1013
Asn Pro Phe Ser Gly Tyr Trp His Trp Ser Glu Asn Thr Ser Leu Asn	
310 315 320 325	
tat gca gct cat gct gtg aaa tcc agg gtc cag gaa cac cca gcc tct	1061
Tyr Ala Ala His Ala Val Lys Ser Arg Val Gln Glu His Pro Ala Ser	
330 335 340	
gct gag ttt gtt tta aag gga gaa aca gaa gag ctc caa gct aat gcc	1109
Ala Glu Phe Val Leu Lys Gly Glu Thr Glu Glu Leu Gln Ala Asn Ala	
345 350 355	
tgc acc aat cca gct gtg cat gaa aag ctg aag aaa tga attgtttctg	1158
Cys Thr Asn Pro Ala Val His Glu Lys Leu Lys Lys *	
360 365 370	
agaactatag taatatggct tggatatctg atgttttcaa atacaagaaa tgtacaattt	1218
atccttttgag agagaatcat gaagaaaaga aggtcaataa aaagggtctaa aaccttggac	1278
aaaagttttt gttatttcgt ctaatagcta ctttcaaggg attctgtgaa taaaaagttt	1338
tgtcaagaaa aaaaaaaaaa	1357

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 <213> Homo sapiens

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catatacttc ccatgataaa ctttaagtggc gagtaagaaa agaagct atg atg ggt	176
	Met Met Gly
	1
ctg gct cag ctt tat aag aaa tac tgt ctt cat ggt gaa gca gga aag	224
Leu Ala Gln Leu Tyr Lys Lys Tyr Cys Leu His Gly Glu Ala Gly Lys	
5 10 15	
gaa gct gca gag aaa gtc agc tgg ata aag gac aaa ctt ctg cat att	272

Glu	Ala	Ala	Glu	Lys	Val	Ser	Trp	Ile	Lys	Asp	Lys	Leu	Leu	His	Ile		
20					25					30					35		
tat	tat	cag	aac	agc	att	gac	gac	aaa	ctg	ttg	gta	gag	aaa	atc	ttt	320	
Tyr	Tyr	Gln	Asn	Ser	Ile	Asp	Asp	Lys	Leu	Leu	Val	Glu	Lys	Ile	Phe		
			40					45						50			
gct	cag	tat	ctt	gtc	ccc	cac	aac	ctg	gaa	aca	gaa	gag	aga	atg	aaa	368	
Ala	Gln	Tyr	Leu	Val	Pro	His	Asn	Leu	Glu	Thr	Glu	Glu	Arg	Met	Lys		
			55					60					65				
tgc	tta	tat	tac	tta	tat	gct	agt	ttg	gat	cca	aat	gct	gta	aaa	gct	416	
Cys	Leu	Tyr	Tyr	Leu	Tyr	Ala	Ser	Leu	Asp	Pro	Asn	Ala	Val	Lys	Ala		
		70				75						80					
ctc	aac	gaa	atg	tgg	aag	tgt	cag	aac	atg	ctt	cgg	agc	cat	gta	cgc	464	
Leu	Asn	Glu	Met	Trp	Lys	Cys	Gln	Asn	Met	Leu	Arg	Ser	His	Val	Arg		
	85					90				95							
gaa	cta	ttg	gat	ttg	cac	aag	cag	cct	aca	tca	gag	gct	aac	tgt	tct	512	
Glu	Leu	Leu	Asp	Leu	His	Lys	Gln	Pro	Thr	Ser	Glu	Ala	Asn	Cys	Ser		
100					105				110					115			
gcc	atg	ttt	gga	aaa	ctg	atg	acc	ata	gca	aag	aat	ttg	cct	gac	ccc	560	
Ala	Met	Phe	Gly	Lys	Leu	Met	Thr	Ile	Ala	Lys	Asn	Leu	Pro	Asp	Pro		
			120						125					130			
ggg	aaa	gca	caa	gat	ttt	gtg	aag	aaa	ttt	aac	cag	gtt	ctc	ggc	gat	608	
Gly	Lys	Ala	Gln	Asp	Phe	Val	Lys	Lys	Phe	Asn	Gln	Val	Leu	Gly	Asp		
			135					140					145				
gat	gag	aaa	ctt	cgg	tct	cag	ttg	gag	tta	tta	att	agc	cca	acc	tgt	656	
Asp	Glu	Lys	Leu	Arg	Ser	Gln	Leu	Glu	Leu	Leu	Ile	Ser	Pro	Thr	Cys		
		150				155						160					
tct	tgc	aaa	caa	gca	gat	att	tgt	gtg	aga	gaa	ata	gcc	cgg	aaa	ctt	704	
Ser	Cys	Lys	Gln	Ala	Asp	Ile	Cys	Val	Arg	Glu	Ile	Ala	Arg	Lys	Leu		
	165					170					175						
gca	aat	cct	aag	caa	cca	aca	aat	cct	ttt	cta	gag	atg	gtc	aaa	ttt	752	
Ala	Asn	Pro	Lys	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met	Val	Lys	Phe		
180					185					190					195		
ctg	ttg	gaa	aga	atc	gca	cct	gtg	cac	att	gat	tca	gaa	gcc	ata	agt	800	
Leu	Leu	Glu	Arg	Ile	Ala	Pro	Val	His	Ile	Asp	Ser	Glu	Ala	Ile	Ser		
			200						205					210			
gcg	cta	gtg	aaa	ttg	atg	aat	aag	tca	ata	gag	ggg	aca	gca	gat	gat	848	
Ala	Leu	Val	Lys	Leu	Met	Asn	Lys	Ser	Ile	Glu	Gly	Thr	Ala	Asp	Asp		
			215					220					225				
gaa	gag	gag	ggg	gta	agt	cca	gat	aca	gct	atc	cgt	tca	gga	ctt	gaa	896	
Glu	Glu	Glu	Gly	Val	Ser	Pro	Asp	Thr	Ala	Ile	Arg	Ser	Gly	Leu	Glu		
		230					235					240					
ctt	ctt	aag	gtt	ctg	tct	ttt	aca	cat	cct	acc	tcg	ttc	cac	tct	gca	944	
Leu	Leu	Lys	Val	Leu	Ser	Phe	Thr	His	Pro	Thr	Ser	Phe	His	Ser	Ala		

245	250	255	
gag aca tat gag tcc ttg tta cag tgc cta aga atg gag gat gac aag Glu Thr Tyr Glu Ser Leu Leu Gln Cys Leu Arg Met Glu Asp Asp Lys 260 265 270 275			992
gta gca gaa gct gct att caa att ttt aga aat aca ggt cac aaa ata Val Ala Glu Ala Ala Ile Gln Ile Phe Arg Asn Thr Gly His Lys Ile 280 285 290			1040
gaa aca gac ctt ccc cag ata cga tcg acc tta att ccc att tta cat Glu Thr Asp Leu Pro Gln Ile Arg Ser Thr Leu Ile Pro Ile Leu His 295 300 305			1088
caa aaa gca aag agg ggt act cca cac caa gca aaa cag gct gtg cac Gln Lys Ala Lys Arg Gly Thr Pro His Gln Ala Lys Gln Ala Val His 310 315 320			1136
tgt ata cac gcc ata ttc aca aat aaa gaa gtc cag ctt gca cag att Cys Ile His Ala Ile Phe Thr Asn Lys Glu Val Gln Leu Ala Gln Ile 325 330 335			1184
ttt gag cca ctc agt agg agt ctg aat gct gat gtg cca gaa caa ctt Phe Glu Pro Leu Ser Arg Ser Leu Asn Ala Asp Val Pro Glu Gln Leu 340 345 350 355			1232
ata act cca tta gtt tca ttg ggc cac att tct atg tta gca cca gat Ile Thr Pro Leu Val Ser Leu Gly His Ile Ser Met Leu Ala Pro Asp 360 365 370			1280
cag ttt gct tcc cca atg aaa tct gta gta gca aat ttt att gtg aaa Gln Phe Ala Ser Pro Met Lys Ser Val Val Ala Asn Phe Ile Val Lys 375 380 385			1328
gat ctg cta atg aat gac agg tca aca ggt gaa aag aat gga aaa ctg Asp Leu Leu Met Asn Asp Arg Ser Thr Gly Glu Lys Asn Gly Lys Leu 390 395 400			1376
tgg tct cca gat gaa gag gtt tcc cct gaa gta cta gca aag gta cag Trp Ser Pro Asp Glu Glu Val Ser Pro Glu Val Leu Ala Lys Val Gln 405 410 415			1424
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Ser	Glu	Ser	Glu	Asp	Asp	Ser	Arg	Asp	Glu	Ser	Gln	Glu	Ser	Ser	Asp		
			120					125					130				
gct	ttg	ctg	aaa	agg	acc	atg	aac	atc	aag	gag	aac	aaa	gcc	atg	ctt	487	
Ala	Leu	Leu	Lys	Arg	Thr	Met	Asn	Ile	Lys	Glu	Asn	Lys	Ala	Met	Leu		
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gcc	cag	tta	ttg	gcg	gaa	ttg	aac	tcg	atg	cca	gat	ttc	ttc	cca	gta	535	
Ala	Gln	Leu	Leu	Ala	Glu	Leu	Asn	Ser	Met	Pro	Asp	Phe	Phe	Pro	Val		
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cga	acc	cca	acc	tca	gct	tct	agg	aag	aag	aca	gtg	agg	cgg	gcc	ttc	583	
Arg	Thr	Pro	Thr	Ser	Ala	Ser	Arg	Lys	Lys	Thr	Val	Arg	Arg	Ala	Phe		
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tcg	gag	gga	cag	atc	acg	cgg	cgt	atg	aac	cca	acc	cgg	agt	gcg	cgg	631	
Ser	Glu	Gly	Gln	Ile	Thr	Arg	Arg	Met	Asn	Pro	Thr	Arg	Ser	Ala	Arg		
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cct	cct	gag	aag	ttt	gct	cta	gag	aac	ttc	act	gtc	tca	gcc	gct	aaa	679	
Pro	Pro	Glu	Lys	Phe	Ala	Leu	Glu	Asn	Phe	Thr	Val	Ser	Ala	Ala	Lys		
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Phe	Ala	Glu	Glu	Phe	Tyr	Ser	Phe	Arg	Arg	Arg	Lys	Thr	Ile	Gly	Gly		
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Lys	Cys	Arg	Glu	Tyr	Arg	Arg	Arg	His	Arg	Ile	Ser	Ser	Phe	Arg	Pro		
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gtg	gag	gat	atc	acc	gaa	gag	gac	tta	gaa	aat	gtt	gcc	ata	act	gtt	823	
Val	Glu	Asp	Ile	Thr	Glu	Glu	Asp	Leu	Glu	Asn	Val	Ala	Ile	Thr	Val		
	245				250					255					260		
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Arg	Asp	Lys	Ile	Tyr	Asp	Lys	Val	Leu	Gly	Asn	Thr	Cys	His	Gln	Cys		

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Arg Gln Lys Thr Ile Asp Thr Lys	Thr Val Cys Arg Asn Gln Gly Cys		
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Cys Gly Val Arg Gly Gln Phe	Cys Gly Pro Cys Leu Arg Asn Arg Tyr		
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Gly Glu Asp Val Arg Ser Ala	Leu Leu Asp Pro Asp Trp Val Cys Pro		
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Pro Cys Arg Gly Ile Cys Asn Cys	Ser Tyr Cys Arg Lys Arg Asp Gly		
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Asp Asn Val Lys Glu Tyr Leu Glu	Ser Leu Gln Lys Glu Leu Val Glu		
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gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct 360
taaccaacac aggccccagc acccgcagag cagacactgc g atg aca acg gac 413
Met Thr Thr Asp
1

gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg 461
Asp Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu
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gaa act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca 509
Glu Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro
25 30 35

gcc gcc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc 557
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Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met	
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Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro	
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gag gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc	701
Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro	
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Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu	
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Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr	
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His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser	
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Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser	
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Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Leu His Pro Val Ile	
215 220 225	
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Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His	
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Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu	
245 250 255 260	
gct gaa gcc ctg gtg act gtc aca aac atc gag gtt att aat tgc agc	1229
Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser	

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Ile	Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp									
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aca	gat	ctc	atc	ccc	acg	gaa	ggg	gtg	aag	gcc	tcg	tcc	acc	tcc	gat									1325
Thr	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	Asp									
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cca	cca	gct	ctg	cct	gac	tcc	act	gaa	gca	aaa	cca	cac	atc	act	gag									1373
Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	Thr	Glu									
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gtc	aca	gcc	tct	gcc	gag	acc	ctg	tcc	aca	gcc	ggc	acc	aca	gag	tca									1421
Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	Thr	Glu	Ser									
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gct	gca	cct	cat	gcc	acg	gtt	ggg	acc	cca	ctc	ccc	act	aac	agc	gcc									1469
Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	Thr	Asn	Ser	Ala									
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Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	Thr	Leu	Ser	Gly	Ala									
			360					365						370										
ctg	gtc	aca	gtt	agc	agg	aat	ccc	ctg	gaa	gaa	acc	tca	gcc	ctc	tct									1565
Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	Glu	Thr	Ser	Ala	Leu	Ser									
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Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	Ser	Gly	Ala	Ala	Pro	Val	Ser									
			390			395					400													
ata	gag	gct	ggg	tca	gca	gtg	ggc	aaa	aca	act	tcc	ttt	gct	ggg	agc									1661
Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser									
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Ser	Ala	Ser	Ser	Tyr	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr									
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cct	tca	gag	aca	ccg	acc	atg	gac	atc	gca	acc	aag	ggg	ccc	ttc	ccc									1757
Pro	Ser	Glu	Thr	Pro	Thr	Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro									
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Thr	Ser	Arg	Asp	Pro	Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser									
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agc	cga	ggg	acg	aac	agc	acc	tta	gcc	aag	atc	aca	acc	tca	gcg	aag									1853
Ser	Arg	Gly	Thr	Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys									
		470				475					480													
acc	acg	atg	aag	ccc	cca	aca	gcc	acg	ccc	acg	act	gcc	cgg	acg	agg									1901
Thr	Thr	Met	Lys	Pro	Pro	Thr	Ala	Thr	Pro	Thr	Thr	Ala	Arg	Thr	Arg									
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Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu Leu
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cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg gca      1997
Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala
      520                      525                      530

gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg cct      2045
Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro
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cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacatcag      2094
His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly *
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tgtatgtatg gggaggggct tcacctgttc ccagaggtgt ccttggactc accttggcac      2334

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gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct      360

taaccaacac aggccccagc acccgagag cagacactgc g      atg aca acg gac      413
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gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg      461

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Ala Gly Pro 40 Ile Pro Glu Ala Glu Thr 45 Arg Gly Ala Lys Arg Ile Ser 50																	
cct gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg																	
Pro Ala Arg Glu Thr 55 Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met 60 65																	
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Val Leu Ile Ala Thr 70 Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro 75 80																	
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Ala Lys Thr 120 Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr 125 130																	
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Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe			
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Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr			
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agg ccg acc aca gac gtg agt gca ggt gaa aat gga ggt ttc ctc ctc			1661
Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu			
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ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg			1709
Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val			
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gca gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg			1757
Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala			
	440	445	450
cct cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacat			1806
Pro His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly *			
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Met Gln Val Trp Leu Leu Thr
1 5
ctg gaa agg ctg agg gtt ctg ccc aaa cct agg agt gaa ttc gac ttc 462
Leu Glu Arg Leu Arg Val Leu Pro Lys Pro Arg Ser Glu Phe Asp Phe
10 15 20
ttt ccc atc tca cac aca cac ccg aga cgt cac ccg aat cca cgt att 510
Phe Pro Ile Ser His Thr His Pro Arg Arg His Pro Asn Pro Arg Ile
25 30 35
tcc cac gtt cgg ctg cca ctg cct ccc agg tgg gct ttg cag gac cca 558
Ser His Val Arg Leu Pro Leu Pro Pro Arg Trp Ala Leu Gln Asp Pro
40 45 50 55
cca tcg cat ccc ctc tca ctc cac aga aaa ctc gtg ggg ccg tgt tcc 606
Pro Ser His Pro Leu Ser Leu His Arg Lys Leu Val Gly Pro Cys Ser
60 65 70
ccc tgc cac tga ccacgtttc cttgcaga 636

Pro Cys His *
75

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<222> (314) .. (1279)

<400> 13

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agttgttccc ctgctagccc agttggcctc tgattttagg agaagccaga agtccagatt      180
tttctgtgag ctctccttag ttgtccacat tggaagcaaa cttttaaatg ctgtgtatgc      240
gtggcccaag caaaacacat ctggaggcca gattgaatcc acaggctgaa agcagtcaac      300
caggcctgat gtc      atg acc ctg tat cct ctc cac tgg cag gaa gag atg      349
                   Met Thr Leu Tyr Pro Leu His Trp Gln Glu Glu Met
                   1              5              10

tca gga gaa agt gtg gtg agc tca gcg gtg cca gcg gct gct acc cgc      397
Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala Ala Ala Thr Arg
                   15              20              25

acc act tcc ttc aag ggc acg agc ccc agc tcc aaa tac gtg aag ctg      445
Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys Leu
                   30              35              40

aat gtg ggt gga gcc ctc tac tat acc acc atg cag acg ctg acc aag      493
Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr Lys
                   45              50              55              60

cag gac acc atg ctg aag gcc atg ttc agc ggg cgc atg gaa gtg ctc      541
Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val Leu
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acc gac agt gaa ggc tgg atc ctc att gac cgc tgt ggg aag cac ttt      589
Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His Phe
                   80              85              90

ggt acg ata ctc aac tac ctt cga gac ggg gcg gtg cct tta ccc gag      637
Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro Glu
                   95              100              105

agc cgc cgg gag atc gag gag ctg cta gca gaa gcc aag tac tac cta      685
Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu
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110	115	120	
gtc caa ggc ctg gtg gaa gag tgc cag gcg gcc cta caa aac aaa gat			733
Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu Gln Asn Lys Asp			
125	130	135	140
act tat gag cct ttc tgc aag gtc cct gtg atc acc tca tcc aag gaa			781
Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr Ser Ser Lys Glu			
	145	150	155
gaa caa aaa ctt ata gcg act tca aat aag cca gcc gtg aag ttg ctc			829
Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala Val Lys Leu Leu			
	160	165	170
tac aac aga agt aac aac aaa tac tca tat acc agc aat tct gac gac			877
Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp Asp			
	175	180	185
aat atg ttg aaa aac att gaa ctg ttt gat aag ctg tct ctg cgc ttt			925
Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg Phe			
	190	195	200
aac gga agg gtc ctg ttc ata aag gat gtt att ggg gat gaa atc tgc			973
Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile Cys			
	205	210	215
tgc tgg tcc ttt tat ggt cag ggc cgg aag att gct gaa gtc tgt tgt			1021
Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys Cys			
	225	230	235
acc tcc atc gtc tat gcc act gag aag aaa cag acc aag gtg gag ttt			1069
Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr Lys Val Glu Phe			
	240	245	250
ccc gaa gcc cgg att tat gag gag acc ctg aac att ttg ctg tat gag			1117
Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile Leu Leu Tyr Glu			
	255	260	265
gcc cag gat ggc cgg gga cct gac aat gcg ctc ctg gag gcc aca ggc			1165
Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu Glu Ala Thr Gly			
	270	275	280
ggg gcg gcg ggg cgc tcc cac cac ctg gac gag gag gag gag cgg gag			1213
Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp Glu Glu Arg Glu			
	285	290	300
cgg atc gag cgc gtg cgg agg atc cac atc aag cgc cct gat gac cgg			1261
Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg Pro Asp Asp Arg			
	305	310	315
gcc cac ctc cac cag tga gcaggc aagagaccga gccgccctcc tctcaccgcc			1315
Ala His Leu His Gln *			
	320		
cccactccct gccgtgctac acccagatcc tgtgcaggct gccgggcccc ttctgcttcc			1375
cttggagcct ggagatactt ttgtaacaag ccagatgatt attttggtat tgcttgacaa			1435

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<213> Homo sapiens

<220>

<221> CDS

<222> (287)..(1924)

<400> 14

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actcactctc atcctcttcc tctgataaag cccctaccag tgctgataaa gtctttctcg      180
tgagagccta gaggccttaa aaaaaaaagt gcttgaaaga gaagggggaca aaggaacacc      240
agtattaaga ggattttcca gtgtttctgg cagttgggtcc agaagg  atg cct cca      295
                                     Met Pro Pro
                                     1

ttc ctg ctt ctc acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc      343
Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro
      5                      10                      15

gtg gcc cta gat cct tgt tct gct tac atc agc ctg aat gag ccc tgg      391
Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp
      20                      25                      30                      35

agg aac act gac cac cag ttg gat gag tct caa ggt cct cct cta tgt      439
Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys
                        40                      45                      50

gac aac cat gtg aat ggg gag tgg tac cac ttc acg ggc atg gcg gga      487
Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly
                        55                      60                      65

gat gcc atg cct acc ttc tgc ata cca gaa aac cac tgt gga acc cac      535
Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His
                        70                      75                      80

gca cct gtc tgg ctc aat ggc agc cac ccc cta gaa ggc gac ggc att      583
Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile
      85                      90                      95

gtg caa cgc cag gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg      631
Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp
      100                      105                      110                      115

aac acc acg gtg gaa gtc aag gct tgc cct gga ggc tac tat gtg tat      679
Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr
                        120                      125                      130

cgt ctg acc aag ccc agc gtc tgc ttc cac gtc tac tgt ggt cat ttt      727
Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe
                        135                      140                      145

tat gac atc tgc gac gag gac tgc cat ggc agc tgc tca gat acc agc      775
Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser
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150	155	160	
gag tgc aca tgc gct cca gga act gtg cta ggc cct gac agg cag aca Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp Arg Gln Thr 165 170 175			823
tgc ttt gat gaa aat gaa tgt gag caa aac aac ggt ggc tgc agt gag Cys Phe Asp Glu Asn Glu Cys Glu Gln Asn Asn Gly Gly Cys Ser Glu 180 185 190 195			871
atc tgt gtg aac ctc aaa aac tcc tac cgc tgt gag tgt ggg gtt ggc Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val Gly 200 205 210			919
cgt gtg cta aga agt gat ggc aag act tgt gaa gac gtt gaa gga tgc Arg Val Leu Arg Ser Asp Gly Lys Thr Cys Glu Asp Val Glu Gly Cys 215 220 225			967
cac aat aac aat ggt ggc tgc agc cac tct tgc ctt gga tct gag aaa His Asn Asn Asn Gly Gly Cys Ser His Ser Cys Leu Gly Ser Glu Lys 230 235 240			1015
ggc tac cag tgt gaa tgt ccc cgg ggc ctg gtg ctg tct gag gat aac Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu Ser Glu Asp Asn 245 250 255			1063
cac act tgc caa gtc cct gtg ttg tgc aaa tca aat gcc att gaa gtg His Thr Cys Gln Val Pro Val Leu Cys Lys Ser Asn Ala Ile Glu Val 260 265 270 275			1111
aac atc ccc agg gag ctg gtt ggt ggc ctg gag ctc ttc ctg acc aac Asn Ile Pro Arg Glu Leu Val Gly Gly Leu Glu Leu Phe Leu Thr Asn 280 285 290			1159
acc tcc tgc cga gga gtg tcc aac ggc acc cat gtc aac atc ctc ttc Thr Ser Cys Arg Gly Val Ser Asn Gly Thr His Val Asn Ile Leu Phe 295 300 305			1207
tct ctc aag aca tgt ggt aca gtg gtc gat gtg gtg aat gac aag att Ser Leu Lys Thr Cys Gly Thr Val Val Asp Val Val Asn Asp Lys Ile 310 315 320			1255
gtg gcc agc aac ctc gtg aca ggt cta ccc aag cag acc ccg ggg agc Val Ala Ser Asn Leu Val Thr Gly Leu Pro Lys Gln Thr Pro Gly Ser 325 330 335			1303
agc ggg gac ttc atc atc cga acc agc aag ctg ctg atc ccg gtg acc Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys Leu Leu Ile Pro Val Thr 340 345 350 355			1351
tgc gag ttt cca cgc ctg tac acc att tct gaa gga tac gtt ccc aac Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser Glu Gly Tyr Val Pro Asn 360 365 370			1399
ctt cga aac tcc cca ctg gaa atc atg agc cga aat cat ggg atc ttc Leu Arg Asn Ser Pro Leu Glu Ile Met Ser Arg Asn His Gly Ile Phe 375 380 385			1447

cca ttc act ctg gag atc ttc aag gac aat gag ttt gaa gag cct tac	1495
Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn Glu Phe Glu Glu Pro Tyr	
390 395 400	
cgg gaa gct ctg ccc acc ctc aag ctt cgt gac tcc ctc tac ttt ggc	1543
Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly	
405 410 415	
att gag ccc gtg gtg cac gtg agc ggc ttg gaa agc ttg gtg gag agc	1591
Ile Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser	
420 425 430 435	
tgc ttt gcc acc ccc acc tcc aag atc gac gag gtc ctg aaa tac tac	1639
Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr Tyr	
440 445 450	
ctc atc cgg gat ggc tgt gtt tca gat gac tcg gta aag cag tac aca	1687
Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln Tyr Thr	
455 460 465	
tcc cgg gat cac cta gca aag cac ttc cag gtc cct gtc ttc aag ttt	1735
Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val Phe Lys Phe	
470 475 480	
gtg ggc aaa gac cac aag gaa gtg ttt ctg cac tgc cgg gtt ctt gtc	1783
Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu Val	
485 490 495	
tgt gga gtg ttg gac gag cgt tcc cgc tgt gcc cag ggt tgc cac cgg	1831
Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala Gln Gly Cys His Arg	
500 505 510 515	
cga atg cgt cgt ggg gca gga gga gag gac tca gcc ggt cta cag ggc	1879
Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu Gln Gly	
520 525 530	
cag acg cta aca ggc ggc ccg atc cgc atc gac tgg gag gac tag ttc	1927
Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile Asp Trp Glu Asp *	
535 540 545	
gtagccatac ctcgagtccc tgcattggac ggctctgctc tttggagctt ctccccccac	1987
cgccctctaa gaacatctgc caacagctgg gttcagactt cacactgtga gttcagactc	2047
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caatcagacc acaaaatcag aagctgggta taatatttca agttacaaac cctagaaaaa	2287
ttaaacagtt actgaaatta tgacttaaatt acccaatgac tccttaaata tgtaaattat	2347
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2444

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<213> Homo sapiens

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<222> (118)..(828)

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atg ggg gca aag gat cca agc att gag cct tca tcc tct att ccc cat 165
Met Gly Ala Lys Asp Pro Ser Ile Glu Pro Ser Ser Ser Ile Pro His
1 5 10 15

cca gtg ggg tgc cga ggc tca ggc agc atg acg acg gag acc ttt gtg 213
Pro Val Gly Cys Arg Gly Ser Gly Ser Met Thr Thr Glu Thr Phe Val
20 25 30

aag gat atc aag cct ggg ctc aag aat ctg aac ctt atc ttc att gtg 261
Lys Asp Ile Lys Pro Gly Leu Lys Asn Leu Asn Leu Ile Phe Ile Val
35 40 45

ctg gag aca ggc cga gtg acc aag aca aag gac ggg cat gag gtt cgg 309
Leu Glu Thr Gly Arg Val Thr Lys Thr Lys Asp Gly His Glu Val Arg
50 55 60

acc tgc aaa gtg gcg gac aaa aca ggc agc atc aat atc tct gtc tgg 357
Thr Cys Lys Val Ala Asp Lys Thr Gly Ser Ile Asn Ile Ser Val Trp
65 70 75 80

gac gat gtt ggc aat ctg atc cag cct ggg gac att atc cgg ctc acc 405
Asp Asp Val Gly Asn Leu Ile Gln Pro Gly Asp Ile Ile Arg Leu Thr
85 90 95

aaa ggg tac gct tca gtt ttc aaa ggt tgt ctg aca cta tat act ggc 453
Lys Gly Tyr Ala Ser Val Phe Lys Gly Cys Leu Thr Leu Tyr Thr Gly
100 105 110

cgt ggg ggt gat ctg cag aag att gga gaa ttc tgt atg gtt tat tct 501
Arg Gly Gly Asp Leu Gln Lys Ile Gly Glu Phe Cys Met Val Tyr Ser
115 120 125

gag gtt cct aac ttc agt gag cca aac cca gag tac agc acc cag cag 549
Glu Val Pro Asn Phe Ser Glu Pro Asn Pro Glu Tyr Ser Thr Gln Gln
130 135 140

gca ccc aac aag gcg gtg cag aac gac agc aac cct tca gct tcc cag 597
Ala Pro Asn Lys Ala Val Gln Asn Asp Ser Asn Pro Ser Ala Ser Gln
145 150 155 160

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cct acc act gga ccc tct gct gcc tct cca gcc tct gag aac cag aat      645
Pro Thr Thr Gly Pro Ser Ala Ala Ser Pro Ala Ser Glu Asn Gln Asn
      165                      170                      175

ggg aat gga ctg agt gcc cca cca ggt ccc ggt ggt ggc cca cat ccc      693
Gly Asn Gly Leu Ser Ala Pro Pro Gly Pro Gly Gly Gly Pro His Pro
      180                      185                      190

cct cat act ccc tcc cac cca ccc agc acc cga atc act cga agc cag      741
Pro His Thr Pro Ser His Pro Pro Ser Thr Arg Ile Thr Arg Ser Gln
      195                      200                      205

ccc aac cac aca cct gca ggc ccg cct ggc cct ttc agc aac cct gtt      789
Pro Asn His Thr Pro Ala Gly Pro Pro Gly Pro Phe Ser Asn Pro Val
      210                      215                      220

agt aac ggc aaa gaa acc cgg agg agc agc aag aga tag catgacattc      838
Ser Asn Gly Lys Glu Thr Arg Arg Ser Ser Lys Arg *
      225                      230                      235

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gattggctgg ttagcagta ttttagccac tgaacttcag tggaggggtgg tgagcagtgt      958

ccttatccac cctaattctca tactccctca ttgtccagct gaactacctg tcccctggga      1018

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attagccagg catggtggcg tatgcctgta atcccagcta cttaggaggc tgaggcagga      1258

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 <212> DNA
 <213> Homo sapiens

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 <222> (301)..(897)

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atg gcc cag aag ccg aag gtg gac ccc cac gtc ggg cgg ctg gga tac	348
Met Ala Gln Lys Pro Lys Val Asp Pro His Val Gly Arg Leu Gly Tyr	
1 5 10 15	
ctg cag gcg ctg gtc acg gaa ttc cag gag acc caa agc caa gac gcc	396
Leu Gln Ala Leu Val Thr Glu Phe Gln Glu Thr Gln Ser Gln Asp Ala	
20 25 30	
aag gag caa gtc ctc gcc aac ctc gcc aac ttc gct tat gac ccc agc	444
Lys Glu Gln Val Leu Ala Asn Leu Ala Asn Phe Ala Tyr Asp Pro Ser	
35 40 45	
aac tac gag tat ctg cgg cag ctg cag gtc ctg gat tta ttt ctc gat	492
Asn Tyr Glu Tyr Leu Arg Gln Leu Gln Val Leu Asp Leu Phe Leu Asp	
50 55 60	
tcg ctg tcg gag gag aat gag acc ctg gtg gag ttt gct att gga ggc	540
Ser Leu Ser Glu Glu Asn Glu Thr Leu Val Glu Phe Ala Ile Gly Gly	
65 70 75 80	
ctg tgc aac ctg tgc cca gac agg gcc aac aag gag cac atc ctg cac	588
Leu Cys Asn Leu Cys Pro Asp Arg Ala Asn Lys Glu His Ile Leu His	
85 90 95	
gca gga ggt gtc cca ctc atc atc aac tgc cta tcc agc ccc aat gag	636
Ala Gly Gly Val Pro Leu Ile Ile Asn Cys Leu Ser Ser Pro Asn Glu	
100 105 110	
gag acg gtg ctg tct gcc atc acc acg ctc atg cac ctg agc ccg ccg	684
Glu Thr Val Leu Ser Ala Ile Thr Thr Leu Met His Leu Ser Pro Pro	
115 120 125	
ggc cgc agc ttt ctc cca gag ctg acc gcc acg ccc gtg gtg cag tgc	732
Gly Arg Ser Phe Leu Pro Glu Leu Thr Ala Thr Pro Val Val Gln Cys	
130 135 140	
atg ctt cgc ttc tcc ctc tcg gcc agc gcc agg ctc cgg aac ctg gca	780
Met Leu Arg Phe Ser Leu Ser Ala Ser Ala Arg Leu Arg Asn Leu Ala	
145 150 155 160	
cag atc ttc ctg gag gac ttc tgc tcc ccc cgc cag gtg gcc gag gcc	828
Gln Ile Phe Leu Glu Asp Phe Cys Ser Pro Arg Gln Val Ala Glu Ala	
165 170 175	
cgc agc cgg cag gcg cac tct gcc ctg ggt atc cca ctg ccg agg agc	876
Arg Ser Arg Gln Ala His Ser Ala Leu Gly Ile Pro Leu Pro Arg Ser	
180 185 190	

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gtg gcc cca cgg cag cgc tga tc catggagact gcgagaccgt ggcaccccta 929
Val Ala Pro Arg Gln Arg *
195

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ggcgcctttt cagccatctg aaaggcgggt tctttcagca ggacaggcat ttacactgat 1049

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aaagggtcct agaagaaaaa aaaaaaaaaa 2098

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<210> 17
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119) .. (580)

<400> 17

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atg aat gtg ggc aca gcg cac agc gag gtg aac ccc aac acg cgg gtg	166
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val	
1 5 10 15	
atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc	214
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu	
20 25 30	
ctc cac atc gtg ctg ctg agc atc ccg ttt gtg agt gtc cct gtc gtc	262
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val	
35 40 45	
tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc ctg	310
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu	
50 55 60	
cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg	358
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala	
65 70 75 80	
agg ctg cta acc cac tgg gag cag atg gat tat ggg gtc cag ttc acg	406
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr	
85 90 95	
gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc	454
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu	
100 105 110	
acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc	502
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr	
115 120 125	
gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga	550
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly	
130 135 140	
gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttccccctgc	601
Val Arg Ile Phe Gly Ile Asn Lys Tyr *	
145 150	
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<210> 18
<211> 1605
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (535) .. (1050)

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gctggtaact ttggcgctc cgccaagccc tgccagactc ccctggctgt gatggcattc 180
tgtgccatcc tccttgtccc cagcctctgc aggatgcctt ccctaccac ctctccctgg 240

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aggctgcac tcggagtggc ttctgctgga gaggtgcttt gctgtctctc agactcagtc 1188
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aaggattcca caaagggaga gtggcatccc tgctgctgct gtgccagacc agagtttcct 1368
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gggtttgctg actgtaatcc ctgacaccag taaaaccaa aggactcttg ggggctcagt 1488
gtgagagcca gggttaccta ctctgccaag tgaggacaaa ctgctaggct gtatcccata 1548
atttcaggat gagaaacatt aacaataaaa attttagtagt aacataaaaa aaaaaaa 1605

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<210> 19
<211> 1497
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (210)..(1172)

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tgggcgggag cccttgtctg ggtctcgcgg ggggctgcca gatgcgtagg ccacactgac 180
tagttccttc ttgtcgcttt tcccagcaa atg gcg gat gac gcc ggt gca gcg 233
Met Ala Asp Asp Ala Gly Ala Ala
1 5

ggg ggg ccc ggg ggc cct ggt ggc cct ggg atg ggg aac cgc ggt ggc 281
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
10 15 20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt 329
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
25 30 35 40

gga cgg ggc cgg ggc cga ggc cgc gga gct cgc gga ggc aag gcc gag 377
Gly Arg Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu
45 50 55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac 425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
60 65 70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att 473

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Met	Lys	Ile	Lys	Ser	Leu	Glu	Glu	Ile	Tyr	Leu	Phe	Ser	Leu	Pro	Ile		
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Lys	Glu	Ser	Glu	Ile	Ile	Asp	Phe	Phe	Leu	Gly	Ala	Ser	Leu	Lys	Asp		
	90					95				100							
gag	gtt	ttg	aag	att	atg	cca	gtg	cag	aag	cag	acc	cgt	gcc	ggc	cag	569	
Glu	Val	Leu	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	Gly	Gln		
105					110					115					120		
cgc	acc	agg	ttc	aag	gca	ttt	gtt	gct	atc	ggg	gac	tac	aat	ggc	cac	617	
Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Ala	Ile	Gly	Asp	Tyr	Asn	Gly	His		
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Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala	Ile	Arg		
			140					145					150				
ggg	gcc	atc	atc	ctg	gcc	aag	ctc	tcc	atc	gtc	ccc	gtg	cgc	aga	ggc	713	
Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Ile	Val	Pro	Val	Arg	Arg	Gly		
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tac	tgg	ggg	aac	aag	atc	ggc	aag	ccc	cac	act	gtc	cct	tgc	aag	gtg	761	
Tyr	Trp	Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val		
	170					175					180						
aca	gcg	tgg	ggc	cat	cat	cct	ggc	caa	gct	ctc	cat	cgt	ccc	cgt	gcg	809	
Thr	Ala	Trp	Gly	His	His	Pro	Gly	Gln	Ala	Leu	His	Arg	Pro	Arg	Ala		
185					190					195					200		
cag	agg	cta	ctg	ggg	gaa	caa	gat	cgg	caa	gcc	cca	cac	tgt	cac	ctt	857	
Gln	Arg	Leu	Leu	Gly	Glu	Gln	Asp	Arg	Gln	Ala	Pro	His	Cys	His	Leu		
			205					210						215			
gca	agg	gac	agt	gtg	ggg	ctt	gcc	gat	ctt	gtt	ccc	cca	gta	gcc	tct	905	
Ala	Arg	Asp	Ser	Val	Gly	Leu	Ala	Asp	Leu	Val	Pro	Pro	Val	Ala	Ser		
			220					225					230				
gcg	cac	ggg	gac	gat	gga	gag	ctt	ggc	cag	gat	gat	ggc	ccc	acg	gat	953	
Ala	His	Gly	Asp	Asp	Gly	Glu	Leu	Gly	Gln	Asp	Asp	Gly	Pro	Thr	Asp		
	235					240						245					
ggc	ggt	ggc	cac	ctc	ctt	gga	gca	ctt	aac	acc	cag	acc	gac	gtg	gcc	1001	
Gly	Gly	Gly	His	Leu	Leu	Gly	Ala	Leu	Asn	Thr	Gln	Thr	Asp	Val	Ala		
	250					255					260						
att	gta	gtc	ccc	gat	agc	aac	aaa	tgc	ctt	gaa	cct	ggt	gcg	ctg	gcc	1049	
Ile	Val	Val	Pro	Asp	Ser	Asn	Lys	Cys	Leu	Glu	Pro	Gly	Ala	Leu	Ala		
265					270					275					280		
ggc	acg	ggt	ctg	ctt	ctg	cac	tgg	cat	aat	ctt	caa	aac	ctc	atc	ctt	1097	
Gly	Thr	Gly	Leu	Leu	Leu	His	Trp	His	Asn	Leu	Gln	Asn	Leu	Ile	Leu		
			285					290					295				
gag	aga	ggg	cac	cac	aca	gtg	aac	gaa	agt	caa	atg	agt	gct	gct	gat	1145	
Glu	Arg	Gly	His	His	Thr	Val	Asn	Glu	Ser	Gln	Met	Ser	Ala	Ala	Asp		

300	305	310	
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Ser Leu Ile Gly Arg Glu Lys Arg *			
315	320		
tcattgtcctt ggaccaagcg gccacaactt cgggtgacggg gcatccactc cttatcgctc			1257
ggccttgcgc tccagcgagc tccgcaggca catcgggcca caggccacac agtcacacag			1317
gccgcagacc accaggccac cagagtgcac agcatgcaca gaaacactgc cgcaggaagc			1377
acacacagcg gcttcccaca tcacaagggc cacaatgggc ccccaggggc caccgccgtg			1437
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 <213> Homo sapiens

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		Met	
		1	
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt			164
Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe			
5 10 15			
gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg			212
Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp			
20 25 30			
ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct			260
Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala			
35 40 45			
gtg att gga acc agg ctg cat gct gct gtg gca att gct tgt gtt gta			308
Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val			
50 55 60 65			
atg gcc ttt tac gtc ctg ttt ata aaa tga a ttccaaagca cccaagtcac			359
Met Ala Phe Tyr Val Leu Phe Ile Lys *			
70 75			
caactgccaa ccaaggggac ggggatgaag aacctgttgg agacctgaac ccagtgtagg			419


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agagttcagc tgaaatcatc ggtccccagg atgacaccac agcatctgcc cctgctatat 479
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ttcctttgat ctatgtgtaa atcagtcctt ggcagagtgc atataatgtc cggataaatt 599
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<210> 21
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<213> Homo sapiens

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Met Gly Lys Val
1

aag gtc gga gtc aac gga ttt ggt cgt att ggg cgc ctg gtc acc agg 162
Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr Arg
5 10 15 20

gct gct ttt aac tct ggt aaa gtg gat att gtt gcc atc aat gac ccc 210
Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp Pro
25 30 35

ttc att gac ctc aac tac atg gtt tac atg ttc caa tat gat tcc acc 258
Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser Thr
40 45 50

cat ggc aaa ttc cat ggc acc gtc aag gct gag aac ggg aag ctt gtc 306
His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val
55 60 65

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa 354
Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys
70 75 80

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atc aag tgg ggc gat gct ggc gct gag tac gtc gtg gag tcc act ggc Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser Thr Gly 85 90 95 100	402
gtc ttc acc acc atg gag aag gct ggg gct cat ttg cag ggg gga gcc Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Gln Gly Gly Ala 105 110 115	450
aaa agg gtc atc atc tct gcc ccc tct gct gat gcc ccc atg ttc gtc Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe Val 120 125 130	498
atg ggt gtg aac cat gag aag tat gac aac agc ctc aag atc atc agc Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile Ser 135 140 145	546
aat gcc tcc tgc acc acc aac tgc tta gca ccc ctg gcc aag gtc atc Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile 150 155 160	594
cat gac aac ttt ggt atc gtg gaa gga ctc atg acc aca gtc cat gcc His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala 165 170 175 180	642
atc act gcc acc cag aag act gtg gga tgg ccc ctt ccg gga aac tgt Ile Thr Ala Thr Gln Lys Thr Val Gly Trp Pro Leu Pro Gly Asn Cys 185 190 195	690
ggc gtg atg gcc gcg ggg gcg tct gcc aga aac atc atc cct gcc tct Gly Val Met Ala Ala Gly Ala Ser Ala Arg Asn Ile Ile Pro Ala Ser 200 205 210	738
act ggc gct gcc aag gct gtg ggc aag gtc atc cct gag ctg aac ggg Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly 215 220 225	786
aag ctc act ggc atg gcc ttc cgt gtc ccc act gcc aac gtg tca gtg Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val 230 235 240	834
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Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn	
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Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu *	
325 330 335	
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cctgccacac tcagtccccc accacactga atctcccctc ctcacagttg ccatgtagac	1243
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 <213> Homo sapiens

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	Met Pro
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ctc ttc act ctg gcc tcg ctg agc ggc tgc ccg agg agg agc tct agg	585
Leu Phe Thr Leu Ala Ser Leu Ser Gly Cys Pro Arg Arg Ser Ser Arg	
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ccg acg ccc acc gca ggc ctt aca gtc ttc tct gga cgc tcc ctt gca	633
Pro Thr Pro Thr Ala Gly Leu Thr Val Phe Ser Gly Arg Ser Leu Ala	
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gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg	681

Asp	Ala	Pro	Trp	Pro	Gly	Gly	Glu	Pro	Pro	Val	Thr	Phe	Leu	Arg	Thr	
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gaa gag ggg ccg gac gcc acc ttc ccc agg acc att ccc ctg atc caa																729
Glu	Glu	Gly	Pro	Asp	Ala	Thr	Phe	Pro	Arg	Thr	Ile	Pro	Leu	Ile	Gln	
			55						60					65		
cag ttg cta aac gcc acg gag ctc acg cag gac ccg gcc gcc tac tcc																777
Gln	Leu	Leu	Asn	Ala	Thr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Ala	Tyr	Ser	
			70					75					80			
cag ctg gtg gcc gtg ctg gtc tac acc gcc gag cgg gcc aag ttc gcc																825
Gln	Leu	Val	Ala	Val	Leu	Val	Tyr	Thr	Ala	Glu	Arg	Ala	Lys	Phe	Ala	
		85					90					95				
acc ggg gta gag cgg cag gac tgg atg gag ctg ttc att gac acc ttt																873
Thr	Gly	Val	Glu	Arg	Gln	Asp	Trp	Met	Glu	Leu	Phe	Ile	Asp	Thr	Phe	
	100					105					110					
aag ctg gtg cac agg gac atc gtg ggg gac ccc gag acc gcg ctg gcc																921
Lys	Leu	Val	His	Arg	Asp	Ile	Val	Gly	Asp	Pro	Glu	Thr	Ala	Leu	Ala	
	115				120				125					130		
ctc tgc taa agcccg gcacccgcc agccgggctg ggccctccct gccacactag																977
Leu	Cys	*														
cttcccaggg ctgccccga caggctggct ctcagtggag gccagagatc tggaatcggg																1037
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gaggaataaa	gaagtcacct	cccagctgt	catcatcttc	cagcagattg	agcaagaata											180
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ttttcaagaa gaggaatagg gtgaatgaat ctcatcagaa aagcagcaat	atg aat Met Asn 1	296
gct ggc cca tct tgg aat aaa gtg caa cat tca aag aat tct tca gga Ala Gly Pro Ser Trp Asn Lys Val Gln His Ser Lys Asn Ser Ser Gly 5 10 15		344
aaa agg cag agt aaa tcc caa gta ccc cac gct tct tcc cag ccg aga Lys Arg Gln Ser Lys Ser Gln Val Pro His Ala Ser Ser Gln Pro Arg 20 25 30		392
agc agc ctc aca gct gtc acc cag cct act gaa gaa aaa ctt aaa gaa Ser Ser Leu Thr Ala Val Thr Gln Pro Thr Glu Glu Lys Leu Lys Glu 35 40 45 50		440
agc att tcc ccg gaa gca aga cgc aaa agg aat cca ctc ggt tcc agg Ser Ile Ser Pro Glu Ala Arg Arg Lys Arg Asn Pro Leu Gly Ser Arg 55 60 65		488
tgt cag ggg gcc tca ggg aat aaa ctg ttt ctt gat ttt cag tca atg Cys Gln Gly Ala Ser Gly Asn Lys Leu Phe Leu Asp Phe Gln Ser Met 70 75 80		536
aaa att att aaa gag aat gct gat gag gac agt gca agt gat ctc tct Lys Ile Ile Lys Glu Asn Ala Asp Glu Asp Ser Ala Ser Asp Leu Ser 85 90 95		584
gat tcg gaa aga att ccc att cct cct tct ccc ctc aca cct cca gat Asp Ser Glu Arg Ile Pro Ile Pro Pro Ser Pro Leu Thr Pro Pro Asp 100 105 110		632
ctc aat ctt cga gct gaa gaa att gat cca gtt tac ttt gat ctt cac Leu Asn Leu Arg Ala Glu Glu Ile Asp Pro Val Tyr Phe Asp Leu His 115 120 125 130		680
cct ggt cag ggc cat aca aaa cct gaa tac tat tat cct aat ttc ctt Pro Gly Gln Gly His Thr Lys Pro Glu Tyr Tyr Tyr Pro Asn Phe Leu 135 140 145		728
cca tcc cct ttc agc tcc tgg gac cta cga gat atg gcc ctg ctt ctg Pro Ser Pro Phe Ser Ser Trp Asp Leu Arg Asp Met Ala Leu Leu Leu 150 155 160		776
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ggg aag tat atc gat aga ctt att cag ctt gag tgg ctg caa gtc cag Gly Lys Tyr Ile Asp Arg Leu Ile Gln Leu Glu Trp Leu Gln Val Gln 180 185 190		872
act gta cag tgt gaa aaa gca aag ggg ggc aaa gca agg ccc ccc act Thr Val Gln Cys Glu Lys Ala Lys Gly Gly Lys Ala Arg Pro Pro Thr 195 200 205 210		920

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gcc cct ggg acc tca ggg gca ctg aaa agc cct ggg aga agt aag cta      968
Ala Pro Gly Thr Ser Gly Ala Leu Lys Ser Pro Gly Arg Ser Lys Leu
                215                      220                      225

att gct agt gct ctg tcc aag cca cta cct cac cag gaa ggg gct tca      1016
Ile Ala Ser Ala Leu Ser Lys Pro Leu Pro His Gln Glu Gly Ala Ser
                230                      235                      240

aag tca ggc cct tcc cga aag aaa gct ttt cac cat gaa gaa atc cac      1064
Lys Ser Gly Pro Ser Arg Lys Lys Ala Phe His His Glu Glu Ile His
                245                      250                      255

cca tca cat tat gca ttt gag act tcc cct aga ccc att gat gtg ctt      1112
Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro Ile Asp Val Leu
                260                      265                      270

ggg ggt acc agg ttt tgt tct cag agg caa acc ctt gaa atg agg aca      1160
Gly Gly Thr Arg Phe Cys Ser Gln Arg Gln Thr Leu Glu Met Arg Thr
                275                      280                      285                      290

gaa gaa aaa aaa aaa aaa tca agt aag agt acg aag ctg cag cgc tgg      1208
Glu Glu Lys Lys Lys Lys Ser Ser Lys Ser Thr Lys Leu Gln Arg Trp
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gat ctg tcc ggc agt gga agc agc tct aag gtg gaa acc agc ggt cac      1256
Asp Leu Ser Gly Ser Gly Ser Ser Ser Lys Val Glu Thr Ser Gly His
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att cga gtt ccc aaa cag gca gct gtg att ctg gac tca gca gat tcc      1304
Ile Arg Val Pro Lys Gln Ala Ala Val Ile Leu Asp Ser Ala Asp Ser
                325                      330                      335

tgt aag gcc tcc aaa aca caa gca cat gca cat cct agg aaa aag gga      1352
Cys Lys Ala Ser Lys Thr Gln Ala His Ala His Pro Arg Lys Lys Gly
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aag gca gag agc tgt ggt cat gcc act gta tcg agt gag aaa aaa ctg      1400
Lys Ala Glu Ser Cys Gly His Ala Thr Val Ser Ser Glu Lys Lys Leu
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aaa aca aac gga gta aag caa aac aca tat aaa cta aaa taa atatcta      1449
Lys Thr Asn Gly Val Lys Gln Asn Thr Tyr Lys Leu Lys *
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aaatgctgaa ttgccaaagac ctgcaggtac ctcaatgtta gagcgcttcc aaaagtcaaa      1509

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              Met Leu Ser Leu Glu Leu Leu Ser Gln Val Val Gly Phe
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cat cag cca ggt agt atc aga ctt gct acc acc cct gta agg gta gat      156
His Gln Pro Gly Ser Ile Arg Leu Ala Thr Thr Pro Val Arg Val Asp
    15               20               25

gaa ttt aaa tat caa atg act cgg act ggc tgg cat gca aca gaa cag      204
Glu Phe Lys Tyr Gln Met Thr Arg Thr Gly Trp His Ala Thr Glu Gln
    30               35               40               45

tat ctc att gaa cct gaa aaa att caa gag atg ttc cct tta ctc aac      252
Tyr Leu Ile Glu Pro Glu Lys Ile Gln Glu Met Phe Pro Leu Leu Asn
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atg aat aag gtt tta gct gga ttg tat aat cct gga gat ggt cac att      300
Met Asn Lys Val Leu Ala Gly Leu Tyr Asn Pro Gly Asp Gly His Ile
                65               70               75

gat cct tat tct cta act atg gca ctg gct gct ggg gct agg aaa tgt      348
Asp Pro Tyr Ser Leu Thr Met Ala Leu Ala Ala Gly Ala Arg Lys Cys
    80               85               90

ggg gcc ctt tta aaa tat cct gca cca gta act tct ctg aaa gcc agg      396
Gly Ala Leu Leu Lys Tyr Pro Ala Pro Val Thr Ser Leu Lys Ala Arg
    95               100               105

tca gat gga aca tgg gac gtt gaa aca cca cag ggg tct atg aga gca      444
Ser Asp Gly Thr Trp Asp Val Glu Thr Pro Gln Gly Ser Met Arg Ala
   110               115               120               125

aat aga att gtg aat gct gca gga ttt tgg gct cgt gaa gta ggt aaa      492
Asn Arg Ile Val Asn Ala Ala Gly Phe Trp Ala Arg Glu Val Gly Lys
   130               135               140

atg att gga cta gaa cat cct ctc att ccg gtt caa cat caa tat gtt      540
Met Ile Gly Leu Glu His Pro Leu Ile Pro Val Gln His Gln Tyr Val
   145               150               155

gtt aca tcg act ata tct gaa gtg aaa gct ttg aaa cga gaa ctg cct      588
Val Thr Ser Thr Ile Ser Glu Val Lys Ala Leu Lys Arg Glu Leu Pro
   160               165               170

gtg ctc cgt gac ctg gaa gga tca tat tat ctc cga cag gaa agg gat      636
Val Leu Arg Asp Leu Glu Gly Ser Tyr Tyr Leu Arg Gln Glu Arg Asp
   175               180               185

ggg ctt ttg ttt ggt cca tat gaa agt caa gag aaa atg aaa gtt cag      684
Gly Leu Leu Phe Gly Pro Tyr Glu Ser Gln Glu Lys Met Lys Val Gln
   190               195               200               205

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Asp Ser Trp Val Thr Asn Gly Val Pro Pro Gly Phe Gly Lys Glu Leu	
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Phe Glu Ser Asp Leu Asp Arg Ile Met Glu His Ile Lys Ala Ala Met	
225 230 235	
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Glu Met Val Pro Val Leu Lys Lys Ala Asp Ile Ile Asn Val Val Asn	
240 245 250	
ggg cct atc acg tat tct cct gac att ctg cct atg gtg ggg ccc cat	876
Gly Pro Ile Thr Tyr Ser Pro Asp Ile Leu Pro Met Val Gly Pro His	
255 260 265	
cag ggg gtc aga aac tac tgg gtg gct ata ggc ttt gga tat ggc ata	924
Gln Gly Val Arg Asn Tyr Trp Val Ala Ile Gly Phe Gly Tyr Gly Ile	
270 275 280 285	
atc cac gct ggt ggg gta ggg aaa tat ctc agt gac tgg atc ctg cat	972
Ile His Ala Gly Gly Val Gly Lys Tyr Leu Ser Asp Trp Ile Leu His	
290 295 300	
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Lys Trp Thr Thr Thr Gln Tyr Thr Glu Ala Lys Ala Arg Glu Ser Tyr	
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335 340 345	
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Arg Pro Thr Gln Arg Val Ser Gly Leu Tyr Gln Arg Leu Glu Ser Lys	
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Cys Ser Met Gly Phe His Ala Gly Trp Glu Gln Pro His Trp Phe Tyr	
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Lys Pro Gly Gln Asp Thr Gln Tyr Arg Pro Ser Phe Arg His Thr Asn	
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Trp Phe Glu Pro Val Gly Ser Glu Tyr Lys Gln Val Met Gln Arg Val	
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Gly Val Thr Asp Leu Ser Pro Phe Gly Lys Phe Asn Ile Lys Gly Gln	
415 420 425	

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Gly	Asn	Glu	Ser	Ile	Trp	Tyr	Asn	Gly	Lys	Val	Val	Gly	Asn	Thr	Thr		
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Ser	Gly	Ser	Tyr	Ser	Tyr	Ser	Ile	Gln	Lys	Ser	Leu	Ala	Phe	Ala	Tyr		
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gtc	cct	gta	caa	cta	agt	gaa	gtg	gga	cag	caa	gtg	gaa	gtt	gaa	cta	2220	
Val	Pro	Val	Gln	Leu	Ser	Glu	Val	Gly	Gln	Gln	Val	Glu	Val	Glu	Leu		
			705					710						715			
tta	ggc	aaa	aat	tac	cca	gca	gtc	atc	ata	caa	gaa	cct	ttg	gta	ttg	2268	
Leu	Gly	Lys	Asn	Tyr	Pro	Ala	Val	Ile	Ile	Gln	Glu	Pro	Leu	Val	Leu		
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acc	gaa	cca	acc	aga	aac	cgg	ctt	cag	aaa	aaa	ggg	gga	aag	gac	aaa	2316	
Thr	Glu	Pro	Thr	Arg	Asn	Arg	Leu	Gln	Lys	Lys	Gly	Gly	Lys	Asp	Lys		
		735				740					745						
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Thr	*																
750																	
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395 400 405	
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Gly Asp Thr Val Gly Phe Leu Leu Asp Leu Asn Glu Lys Gln Met Ile	
425 430 435 440	
ttc ttt tta aat ggc aac cag ctg cct cct gaa aag caa gtc ttt tca	1997
Phe Phe Leu Asn Gly Asn Gln Leu Pro Pro Glu Lys Gln Val Phe Ser	
445 450 455	
tct act gta tct gga ttt ttt gct gca gct agt ttc atg tca tat caa	2045
Ser Thr Val Ser Gly Phe Phe Ala Ala Ser Phe Met Ser Tyr Gln	
460 465 470	
caa tgt gag ttc aat ttt gga gca aaa cca ttc aaa tac cca cca tct	2093
Gln Cys Glu Phe Asn Phe Gly Ala Lys Pro Phe Lys Tyr Pro Pro Ser	
475 480 485	
atg aaa ttt agc act ttt aat gac tac gcc ttc cta aca gct gaa gaa	2141
Met Lys Phe Ser Thr Phe Asn Asp Tyr Ala Phe Leu Thr Ala Glu Glu	
490 495 500	
aaa atc att ttg cca agg cac agg cgt ctt gct ctg ttg aag caa gtc	2189
Lys Ile Ile Leu Pro Arg His Arg Arg Leu Ala Leu Leu Lys Gln Val	
505 510 515 520	
agt atc cga gaa aac tgc tgt tcc ctt tgt tgt gat gag gta gca gac	2237
Ser Ile Arg Glu Asn Cys Cys Ser Leu Cys Cys Asp Glu Val Ala Asp	
525 530 535	
aca caa ttg aag cca tgt gga cac agt gac ctg tgc atg gat tgt gcc	2285
Thr Gln Leu Lys Pro Cys Gly His Ser Asp Leu Cys Met Asp Cys Ala	
540 545 550	
ttg cag ctg gag acc tgc cca ttg tgt cgt aaa gaa ata gta tct aga	2333
Leu Gln Leu Glu Thr Cys Pro Leu Cys Arg Lys Glu Ile Val Ser Arg	
555 560 565	
atc aga cag att tct cat att tca tga cacat gtgaagaggc atcgtggact	2385
Ile Arg Gln Ile Ser His Ile Ser *	
570 575	
tttttctact caattccagc caatgttgaa aaaaaaaaaa a	2426

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (14)..(475)

<400> 26

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ttttgaaccc tag   atg gcg tcc tat ttc gat gaa cac gac tgc gag ccg   49
                   Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro
                   1             5             10

tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc gca   97
Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala
      15             20             25

agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta gta   145
Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val
      30             35             40

gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt gag   193
Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu
      45             50             55             60

aac ctc ccc agg aca gtc atc aga ggc tct cag gct gag ctc aag tgc   241
Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys
      65             70             75

ccc gtg tgt ctt ttg gaa ttt gag gag gag gag act gcc att gag atg   289
Pro Val Cys Leu Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met
      80             85             90

cct tgc cat cac ctt ttc cat tcc agc tgc att ctg ccc tgg cta agc   337
Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser
      95             100            105

aag aca aat tcc tgt ccc ttg tgc cgc cat gag ctg ccc act gat gac   385
Lys Thr Asn Ser Cys Pro Leu Cys Arg His Glu Leu Pro Thr Asp Asp
     110             115             120

gac act tat gag gag cac aga cga gat aag gct cga aaa cag cag cag   433
Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln
     125             130             135             140

caa cac cga ctg gag aac ctc cat gga gcc atg tac acg tga ggaggtt   482
Gln His Arg Leu Glu Asn Leu His Gly Ala Met Tyr Thr  *
     145             150

ggggctgagt gctggccctc tgcgtcttcc ttattaacct tgaatcctca ttaaaggttt   542

ctttaccac aaaaaaaaaa aa   564

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<210> 27
 <211> 609
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 <213> Homo sapiens

<220>
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 <222> (18)..(581)

<400> 27

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	Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu	
	1 5 10	
ccg tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc		98
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu		
	15 20 25	
gca agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta		146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val		
	30 35 40	
gta gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt		194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val		
	45 50 55	
gag aac ctc ccc agg aca gtc atc aga ggc tct cag gct gct ctc acc		242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Ala Leu Thr		
	60 65 70 75	
gtg ccc tgg gcc cag tac tca agc ttc ttt ctg ttc atg gac tgc tgg		290
Val Pro Trp Ala Gln Tyr Ser Ser Phe Phe Leu Phe Met Asp Cys Trp		
	80 85 90	
ggg atg gaa gaa gag tgg cag ttg gga gca ggg gag ggt ggt tat cag		338
Gly Met Glu Glu Glu Trp Gln Leu Gly Ala Gly Glu Gly Gly Tyr Gln		
	95 100 105	
ctt atg aag atc aga cca agg cta gaa cac tac tct act ttt ctc aga		386
Leu Met Lys Ile Arg Pro Arg Leu Glu His Tyr Ser Thr Phe Leu Arg		
	110 115 120	
caa att cct gtc cct tgt gcc gct atg agc tgc cca ctg atg acg aca		434
Gln Ile Pro Val Pro Cys Ala Ala Met Ser Cys Pro Leu Met Thr Thr		
	125 130 135	
ctt atg agg agc aca gac gag ata agg ctc gaa aac agc agc agc aac		482
Leu Met Arg Ser Thr Asp Glu Ile Arg Leu Glu Asn Ser Ser Ser Asn		
	140 145 150 155	
acc gac tgg aga acc tcc atg gag cca tgt aca cgt gag gag gtt ggg		530
Thr Asp Trp Arg Thr Ser Met Glu Pro Cys Thr Arg Glu Glu Val Gly		
	160 165 170	
gct gag tgc tgg ccc tct gcg tct tcc tta tta acc ttg aat cct cat		578
Ala Glu Cys Trp Pro Ser Ala Ser Ser Leu Leu Thr Leu Asn Pro His		

175

180

185

taa aggtttcttt acccacaataa aaaaaaaaa

609

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<210> 28

<211> 1291

<212> DNA

<213> Homo sapiens

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	Met Trp Ala Ala Ala Gly Gly Leu Trp	
	1 5	

cgc tcc cgc gcg ggt ctc cgg gcc ctg ttc cgt agc cgc gat gct gcg	100
Arg Ser Arg Ala Gly Leu Arg Ala Leu Phe Arg Ser Arg Asp Ala Ala	
10 15 20 25	

cta ttt cca ggc tgc gag cgg gga ctt cac tgc tct gct gtc tcc tgc	148
Leu Phe Pro Gly Cys Glu Arg Gly Leu His Cys Ser Ala Val Ser Cys	
30 35 40	

aag aac tgg ctc aag aaa ttt gcc tcg aaa acc aaa aaa aag gtt tgg	196
Lys Asn Trp Leu Lys Lys Phe Ala Ser Lys Thr Lys Lys Lys Val Trp	
45 50 55	

tat gaa agt cct tcc ttg ggt tct cac tcg act tac aaa cca tcc aag	244
Tyr Glu Ser Pro Ser Leu Gly Ser His Ser Thr Tyr Lys Pro Ser Lys	
60 65 70	

ttg gaa ttc ctc atg agg agc acc tca aag aaa acc agg aag gaa gac	292
Leu Glu Phe Leu Met Arg Ser Thr Ser Lys Lys Thr Arg Lys Glu Asp	
75 80 85	

cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca	340
His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr	
90 95 100 105	

gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac	388
Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn	
110 115 120	

gtg gag ctc tcc aag gtt tcc ctg act cca gac ttc tca gcc tgc cga	436
Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg	
125 130 135	

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag	484
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Ala Tyr Trp Lys Thr Thr Leu Ser Ala Glu Gln Asn Ala His Met Glu	
140 145 150	
gct gtc ctg cag aga agt gcc gcg cac atg agg cac ctt ttg atg tcc	532
Ala Val Leu Gln Arg Ser Ala Ala His Met Arg His Leu Leu Met Ser	
155 160 165	
cag cag acc ctg agg aat gtg cca ccg ata gtg ttt gtt caa gac aag	580
Gln Gln Thr Leu Arg Asn Val Pro Pro Ile Val Phe Val Gln Asp Lys	
170 175 180 185	
gga aat gca gct cta gct gag ctt gat cag tta ctg gca gtc gca gac	628
Gly Asn Ala Ala Leu Ala Glu Leu Asp Gln Leu Leu Ala Val Ala Asp	
190 195 200	
ttt gga ccc cgg gat gaa aga gac aac ttt gta caa aat gat ttc agg	676
Phe Gly Pro Arg Asp Glu Arg Asp Asn Phe Val Gln Asn Asp Phe Arg	
205 210 215	
gac cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc	724
Asp Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser	
220 225 230	
tcc agt ctg tgt ggg atc gat cat gag gcg ctc cac aag cag att atg	772
Ser Ser Leu Cys Gly Ile Asp His Glu Ala Leu His Lys Gln Ile Met	
235 240 245	
gag tac aaa agg agg aaa gat aaa ggg ctc ggg ggc ctg gtg tgg cag	820
Glu Tyr Lys Arg Arg Lys Asp Lys Gly Leu Gly Gly Leu Val Trp Gln	
250 255 260 265	
ggg cag gtg gct gag ctg aca acg cag atg aaa aag gga agg aag agg	868
Gly Gln Val Ala Glu Leu Thr Thr Gln Met Lys Lys Gly Arg Lys Arg	
270 275 280	
gcc aag ccc cgc ctg gag cag gac agc tcc ctc aag agt tac ctg tca	916
Ala Lys Pro Arg Leu Glu Gln Asp Ser Ser Leu Lys Ser Tyr Leu Ser	
285 290 295	
ggc gag gag gtt gaa gat gac ctg gac ctg gtt ggt gcc ccg gag tac	964
Gly Glu Glu Val Glu Asp Asp Leu Asp Leu Val Gly Ala Pro Glu Tyr	
300 305 310	
gaa tgc tat gcc ccg gac aca gag gag ttg gag gca gag aga gga ggt	1012
Glu Cys Tyr Ala Pro Asp Thr Glu Glu Leu Glu Ala Glu Arg Gly Gly	
315 320 325	
ggc aga aca gag gat ggc cac agc tgc gga gca agc agg gag tag atg	1060
Gly Arg Thr Glu Asp Gly His Ser Cys Gly Ala Ser Arg Glu *	
330 335 340	
gagaggctct gcccatccca catttgcagg gaaaagcatt ggcacgcaac gcagcatgtg 1120	
gcttcattga ggcagttgat ggagttaaac catctgctct tctgctactt caacattttc 1180	
tagcttttcc gtgtatctaa acacaatttg ctacacaagt cactgttttt ttttccatgc 1240	

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1291

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<211> 766
<212> DNA
<213> Homo sapiens

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<222> (103)..(759)

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ggcggttgca ggcttcagcc tgcgctggtt ggtgaaacag ag atg tca gaa aag 114
Met Ser Glu Lys
1

gag aac aac ttc ccg cca ctg ccc aag ttc atc cct gtg aag ccc tgc 162
Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro Val Lys Pro Cys
5 10 15 20

ttc tac cag aac ttc tcc gac gag atc cca gtg gag cac cag gtc ctg 210
Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu His Gln Val Leu
25 30 35

gtg aag agg atc tac ccg ctg tgg atg ttt tac tgc gcc acc ctc ggc 258
Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly
40 45 50

gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg 306
Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly
55 60 65

acc aac ttc ggc ctg gcc ttc gtg tgg ctg ctc ctg ttc acg cct tgc 354
Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Phe Thr Pro Cys
70 75 80

ggc tac gtg tgc tgg ttc ccg cct gtc tac aag gcc ttc cga gcc gac 402
Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp
85 90 95 100

agc tcc ttt aat ttc atg gcg ttt ttc ttc atc ttc gga gcc cag ttt 450
Ser Ser Phe Asn Phe Met Ala Phe Phe Phe Ile Phe Gly Ala Gln Phe
105 110 115

gtc ctg acc gtc atc cag gcg att ggc ttc tcc ggc tgg ggc gcg tgc 498
Val Leu Thr Val Ile Gln Ala Ile Gly Phe Ser Gly Trp Gly Ala Cys
120 125 130

ggc tgg ctg tcg gca att gga ttc ttc cag tac agc ccg ggc gct gcc 546
Gly Trp Leu Ser Ala Ile Gly Phe Phe Gln Tyr Ser Pro Gly Ala Ala
135 140 145

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gtg gtc atg ctg ctt cca gcc atc atg ttc tcc gtg tcg gct gcc atg      594
Val Val Met Leu Leu Pro Ala Ile Met Phe Ser Val Ser Ala Ala Met
    150                      155                      160

atg gcc atc gcg atc atg aag gtg cac agg atc tac cga ggg ggc tgg      642
Met Ala Ile Ala Ile Met Lys Val His Arg Ile Tyr Arg Gly Gly Trp
    165                      170                      175                      180

cgg aag ctt cca gaa ggc cag acg gag tgg cac acg ggc ctt ggc gga      690
Arg Lys Leu Pro Glu Gly Gln Thr Glu Trp His Thr Gly Leu Gly Gly
                185                      190                      195

acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc      738
Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro
                200                      205                      210

agt acc ccc ttg tgc ccg taa ccggcgg      766
Ser Thr Pro Leu Cys Pro *
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<210> 30
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<212> DNA
<213> Homo sapiens

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<220>
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<222> (139)..(3633)

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gaggtacggc ctgtggtc  atg gcg ctg ttc cca gcc ttt gcg ggg ctt agt      171
                   Met Ala Leu Phe Pro Ala Phe Ala Gly Leu Ser
                   1                      5                      10

gag gct ccc gat ggc ggg agc tcc agg aaa gag tta gac tgg ctg agc      219
Glu Ala Pro Asp Gly Gly Ser Ser Arg Lys Glu Leu Asp Trp Leu Ser
                15                      20                      25

aac cca agc ttt tgt gtt gga tcc ata acg tcc ctg agc caa caa act      267
Asn Pro Ser Phe Cys Val Gly Ser Ile Thr Ser Leu Ser Gln Gln Thr
                30                      35                      40

gaa gca gct cca gcc cat gtt tct gaa ggg tta ccg ctg aca agg agt      315
Glu Ala Ala Pro Ala His Val Ser Glu Gly Leu Pro Leu Thr Arg Ser
                45                      50                      55

cat ctg aaa tca gag tct tca gat gaa agt gac act aac aaa aag ctc      363
His Leu Lys Ser Glu Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu
    60                      65                      70                      75

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aaa caa aca agt aga aaa aag aag aaa gag aaa aag aaa aaa agg aag	411
Lys Gln Thr Ser Arg Lys Lys Lys Lys Glu Lys Lys Lys Lys Arg Lys	
80 85 90	
cat cag cat cat aag aaa aca aag agg aag cat ggg ccg tcg agt agc	459
His Gln His His Lys Lys Thr Lys Arg Lys His Gly Pro Ser Ser Ser	
95 100 105	
agc agg tct gag aca gac acc gat tct gaa aag gac aaa cct tcc aga	507
Ser Arg Ser Glu Thr Asp Thr Asp Ser Glu Lys Asp Lys Pro Ser Arg	
110 115 120	
ggc gtt gga ggc agt aaa aag gaa tct gag gaa ccg aat caa gga aat	555
Gly Val Gly Gly Ser Lys Lys Glu Ser Glu Glu Pro Asn Gln Gly Asn	
125 130 135	
aat gct gca gct gat act gga cat cgc ttt gtt tgg ctt gag gac att	603
Asn Ala Ala Ala Asp Thr Gly His Arg Phe Val Trp Leu Glu Asp Ile	
140 145 150 155	
cag gct gtg acg gga gaa acc ttc aga aca gat aag aaa cca gat cct	651
Gln Ala Val Thr Gly Glu Thr Phe Arg Thr Asp Lys Lys Pro Asp Pro	
160 165 170	
gcg aac tgg gag tac aag tct ctc tac cga ggg gat ata gca aga tac	699
Ala Asn Trp Glu Tyr Lys Ser Leu Tyr Arg Gly Asp Ile Ala Arg Tyr	
175 180 185	
aag agg aaa gga gac tcc tgc ctt ggc att aac cct aag aag cag tgc	747
Lys Arg Lys Gly Asp Ser Cys Leu Gly Ile Asn Pro Lys Lys Gln Cys	
190 195 200	
ata tct tgg gaa ggg act tcc aca gag aag aag cat tca cgc aag cag	795
Ile Ser Trp Glu Gly Thr Ser Thr Glu Lys Lys His Ser Arg Lys Gln	
205 210 215	
gtt gaa cgc tat ttt act aag aag agt gtg gga tta atg aac atc gat	843
Val Glu Arg Tyr Phe Thr Lys Lys Ser Val Gly Leu Met Asn Ile Asp	
220 225 230 235	
gga gtt gcc att agc agt aaa act gaa cct ccc tca tct gag ccc atc	891
Gly Val Ala Ile Ser Ser Lys Thr Glu Pro Pro Ser Ser Glu Pro Ile	
240 245 250	
tcc ttt ata cca gtg aag gac ttg gaa gat gcg gct cct gtt aca acc	939
Ser Phe Ile Pro Val Lys Asp Leu Glu Asp Ala Ala Pro Val Thr Thr	
255 260 265	
tgg ttg aat cct ctg ggg att tat gat cag tca acc aca cat tgg cta	987
Trp Leu Asn Pro Leu Gly Ile Tyr Asp Gln Ser Thr Thr His Trp Leu	
270 275 280	
caa gga cag ggt cct cca gag cag gaa tca aag cag cca gac gca cag	1035
Gln Gly Gln Gly Pro Pro Glu Gln Glu Ser Lys Gln Pro Asp Ala Gln	
285 290 295	

Asp	Ser	Gly	Glu	Pro	Arg	Ala	Gly	Glu	Lys	Gly	Ala	Arg	Gly	Trp	Lys		
525						530					535						
gcg	tgg	atg	cac	cag	cag	gaa	cga	ggt	ggc	tgg	gtg	gtc	atc	aac	cca	1803	
Ala	Trp	Met	His	Gln	Gln	Glu	Arg	Gly	Gly	Trp	Val	Val	Ile	Asn	Pro		
540					545					550					555		
gat	gag	gat	gac	gat	gaa	cca	gaa	gag	gat	gac	cag	gaa	ata	aaa	gat	1851	
Asp	Glu	Asp	Asp	Asp	Glu	Pro	Glu	Glu	Asp	Asp	Gln	Glu	Ile	Lys	Asp		
				560					565					570			
aag	act	ctg	ccc	agg	tgg	cag	atc	tgg	ctt	gct	gct	gag	cgt	tcc	cgt	1899	
Lys	Thr	Leu	Pro	Arg	Trp	Gln	Ile	Trp	Leu	Ala	Ala	Glu	Arg	Ser	Arg		
			575					580					585				
gac	cag	agg	cac	tgg	cgg	ccc	tgg	cgc	cct	gat	aag	acc	aag	aag	caa	1947	
Asp	Gln	Arg	His	Trp	Arg	Pro	Trp	Arg	Pro	Asp	Lys	Thr	Lys	Lys	Gln		
			590				595					600					
acc	gag	gaa	gac	tgt	gag	gat	ccc	gag	aga	cag	ggg	gtg	ttt	gat	gat	1995	
Thr	Glu	Glu	Asp	Cys	Glu	Asp	Pro	Glu	Arg	Gln	Gly	Val	Phe	Asp	Asp		
	605					610					615						
att	ggg	caa	tct	ttg	atc	aga	ctt	tcc	agc	cat	gat	ctt	cag	ttc	cag	2043	
Ile	Gly	Gln	Ser	Leu	Ile	Arg	Leu	Ser	Ser	His	Asp	Leu	Gln	Phe	Gln		
	620				625					630					635		
ctg	gtg	gag	gcc	ttc	ctg	cag	ttc	ttg	ggt	gtg	cct	tct	ggc	ttt	act	2091	
Leu	Val	Glu	Ala	Phe	Leu	Gln	Phe	Leu	Gly	Val	Pro	Ser	Gly	Phe	Thr		
				640					645					650			
cct	cca	gcc	tcc	tgt	ctt	tat	ctg	gcc	atg	gat	gag	aac	agc	atc	ttt	2139	
Pro	Pro	Ala	Ser	Cys	Leu	Tyr	Leu	Ala	Met	Asp	Glu	Asn	Ser	Ile	Phe		
			655					660					665				
gat	aat	gga	ctt	tat	gat	gaa	aag	ccc	ttg	act	ttt	ttc	aac	cct	ttg	2187	
Asp	Asn	Gly	Leu	Tyr	Asp	Glu	Lys	Pro	Leu	Thr	Phe	Phe	Asn	Pro	Leu		
		670					675					680					
ttt	tct	ggg	gct	agc	tgt	gtt	ggc	cgc	atg	gat	agg	ttg	ggc	tat	cct	2235	
Phe	Ser	Gly	Ala	Ser	Cys	Val	Gly	Arg	Met	Asp	Arg	Leu	Gly	Tyr	Pro		
	685					690					695						
cgc	tgg	acc	agg	ggt	cag	aac	cga	gag	ggc	gag	gag	ttc	atc	cgc	aat	2283	
Arg	Trp	Thr	Arg	Gly	Gln	Asn	Arg	Glu	Gly	Glu	Glu	Phe	Ile	Arg	Asn		
	700				705				710						715		
gtc	ttc	cac	ctt	gtc	atg	cct	tta	ttt	tca	ggc	aaa	gag	aag	tcc	cag	2331	
Val	Phe	His	Leu	Val	Met	Pro	Leu	Phe	Ser	Gly	Lys	Glu	Lys	Ser	Gln		
				720					725					730			
ctc	tgc	ttc	tcc	tgg	tta	cag	tat	gag	att	gca	aag	gtc	att	tgg	tgc	2379	
Leu	Cys	Phe	Ser	Trp	Leu	Gln	Tyr	Glu	Ile	Ala	Lys	Val	Ile	Trp	Cys		
			735					740					745				
ctg	cac	act	aaa	aac	aag	aag	aga	tta	aag	tct	caa	ggg	aag	aac	tgc	2427	
Leu	His	Thr	Lys	Asn	Lys	Lys	Arg	Leu	Lys	Ser	Gln	Gly	Lys	Asn	Cys		

750	755	760	
aaa aaa cta gcc aag aat ctc ctt aag gag cca gaa aac tgc aac aac			2475
Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn			
765	770	775	
ttt tgc ctg tgg aag cag tat gca cat ctg gag tgg ttg ctt ggc aac			2523
Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn			
780	785	790	795
acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga			2571
Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly			
	800	805	810
agc aga gaa ctg aaa gac tct gac ctc tgt gag ctc agt ctg ctc tat			2619
Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr			
	815	820	825
gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca			2667
Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr			
	830	835	840
gct cga gct gtt cac ata tta acc aag ctg act gag agc agc ccc tat			2715
Ala Arg Ala Val His Ile Leu Thr Lys Leu Thr Glu Ser Ser Pro Tyr			
	845	850	855
ggg ccc tac act gga cag gtg ttg gct gtt cac att ttg aaa gcg cga			2763
Gly Pro Tyr Thr Gly Gln Val Leu Ala Val His Ile Leu Lys Ala Arg			
	860	865	870
875			
aag gct tat gag cac gca ctg cag gac tgt ttg ggt gac agc tgt gtc			2811
Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val			
	880	885	890
tcc aat cca gct ccc acc gat tcc tgt agc cgc cta att agc ctg gct			2859
Ser Asn Pro Ala Pro Thr Asp Ser Cys Ser Arg Leu Ile Ser Leu Ala			
	895	900	905
aaa tgc ttc atg ctc ttc cag tat ttg acc ata ggg att gat gct gct			2907
Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala			
	910	915	920
gtg cag ata tac gaa cag gtg ttt gca aaa ctg aac agt tct gtt ttc			2955
Val Gln Ile Tyr Glu Gln Val Phe Ala Lys Leu Asn Ser Ser Val Phe			
	925	930	935
cca gaa ggc tct ggc gag ggg gac agt gcc agc tcc cag agt tgg acc			3003
Pro Glu Gly Ser Gly Glu Gly Asp Ser Ala Ser Ser Gln Ser Trp Thr			
	940	945	950
955			
agt gtt ctc gaa gcc atc aca ctg atg cac acg agc ctg ctg aga ttc			3051
Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe			
	960	965	970
cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc			3099
His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu			
	975	980	985

tca cag gct tta aag ttg tat cca ggc aac cag gtt ctt tgg agg tcc	3147
Ser Gln Ala Leu Lys Leu Tyr Pro Gly Asn Gln Val Leu Trp Arg Ser	
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tat gta cag att cag aat aag tcc cac agt gcc agc aaa acc agg aga	3195
Tyr Val Gln Ile Gln Asn Lys Ser His Ser Ala Ser Lys Thr Arg Arg	
1005 1010 1015	
ttt ttt gac aca atc acc agg tct gcc aaa ccc ttg gag cct tgg ttg	3243
Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu	
1020 1025 1030 1035	
ttt gca att gaa gct gag aaa ctg agg aag aga ctg gtg gaa act gtc	3291
Phe Ala Ile Glu Ala Glu Lys Leu Arg Lys Arg Leu Val Glu Thr Val	
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cag agg tta gac ggt aga gag atc cac gcc aca att cct gag acc ggc	3339
Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly	
1055 1060 1065	
tta atg cat cgg atc caa gcc ctg ttt gaa aat gcc atg cgc agc gac	3387
Leu Met His Arg Ile Gln Ala Leu Phe Glu Asn Ala Met Arg Ser Asp	
1070 1075 1080	
agt ggc agc cag tgc ccc ttg ctg tgg agg atg tat ttg aac ttt ctg	3435
Ser Gly Ser Gln Cys Pro Leu Leu Trp Arg Met Tyr Leu Asn Phe Leu	
1085 1090 1095	
gtt tcc tta gga aat aaa gaa aga agc aaa ggt gta ttc tac aaa gca	3483
Val Ser Leu Gly Asn Lys Glu Arg Ser Lys Gly Val Phe Tyr Lys Ala	
1100 1105 1110 1115	
ctt cag aat tgc cct tgg gca aag gtg ttg tac ctg gac gcc gtg gag	3531
Leu Gln Asn Cys Pro Trp Ala Lys Val Leu Tyr Leu Asp Ala Val Glu	
1120 1125 1130	
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Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys	
1135 1140 1145	
gag ctc cgg gtg cgc ctg ccg ctg gag gag ctg gag ctg ctg ctg gag	3627
Glu Leu Arg Val Arg Leu Pro Leu Glu Glu Leu Glu Leu Leu Glu	
1150 1155 1160	
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Asp *	
1165	
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gtgtaaataa caaaaagtt atttacatat tatatatgtg aatatgtgta tatatgtaca	3863
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                  Met Ala Ser Ser Ser Gly Ala Gly Ala Ala Ala Ala
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gcc gcg gcg gcg aat ctg aat gcg gtg cgg gag acc atg gac gtt ctg   97
Ala Ala Ala Ala Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu
                   15                   20                   25

ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg   145
Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu
                   30                   35                   40

tct att tgt gta cgg ctt tgt gaa caa gga att aac cca gaa gct tta   193
Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu
                   45                   50                   55                   60

tca tcg gtt att aag gag ctt cgc aag gct act gaa gca ctg aag gct   241
Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala
                   65                   70                   75

gct gaa aat atg aca agc tga ct ttctggagaa attctgatga gatatgtcaa   294
Ala Glu Asn Met Thr Ser *
                   80

gctctgcaag agggttagaa gattgcattg tagttgagaa tgtacaatga aattactgca   354

tgcagcagtg tagaaaaatt ttacttttta aaagaattat aaaaccatag ctttataaat   414

cagtggaaag tggcttacag agagaactat cagatgtggt tacatcacat cttattcact   474

ttttttaaca gctctaattgc tttggcattg ctatgttcat atttatgtat tccttattta   534

tagctctgat agctttaatt ttctaagcag tctgtctatc agatgtgcac atctgctgtg   594

ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttggtgac   654

atttccatta taaactttta ttttgaattg tttatgcatt ataactgtgg atttatattg   714

tattgggctg aaagttgaca ggatttcagc caccacttgt gaatttttat ttagattcat   774

tatgtatatc agaatcttgt tttttgaaat aagagcatgg aaaacatttc ttgtaatcta   834

ctcttgaaca aagaatattt agtttttcaa acagtttggt gggcagctaa tagtgtgaac   894

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caggtcattt ttgtattgag taaaaaaatc aaactttgag aaacttggat tttaaaagta 954
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aaaatgaaac aacaaaaaaa aaaaa 1099

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acctcgcgat agctactggc cctgggcgag ccgttgggat tgcgcttgcg cacagcgtgt 180
cttctggatc gccataccta cctgtgggtc ctcatcttcc tggcctcata gctcctctc 240
tccaagc atg tct tcc ccg ttg caa aga gct gtg gga gat acc aag agg 289
Met Ser Ser Pro Leu Gln Arg Ala Val Gly Asp Thr Lys Arg
1 5 10
gcc ttt tct gca tct tct agt tcc tct gcc agt cta ccc ttt gat gac 337
Ala Phe Ser Ala Ser Ser Ser Ser Ser Ala Ser Leu Pro Phe Asp Asp
15 20 25 30
agg gac tca aac cat acc tca gag ggg aat ggc gac tct ttg tta gct 385
Arg Asp Ser Asn His Thr Ser Glu Gly Asn Gly Asp Ser Leu Leu Ala
35 40 45
gat gaa gac act gac ttt gaa gac agc ttg aat cgc aat gtg aag aag 433
Asp Glu Asp Thr Asp Phe Glu Asp Ser Leu Asn Arg Asn Val Lys Lys
50 55 60
aga gca gca aaa cga cca ccg aaa aca aca ccg gtg gca aaa cat cca 481
Arg Ala Ala Lys Arg Pro Pro Lys Thr Thr Pro Val Ala Lys His Pro
65 70 75
aag aaa ggg tcc cga gtg gta cat cgt cat agc cgg aaa cag tca gag 529
Lys Lys Gly Ser Arg Val Val His Arg His Ser Arg Lys Lys Ser Glu
80 85 90
cca cca gcc aat gat ctt ttc aat gct gtg aaa gcc gcc aaa agt gac 577
Pro Pro Ala Asn Asp Leu Phe Asn Ala Val Lys Ala Ala Lys Ser Asp
95 100 105 110

Tyr	Ser	Thr	Ser	Phe	Leu	Thr	Asp	Ser	Tyr	Leu	Lys	Tyr	Ile	Gly	Trp	
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act	ctg	cat	gat	aag	cac	cga	gaa	gtc	cgc	gtg	aag	tgc	gtg	aag	gct	1345
Thr	Leu	His	Asp	Lys	His	Arg	Glu	Val	Arg	Val	Lys	Cys	Val	Lys	Ala	
				355					360					365		
ctg	aaa	ggg	ctg	tac	ggg	aac	cgg	gac	ctg	acc	gca	cgc	ctg	gag	ctc	1393
Leu	Lys	Gly	Leu	Tyr	Gly	Asn	Arg	Asp	Leu	Thr	Ala	Arg	Leu	Glu	Leu	
			370					375					380			
ttc	acc	agc	cgc	ttc	aag	gac	cgg	atg	gtt	tcc	atg	atc	atg	gac	aga	1441
Phe	Thr	Ser	Arg	Phe	Lys	Asp	Arg	Met	Val	Ser	Met	Ile	Met	Asp	Arg	
		385					390					395				
gag	tac	agt	gtg	gca	gtg	gag	gcc	gtc	aga	tta	ctg	ata	ctt	ata	ctt	1489
Glu	Tyr	Ser	Val	Ala	Val	Glu	Ala	Val	Arg	Leu	Leu	Ile	Leu	Ile	Leu	
	400					405				410						
aag	aac	atg	gaa	ggg	ttg	ctg	acg	gac	gcg	gat	tgt	gag	agc	gtc	tac	1537
Lys	Asn	Met	Glu	Gly	Leu	Leu	Thr	Asp	Ala	Asp	Cys	Glu	Ser	Val	Tyr	
415					420				425					430		
ccc	gtt	gtg	tat	cct	tct	aat	cga	ggc	ctg	gct	tct	gcc	gca	ggc	gaa	1585
Pro	Val	Val	Tyr	Pro	Ser	Asn	Arg	Gly	Leu	Ala	Ser	Ala	Ala	Gly	Glu	
				435					440					445		
ttt	ctg	tac	tgg	aaa	ctt	ttc	tac	cct	gag	tgc	gag	ata	aga	acg	atg	1633
Phe	Leu	Tyr	Trp	Lys	Leu	Phe	Tyr	Pro	Glu	Cys	Glu	Ile	Arg	Thr	Met	
			450					455					460			
ggg	gga	aga	gag	caa	cgc	cag	agc	cca	ggc	gcc	cag	agg	act	ttc	ttc	1681
Gly	Gly	Arg	Glu	Gln	Arg	Gln	Ser	Pro	Gly	Ala	Gln	Arg	Thr	Phe	Phe	
		465				470						475				
cag	ctt	ctg	ctg	tcc	ttc	ttt	gtg	gag	agc	gag	ctc	cat	gac	cac	gct	1729
Gln	Leu	Leu	Leu	Ser	Phe	Phe	Val	Glu	Ser	Glu	Leu	His	Asp	His	Ala	
	480					485					490					
gct	tac	tta	gta	gac	agt	ctg	tgg	gac	tgt	gca	ggg	gct	cgg	ctg	aag	1777
Ala	Tyr	Leu	Val	Asp	Ser	Leu	Trp	Asp	Cys	Ala	Gly	Ala	Arg	Leu	Lys	
495					500					505					510	
gac	tgg	gag	ggg	ctg	aca	agc	ctg	ctg	ctg	gag	aag	gac	cag	aac	ctg	1825
Asp	Trp	Glu	Gly	Leu	Thr	Ser	Leu	Leu	Leu	Glu	Lys	Asp	Gln	Asn	Leu	
				515					520					525		
ggg	gat	gtg	cag	gag	agc	aca	ctg	ata	gaa	atc	ctt	gtg	tcc	agt	gcc	1873
Gly	Asp	Val	Gln	Glu	Ser	Thr	Leu	Ile	Glu	Ile	Leu	Val	Ser	Ser	Ala	
			530					535					540			
cgg	caa	gct	tca	gag	ggg	cac	cgg	cct	gtg	ggc	cgg	gtc	act	ggg	agg	1921
Arg	Gln	Ala	Ser	Glu	Gly	His	Pro	Pro	Val	Gly	Arg	Val	Thr	Gly	Arg	
		545					550					555				
aag	ggc	tta	acc	tct	aag	gag	cgc	aag	acc	caa	gcc	gat	gac	agg	gtg	1969
Lys	Gly	Leu	Thr	Ser	Lys	Glu	Arg	Lys	Thr	Gln	Ala	Asp	Asp	Arg	Val	

560	565	570	
aag ttg act gag cac ctc atc ccc ctg ctg ccc cag ctc ctg gcc aag			2017
Lys Leu Thr Glu His Leu Ile Pro Leu Leu Pro Gln Leu Leu Ala Lys			
575	580	585	590
ttc tca gct gat gca gag aag gtc act ccc ctg ctc cag ctt ctc agc			2065
Phe Ser Ala Asp Ala Glu Lys Val Thr Pro Leu Leu Gln Leu Leu Ser			
	595	600	605
tgc ttt gac ctc cac atc tac tgc act ggg cgc ttg gag aag cac ctg			2113
Cys Phe Asp Leu His Ile Tyr Cys Thr Gly Arg Leu Glu Lys His Leu			
	610	615	620
gag ctg ttc ctg cag caa ctc cag gag gtg gtg gtg aag cat gca gag			2161
Glu Leu Phe Leu Gln Gln Leu Gln Glu Val Val Val Lys His Ala Glu			
	625	630	635
cca gcg gtg ctt gag gct ggg gcg cat gcc ctc tac ctg ctc tgt aat			2209
Pro Ala Val Leu Glu Ala Gly Ala His Ala Leu Tyr Leu Leu Cys Asn			
	640	645	650
ccc gaa ttc act ttc ttc agc cgg gcg gac ttt gcc cgc agc cag cta			2257
Pro Glu Phe Thr Phe Phe Ser Arg Ala Asp Phe Ala Arg Ser Gln Leu			
	655	660	665
gta gat ttg ctg act gac cgc ttc cag cag gag ctt gaa gag ctg tta			2305
Val Asp Leu Leu Thr Asp Arg Phe Gln Gln Glu Leu Glu Glu Leu Leu			
	675	680	685
cag tcg tcc ttc cta gat gag gat gag gta tat aat ctg gca gcc act			2353
Gln Ser Ser Phe Leu Asp Glu Asp Glu Val Tyr Asn Leu Ala Ala Thr			
	690	695	700
ctg aaa cgc ctc tct gcc ttc tac aac act cat gac ctg act cgc tgg			2401
Leu Lys Arg Leu Ser Ala Phe Tyr Asn Thr His Asp Leu Thr Arg Trp			
	705	710	715
gag ctc tat gag cca tgt tgc caa ctc ctg cag aag gct gtg gac aca			2449
Glu Leu Tyr Glu Pro Cys Cys Gln Leu Leu Gln Lys Ala Val Asp Thr			
	720	725	730
gga gag gtt cct cac cag gtt atc ctg cca gcc ttg act ctt gtc tat			2497
Gly Glu Val Pro His Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr			
	735	740	745
ttt tcc att ctc tgg aca cta acc cac att tct aaa tca gat gct tcc			2545
Phe Ser Ile Leu Trp Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser			
	755	760	765
cag aag cag ctg tcg agt ttg agg gac aga atg gtg gcc ttc tgt gaa			2593
Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu			
	770	775	780
ctc tgc cag agt tgc ctc tca gat gtg gat act gag atc cag gag cag			2641
Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln			
	785	790	795

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tcc cag gca cct ggc cat ccc tgg ggc cca gtc acc acc tac tgc cac Ser Gln Ala Pro Gly His Pro Trp Gly Pro Val Thr Thr Tyr Cys His 1040 1045 1050	3409
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ccc agc tcc aag agg agg cgc gtt gaa ggg cct gcc aag cct aac aga Pro Ser Ser Lys Arg Arg Arg Val Glu Gly Pro Ala Lys Pro Asn Arg 1075 1080 1085	3505
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tgggcattgt ttttctaacc taacctttcc ctctggggta gagaagccga gagaccctgt	4118

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aagggcagca cctctgtgtt taatggaaat agcccatagt ctcttgatt tttggaacat 4238
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1 5

ctg gag aac gcg cag cat gtg gcg ttg gtg tgc gcc cgc ggc gag cgc 100
Leu Glu Asn Ala Gln His Val Ala Leu Val Cys Ala Arg Gly Glu Arg
10 15 20

ttc ctg gcg cgg gat gcg ctg cgc agc ctg gcg gtg ctg gaa ggc gcc 148
Phe Leu Ala Arg Asp Ala Leu Arg Ser Leu Ala Val Leu Glu Gly Ala
25 30 35 40

agc ctg gtg gtg ggc aaa gat gga ttt ata aaa gct att ggt cct gct 196
Ser Leu Val Val Gly Lys Asp Gly Phe Ile Lys Ala Ile Gly Pro Ala
45 50 55

gat gtt att caa aga cag ttt tct gga gaa act ttt gaa gaa tta att 244
Asp Val Ile Gln Arg Gln Phe Ser Gly Glu Thr Phe Glu Glu Leu Ile
60 65 70

gac tgc tct ggg aaa tgt atc cta cca ggt ttg gtg gat gca cac aca 292
Asp Cys Ser Gly Lys Cys Ile Leu Pro Gly Leu Val Asp Ala His Thr
75 80 85

cat cca gta tgg gct ggt gaa aga gtt cac gaa ttt gca atg aag ttg 340
His Pro Val Trp Ala Gly Glu Arg Val His Glu Phe Ala Met Lys Leu
90 95 100

gca gga gcc acc tac atg gaa att cac cag gcc gga gga ggg atc cac 388
Ala Gly Ala Thr Tyr Met Glu Ile His Gln Ala Gly Gly Gly Ile His
105 110 115 120

ttt acc gtg gag cgc acg cgc caa gcc aca gag gag gag ctg ttc cgc 436
Phe Thr Val Glu Arg Thr Arg Gln Ala Thr Glu Glu Glu Leu Phe Arg
125 130 135

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Val Glu Cys Lys Ser Gly Tyr Gly Leu Asp Leu Glu Thr Glu Leu Lys	
155 160 165	
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Met Leu Arg Val Ile Glu Arg Ala Arg Arg Glu Leu Asp Ile Gly Ile	
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Ser Ala Thr Tyr Cys Gly Ala His Ser Val Pro Lys Gly Lys Thr Ala	
185 190 195 200	
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Thr Glu Ala Ala Asp Asp Ile Ile Asn Asn His Leu Pro Lys Leu Lys	
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Glu Leu Gly Arg Asn Gly Glu Ile His Val Asp Asn Ile Asp Val Phe	
220 225 230	
tgt gag aaa ggt gtc ttt gat ctc gat tcc acc aga agg att ctt caa	772
Cys Glu Lys Gly Val Phe Asp Leu Asp Ser Thr Arg Arg Ile Leu Gln	
235 240 245	
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Arg Gly Lys Asp Ile Gly Leu Gln Ile Asn Phe His Gly Asp Glu Leu	
250 255 260	
cac ccg atg aag gct gct gag ctt ggg gct gaa ctg gga gcg cag gca	868
His Pro Met Lys Ala Ala Glu Leu Gly Ala Glu Leu Gly Ala Gln Ala	
265 270 275 280	
atc agc cac ctg gaa gaa gtg agt gat gaa ggc atc gtt gcc atg gca	916
Ile Ser His Leu Glu Glu Val Ser Asp Glu Gly Ile Val Ala Met Ala	
285 290 295	
acg gcc agg tgc tct gcc atc ctt ctg ccc acc aca gcc tac atg ctg	964
Thr Ala Arg Cys Ser Ala Ile Leu Leu Pro Thr Thr Ala Tyr Met Leu	
300 305 310	
aga ctg aaa caa cct cga gcc agg aag atg tta gat gaa gga gta ata	1012
Arg Leu Lys Gln Pro Arg Ala Arg Lys Met Leu Asp Glu Gly Val Ile	
315 320 325	
gtt gct ctg gga agt gat ttc aac ccc aat gca tat tgc ttt tca atg	1060
Val Ala Leu Gly Ser Asp Phe Asn Pro Asn Ala Tyr Cys Phe Ser Met	
330 335 340	
cca atg gtc atg cat ctg gcc tgt gta aac atg aga atg tcc atg cct	1108
Pro Met Val Met His Leu Ala Cys Val Asn Met Arg Met Ser Met Pro	
345 350 355 360	

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365 370 375	
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Ile Ile Asn Ser Ser Arg Trp Glu His Leu Ile Tyr Gln Phe Gly Gly	
395 400 405	
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His His Glu Leu Ile Glu Tyr Val Ile Ala Lys Gly Lys Leu Ile Tyr	
410 415 420	
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Lys Thr *	
425	
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Cys Gly Ala Val Gly Leu Leu Pro Pro Gly Thr Ala Ala Pro Ser Gly
885                      890                      895                      900

tgg gcc cag gct cca ctc agt gac acg gct caa gtc tac atg gag ctg      2850
Trp Ala Gln Ala Pro Leu Ser Asp Thr Ala Gln Val Tyr Met Glu Leu
                      905                      910                      915

cag ggc ctg gtg gac ccg cag atc cag cta cct ctg tta gcc gcc cga      2898
Gln Gly Leu Val Asp Pro Gln Ile Gln Leu Pro Leu Leu Ala Ala Arg
                      920                      925                      930

agg tac aag ttg cag aag cag ctt gat agc ctc aca gcc agg acc cca      2946
Arg Tyr Lys Leu Gln Lys Gln Leu Asp Ser Leu Thr Ala Arg Thr Pro
                      935                      940                      945

tca gaa ggg gag gca ggg act cag agg caa caa aag ctt tct tcc ctc      2994
Ser Glu Gly Glu Ala Gly Thr Gln Arg Gln Gln Lys Leu Ser Ser Leu
                      950                      955                      960

cag ctg gaa ttg tca aaa ctg gac aag gca gcc tct cac ctc cag cag      3042
Gln Leu Glu Leu Ser Lys Leu Asp Lys Ala Ala Ser His Leu Gln Gln
965                      970                      975                      980

ctg atg gat gag cct cca gcc cca ggg agc ccg gag ctc taa ctcacata      3091
Leu Met Asp Glu Pro Pro Ala Pro Gly Ser Pro Glu Leu *
                      985                      990

tccccatcag ttttctctccc tctcagacct gtctttgagg acaaacagat ttgtcagctg      3151

tcaggggtgca gtgggacgtc agagactatg tgggtccatcg ccttcattgt gtaaattgagg      3211

acacagactg gcttggtcgc agtgactgtg gtgtccttga gatgctcaca ttactgccccg      3271

gcctgcctcc cacctggaag tctgggaatg aggagattga gataaaacttt tgaaatccca      3331

aacatgtctg tttatggctc tttggtcccc tttgctccca gtggtgactt ttgtgcttct      3391

gagttgtccc ctgagagctt ggtctgggaa aagaggagga ggggtcctca ctggaggaag      3451

aggaaccttt tagtcatggg taaggggatg gggacagttg gttcccggtt ctacctccct      3511

ttctggactg acaattgccc tggctttttg cagggtcctt tctccccccac tttcactaaa      3571

ttggaagttc cccgtcctt gggttt                                     3596

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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (555)..(1406)

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Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn	
160 165 170	
atg ttg gtt gca atc act gtg ctt att tat cca aac tcc att cag gaa	1118
Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu	
175 180 185	
tac ata cgg caa ctg cct cct aat ttt ccc tac aga gat gat gtc atg	1166
Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met	
190 195 200	
tca gtg aat cct acc tgt ttg gtc ctt att att ctt ctg ttt att agc	1214
Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser	
205 210 215 220	
att atc ttg act ttt aag ggt tac ttg att agc tgt gtt tgg aac tgc	1262
Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys	
225 230 235	
tac cga tac atc aat ggt agg aac tcc tct gat gtc ctg gtt tat gtt	1310
Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu Val Tyr Val	
240 245 250	
acc agc aat gac act acg gtg ctg cta ccc ccg tat gat gat gcc act	1358
Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr	
255 260 265	
gtg aat ggt gct gcc aag gag cca ccg cca cct tac gtg tct gcc taa	1406
Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Tyr Val Ser Ala *	
270 275 280	

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 Met
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 Leu Pro Gly Ala Trp Leu Leu Trp Thr Ser Leu Leu Leu Ala Arg
 5 10 15

cct gcc cag ccc tgt ccc atg ggt tgt gac tgc ttc gtc cag gag gtg Pro Ala Gln Pro Cys Pro Met Gly Cys Asp Cys Phe Val Gln Glu Val 20 25 30	153
ttc tgc tca gat gag gag ctt gcc acc gtc ccg ctg gac atc ccg cca Phe Cys Ser Asp Glu Glu Leu Ala Thr Val Pro Leu Asp Ile Pro Pro 35 40 45	201
tat acg aaa aac atc atc ttt gtg gag acc tcg ttc acc aca ttg gaa Tyr Thr Lys Asn Ile Ile Phe Val Glu Thr Ser Phe Thr Thr Leu Glu 50 55 60 65	249
acc aga gct ttt ggc agt aac ccc aac ttg acc aag gtg gtc ttc ctc Thr Arg Ala Phe Gly Ser Asn Pro Asn Leu Thr Lys Val Val Phe Leu 70 75 80	297
aac act cag ctc tgc cag ttt agg ccg gat gcc ttt ggg ggg ctg ccc Asn Thr Gln Leu Cys Gln Phe Arg Pro Asp Ala Phe Gly Gly Leu Pro 85 90 95	345
agg ctg gag gac ctg gag gtc aca ggc agt agc ttc ttg aac ctc agc Arg Leu Glu Asp Leu Glu Val Thr Gly Ser Ser Phe Leu Asn Leu Ser 100 105 110	393
acc aac atc ttc tcc aac ctg acc tcg ctg ggc aag ctc acc ctc aac Thr Asn Ile Phe Ser Asn Leu Thr Ser Leu Gly Lys Leu Thr Leu Asn 115 120 125	441
ttc aac atg ctg gag gct ctg ccc gag ggt ctt ttc cag cac ctg gct Phe Asn Met Leu Glu Ala Leu Pro Glu Gly Leu Phe Gln His Leu Ala 130 135 140 145	489
gcc ctg gag tcc ctc cac ctg cag ggg aac cag ctc cag gcc ctg ccc Ala Leu Glu Ser Leu His Leu Gln Gly Asn Gln Leu Gln Ala Leu Pro 150 155 160	537
agg agg ctc ttc cag cct ctg acc cat ctg aag aca ctc aac ctg gcc Arg Arg Leu Phe Gln Pro Leu Thr His Leu Lys Thr Leu Asn Leu Ala 165 170 175	585
cag aac ctc ctg gcc cag ctc ccg gag gag ctg ttc cac cca ctc acc Gln Asn Leu Leu Ala Gln Leu Pro Glu Glu Leu Phe His Pro Leu Thr 180 185 190	633
agc ctg cag acc ctg aag ctg agc aac aac gcg ctc tct ggt ctc ccc Ser Leu Gln Thr Leu Lys Leu Ser Asn Asn Ala Leu Ser Gly Leu Pro 195 200 205	681
cag ggt gtg ttt ggc aaa ctg ggc agc ctg cag gag ctc ttc ctg gac Gln Gly Val Phe Gly Lys Leu Gly Ser Leu Gln Glu Leu Phe Leu Asp 210 215 220 225	729
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tgc cta gag agg ctg tgg ctg caa cgc aac gcc atc acg cac ctg ccg	825

Cys	Leu	Glu	Arg	Leu	Trp	Leu	Gln	Arg	Asn	Ala	Ile	Thr	His	Leu	Pro		
			245					250					255				
ctc	tcc	atc	ttt	gcc	tcc	ctg	ggt	aat	ctg	acc	ttt	ctg	agc	ttg	cag	873	
Leu	Ser	Ile	Phe	Ala	Ser	Leu	Gly	Asn	Leu	Thr	Phe	Leu	Ser	Leu	Gln		
		260					265					270					
tgg	aac	atg	ctt	cgg	gtc	ctg	cct	gcc	ggc	ctc	ttt	gcc	cac	acc	cca	921	
Trp	Asn	Met	Leu	Arg	Val	Leu	Pro	Ala	Gly	Leu	Phe	Ala	His	Thr	Pro		
	275					280					285						
tgc	ctg	gtt	ggc	ctg	tct	ctg	acc	cat	aac	cag	ctg	gag	act	gtc	gct	969	
Cys	Leu	Val	Gly	Leu	Ser	Leu	Thr	His	Asn	Gln	Leu	Glu	Thr	Val	Ala		
290					295					300					305		
gag	ggc	acc	ttt	gcc	cac	ctg	tcc	aac	ctg	cgt	tcc	ctc	atg	ctc	tca	1017	
Glu	Gly	Thr	Phe	Ala	His	Leu	Ser	Asn	Leu	Arg	Ser	Leu	Met	Leu	Ser		
			310						315					320			
tac	aat	gcc	att	acc	cac	ctc	cca	gct	ggc	atc	ttc	aga	gac	ctg	gag	1065	
Tyr	Asn	Ala	Ile	Thr	His	Leu	Pro	Ala	Gly	Ile	Phe	Arg	Asp	Leu	Glu		
		325						330					335				
gag	ttg	gtc	aaa	ctc	tac	ctg	ggc	agc	aac	aac	ctt	acg	gcg	ctg	cac	1113	
Glu	Leu	Val	Lys	Leu	Tyr	Leu	Gly	Ser	Asn	Asn	Leu	Thr	Ala	Leu	His		
		340					345					350					
cca	gcc	ctc	ttc	cag	aac	ctg	tcc	aag	ctg	gag	ctg	ctc	agc	ctc	tcc	1161	
Pro	Ala	Leu	Phe	Gln	Asn	Leu	Ser	Lys	Leu	Glu	Leu	Leu	Ser	Leu	Ser		
		355				360					365						
aag	aac	cag	ctg	acc	aca	ctt	ccg	gag	ggc	atc	ttc	gac	acc	aac	tac	1209	
Lys	Asn	Gln	Leu	Thr	Thr	Leu	Pro	Glu	Gly	Ile	Phe	Asp	Thr	Asn	Tyr		
370					375					380					385		
aac	ctg	ttc	aac	ctg	gcc	ctg	cac	ggt	aac	ccc	tgg	cag	tgc	gac	tgc	1257	
Asn	Leu	Phe	Asn	Leu	Ala	Leu	His	Gly	Asn	Pro	Trp	Gln	Cys	Asp	Cys		
			390						395					400			
cac	ctg	gcc	tac	ctc	ttc	aac	tgg	ctg	cag	cag	tac	acc	gat	cgg	ctc	1305	
His	Leu	Ala	Tyr	Leu	Phe	Asn	Trp	Leu	Gln	Gln	Tyr	Thr	Asp	Arg	Leu		
		405						410					415				
ctg	aac	atc	cag	acc	tac	tgc	gct	ggc	cct	gcc	tac	ctc	aaa	ggc	cag	1353	
Leu	Asn	Ile	Gln	Thr	Tyr	Cys	Ala	Gly	Pro	Ala	Tyr	Leu	Lys	Gly	Gln		
		420					425					430					
gtg	gtg	ccc	gcc	ttg	aat	gag	aag	cag	ctg	gtg	tgt	ccc	gtc	acc	cgg	1401	
Val	Val	Pro	Ala	Leu	Asn	Glu	Lys	Gln	Leu	Val	Cys	Pro	Val	Thr	Arg		
		435				440					445						
gac	cac	ttg	ggc	ttc	cag	gtc	acg	tgg	ccg	gac	gaa	agc	aag	gca	ggg	1449	
Asp	His	Leu	Gly	Phe	Gln	Val	Thr	Trp	Pro	Asp	Glu	Ser	Lys	Ala	Gly		
450					455					460					465		
ggc	agc	tgg	gat	ctg	gct	gtg	cag	gaa	agg	gca	gcc	cgg	agc	cag	tgc	1497	
Gly	Ser	Trp	Asp	Leu	Ala	Val	Gln	Glu	Arg	Ala	Ala	Arg	Ser	Gln	Cys		

470	475	480	
acc tac agc aac ccc gag ggc acc	gtg gtg ctc gcc tgt gac cag gcc	1545	
Thr Tyr Ser Asn Pro Glu Gly Thr	Val Val Leu Ala Cys Asp Gln Ala		
485	490	495	
cag tgt cgc tgg ctg aac gtc cag	ctc tct cct cgg cag ggc tcc ctg	1593	
Gln Cys Arg Trp Leu Asn Val Gln	Leu Ser Pro Arg Gln Gly Ser Leu		
500	505	510	
gga ctg cag tac aat gct agt cag	gag tgg gac ctg agg tgc agc tgc	1641	
Gly Leu Gln Tyr Asn Ala Ser Gln	Glu Trp Asp Leu Arg Ser Ser Cys		
515	520	525	
ggg tct ctg cgg ctc acc gtg tct	atc gag gct cgg gca gca ggg ccc	1689	
Gly Ser Leu Arg Leu Thr Val Ser	Ile Glu Ala Arg Ala Ala Gly Pro		
530	535	540	545
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tcccaggtct tcagctaagc tcaaccaatt	gtcaaccaga aaatgtttaa atttacctac	2766	
agcctggaag caccacccc cgctgcttcg	agttgtcctg cctttctgaa ctcaaccaat	2826	

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 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly
 1 5 10
 cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg 157
 Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met
 15 20 25 30
 ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac 205
 Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His
 35 40 45
 atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc 253
 Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe
 50 55 60
 aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg 301
 Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala
 65 70 75
 tac tcc gtg aag tct agg gac agg aag atg gtt ggc gac gtg acc ggg 349
 Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly
 80 85 90
 gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg 397
 Ala Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu
 95 100 105 110
 att ttg ggc atc ttc atg acc att ctg ctc atc atc atc cca gtg ttg 445
 Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Ile Pro Val Leu
 115 120 125
 gtc gtc cag gcc cag cga tag at caggaggcat cattgaggcc aggagctctg 498
 Val Val Gln Ala Gln Arg *
 130

cccgtgagct gtatccacgt actctatctt ccattcttcg cctgccccca gaggccagag 558
ctctgccctt gactgtattc acttattcag ctccattctg cctgtccaaa gcgagtctga 618
ttagccttta caa 631

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<212> DNA
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<220>
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<222> (274)..(2271)

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cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgcct 180
ggatcccagc gcccgatcc cgggcggccc acccccacgc ccgcctccgc caactttcac 240
gctgcctcgg cggcccgccc cggtcgcagc cca atg gtg gag gcc ata gtg gag 294
Met Val Glu Ala Ile Val Glu
1 5
ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt 342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
10 15 20
gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga 390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
25 30 35
cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa 438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
40 45 50 55
ata aag aaa gag atg aag aaa gac cct ctg acc aac aaa gct cca gaa 486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
60 65 70
aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa 534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
75 80 85
acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc 582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
90 95 100
cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg 630

Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu	
105 110 115	
aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg	678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp	
120 125 130 135	
tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc	726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe	
140 145 150	
atc aag gag ctg tca ggg gag tcg gat gag ctt ggc att tcc cag gat	774
Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp	
155 160 165	
gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt	822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
170 175 180	
gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca	870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
185 190 195	
gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt	918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
200 205 210 215	
gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att	966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
220 225 230	
gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag	1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
235 240 245	
tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac	1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
250 255 260	
agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag	1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg	1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
300 305 310	
aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	

330	335	340	
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gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg 360 365 370 375			1398
aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag Thr Glu Glu Lys Glu Arg Pro Glu Arg Glu Pro Lys Leu Asp Leu Gln 380 385 390			1446
aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys 395 400 405			1494
acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu 410 415 420			1542
aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile 425 430 435			1590
gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser 440 445 450 455			1638
gac cgc agc aat gac att gac tta gaa ggt ttt gac tcc gtg gta tca Asp Arg Ser Asn Asp Ile Asp Leu Glu Gly Phe Asp Ser Val Val Ser 460 465 470			1686
tct act gag aaa ctc agt cat ccg acc aca agc aga cca aaa gct aca Ser Thr Glu Lys Leu Ser His Pro Thr Thr Ser Arg Pro Lys Ala Thr 475 480 485			1734
ggg agg cgg cct ccg tcc cag tcc ctc aca tct tca tcc ctt tca agc Gly Arg Arg Pro Pro Ser Gln Ser Leu Thr Ser Ser Ser Leu Ser Ser 490 495 500			1782
cct gat atc ttc gac tcc cca agt ccc gaa gag gat aag gag gaa cac Pro Asp Ile Phe Asp Ser Pro Ser Pro Glu Glu Asp Lys Glu Glu His 505 510 515			1830
att tca ctt gcg cac aga gga gtg gac gcg tca aag aaa act tcc aag Ile Ser Leu Ala His Arg Gly Val Asp Ala Ser Lys Lys Thr Ser Lys 520 525 530 535			1878
act gtt acc ata tcc caa gtg tct gac aac aaa gca tcc ctg ccg ccc Thr Val Thr Ile Ser Gln Val Ser Asp Asn Lys Ala Ser Leu Pro Pro 540 545 550			1926
aag ccg ggg acc atg gca gca ggt ggc ggt ggg cca gcc cct ctg tcc Lys Pro Gly Thr Met Ala Ala Gly Gly Gly Gly Pro Ala Pro Leu Ser 555 560 565			1974

<211> 2866
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 <213> Homo sapiens

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cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgccct      180
ggatcccagc gccccgatcc cggcgcccca acccccacgc ccgcctccgc caactttcac      240
gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
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Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
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gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga      390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
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cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa      438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
                               40                               45                               50                               55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa      486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
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aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa      534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
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acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc      582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
                               90                               95                               100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg      630
Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu
                               105                               110                               115

aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg      678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
                               120                               125                               130                               135

tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc      726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe
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Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
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Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
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gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt	918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
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gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att	966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
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Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
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Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
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agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag	1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
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Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
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aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	
330 335 340	
tcc gct cct gtc atc aaa caa ggg gca ggc acc act gag aga aaa cat	1350
Ser Ala Pro Val Ile Lys Gln Gly Ala Gly Thr Thr Glu Arg Lys His	
345 350 355	
gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga	1398
Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg	
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				380					385					390		
aag	ccc	tcc	gtt	cct	gcc	ata	ccg	cca	aaa	aag	cct	cgg	cca	cct	aag	1494
Lys	Pro	Ser	Val	Pro	Ala	Ile	Pro	Pro	Lys	Lys	Pro	Arg	Pro	Pro	Lys	
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Thr	Asn	Ser	Leu	Ser	Arg	Pro	Gly	Ala	Leu	Pro	Pro	Arg	Arg	Pro	Glu	
		410					415					420				
aga	ccg	gtg	ggc	ccg	ctg	aca	cac	acc	agg	ggc	gac	agt	cca	aag	att	1590
Arg	Pro	Val	Gly	Pro	Leu	Thr	His	Thr	Arg	Gly	Asp	Ser	Pro	Lys	Ile	
	425					430				435						
gac	ttg	gcc	ggc	agt	tcg	cta	tct	ggc	atc	ctg	gac	aaa	gat	ctc	tcg	1638
Asp	Leu	Ala	Gly	Ser	Ser	Leu	Ser	Gly	Ile	Leu	Asp	Lys	Asp	Leu	Ser	
440					445				450						455	
gac	cgc	agc	aat	gac	att	gac	tta	gaa	ggc	ttt	gac	tcc	gtg	gta	tca	1686
Asp	Arg	Ser	Asn	Asp	Ile	Asp	Leu	Glu	Gly	Phe	Asp	Ser	Val	Val	Ser	
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tct	act	gag	aaa	ctc	agt	cat	ccg	acc	aca	agc	aga	cca	aaa	gct	aca	1734
Ser	Thr	Glu	Lys	Leu	Ser	His	Pro	Thr	Thr	Ser	Arg	Pro	Lys	Ala	Thr	
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Gly	Arg	Arg	Pro	Pro	Ser	Gln	Ser	Leu	Thr	Ser	Val	Ser	Asp	Asn	Lys	
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Ala	Ser	Leu	Pro	Pro	Lys	Pro	Gly	Thr	Met	Ala	Ala	Gly	Gly	Gly	Gly	
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Pro	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Leu	
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Gly	Thr	Ala	Gly	His	Arg	Ala	Asn	Ser	Pro	Ser	Leu	Phe	Gly	Thr	Glu	
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Gly	Lys	Pro	Lys	Met	Glu	Pro	Ala	Ala	Ser	Ser	Gln	Ala	Ala	Val	Glu	
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Glu	Leu	Arg	Thr	Gln	Val	Arg	Glu	Leu	Arg	Ser	Ile	Ile	Glu	Thr	Met	
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Lys	Asp	Gln	Gln	Lys	Arg	Glu	Ile	Lys	Gln	Leu	Leu	Ser	Glu	Leu	Asp	
	585					590				595						
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Glu	Glu	Lys	Lys	Ile	Arg	Leu	Arg	Leu	Gln	Met	Glu	Val	Asn	Asp	Ile	

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Lys Lys Ala Leu Gln Ser Lys *				
620				
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cacaaattcc atccaagagg agaatcttcc ccagggttta gtcctggggc tggcactcgt				2352
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			Met Phe Arg Lys	

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Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro Gln Asn Phe Gln His	
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Arg Val His Thr Ser Phe Asp Pro Lys Glu Gly Lys Phe Val Gly Leu	
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Pro Pro Gln Trp Gln Asn Ile Leu Asp Thr Leu Arg Arg Pro Lys Pro	
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Val Val Asp Pro Ser Arg Ile Thr Arg Val Gln Leu Gln Pro Met Lys	
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Thr Val Val Arg Gly Ser Ala Met Pro Val Asp Gly Tyr Ile Ser Gly	
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Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr Leu	
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Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu	
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Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser	
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Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn	
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Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu	
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Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu Gly	
185 190 195	
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Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly Thr	
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Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala Arg	
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Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg Leu	
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Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser Ser	
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Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe Arg	
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Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln Ser	
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Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly	
325 330 335 340	
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Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His	
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Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val	
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Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu	
375 380 385	
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Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg	
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Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile	
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Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val Lys	
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440 445 450	

Gln Thr Ser Thr Cys *
680

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tctctccaaa gattgaaatg tgaagcccca gccccaccct ctgcccttca gcctactggg 2605
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ggtgacaggc gttgagacca ccgaagggaa ccc atg gct agg atc agt ttt tcc 174
Met Ala Arg Ile Ser Phe Ser
1 5
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Tyr Leu Cys Pro Ala Ser Trp Tyr Phe Thr Val Pro Thr Val Ser Pro
10 15 20
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Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys
25 30 35
ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318
Leu Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser
40 45 50 55

tta cca cga gat agg caa tac gaa agg tat ttg gct cga gta ggg gag Leu Pro Arg Asp Arg Gln Tyr Glu Arg Tyr Leu Ala Arg Val Gly Glu	366
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75 80 85	
gtt gac tgt ggc agc agt ggt tcc cgg att ttt gtt tat ttc tgg cca Val Asp Cys Gly Ser Ser Gly Ser Arg Ile Phe Val Tyr Phe Trp Pro	462
90 95 100	
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105 110 115	
gac cgc aac agc caa cca gtg gtt aaa aaa atc aag cca gga atc tct Asp Arg Asn Ser Gln Pro Val Val Lys Lys Ile Lys Pro Gly Ile Ser	558
120 125 130 135	
gca atg gca gac act cca gaa cat gcc agt gat tac ctt cgt cct ctg Ala Met Ala Asp Thr Pro Glu His Ala Ser Asp Tyr Leu Arg Pro Leu	606
140 145 150	
ctg agc ttt gct gct gct cat gtg cct gtg aag aag cac aag gag acc Leu Ser Phe Ala Ala Ala His Val Pro Val Lys Lys His Lys Glu Thr	654
155 160 165	
cct ctt tac atc ctc tgc aca gca ggc atg agg ctt ctc cct gag agg Pro Leu Tyr Ile Leu Cys Thr Ala Gly Met Arg Leu Leu Pro Glu Arg	702
170 175 180	
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185 190 195	
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200 205 210 215	
cag gaa ggg gtt tat gca tgg att gga atc aac ttt gtt ttg gga aga Gln Glu Gly Val Tyr Ala Trp Ile Gly Ile Asn Phe Val Leu Gly Arg	846
220 225 230	
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250 255 260	
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265 270 275	

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Lys Gln Glu Glu Ala Ala Lys Ile Leu Leu Ala Glu Phe Asn Leu Gly	
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Cys Asp Val Gln His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr	
300 305 310	
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Phe Leu Gly Phe Gly Gly Asn Phe Ala Arg Gln Arg Tyr Glu Asp Leu	
315 320 325	
gtt ctg aat gaa act ctt aac aaa aac aga ttg ctt ggt cag aag aca	1182
Val Leu Asn Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr	
330 335 340	
ggt ctg agt ccc gac aat cca ttt ctg gat ccc tgc ctg cca gtg gga	1230
Gly Leu Ser Pro Asp Asn Pro Phe Leu Asp Pro Cys Leu Pro Val Gly	
345 350 355	
ctc aca gat gtg gtg gag agg aac agc caa gtc tta cat gtc cga gga	1278
Leu Thr Asp Val Val Glu Arg Asn Ser Gln Val Leu His Val Arg Gly	
360 365 370 375	
aga gga gac tgg gtg tct tgt ggg gca atg ctg agc ccc ctg ctg gct	1326
Arg Gly Asp Trp Val Ser Cys Gly Ala Met Leu Ser Pro Leu Leu Ala	
380 385 390	
cgc tcc aac acc agc cag gcc tca ctc aat ggc ata tat caa tcg cct	1374
Arg Ser Asn Thr Ser Gln Ala Ser Leu Asn Gly Ile Tyr Gln Ser Pro	
395 400 405	
att gac ttc aac aac agc gag ttc tac ggc ttc tct gag ttt ttt tat	1422
Ile Asp Phe Asn Asn Ser Glu Phe Tyr Gly Phe Ser Glu Phe Phe Tyr	
410 415 420	
tgt aca gag gat gtg ttg cgc att ggt ggc cgc tac cat ggg cca aca	1470
Cys Thr Glu Asp Val Leu Arg Ile Gly Gly Arg Tyr His Gly Pro Thr	
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Phe Ala Lys Ala Ala Gln Asp Tyr Cys Gly Met Ala Trp Ser Val Leu	
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act cag aga ttc aag aat ggc ctc ttt tca tca cat gca gat gag cat	1566
Thr Gln Arg Phe Lys Asn Gly Leu Phe Ser Ser His Ala Asp Glu His	
460 465 470	
cga ctc aaa tat cag tgt ttt aaa tcg gct tgg atg tac caa gtc tta	1614
Arg Leu Lys Tyr Gln Cys Phe Lys Ser Ala Trp Met Tyr Gln Val Leu	
475 480 485	
cat gaa gga ttc cac ttt ccc tat gac tac cca aac ctg cgg aca gcc	1662
His Glu Gly Phe His Phe Pro Tyr Asp Tyr Pro Asn Leu Arg Thr Ala	
490 495 500	
cag ctg gtg tat gac cga gag gtt cag tgg acg ctg gga gcc att cta	1710

Gln	Leu	Val	Tyr	Asp	Arg	Glu	Val	Gln	Trp	Thr	Leu	Gly	Ala	Ile	Leu		
505						510					515						
tat	aaa	aca	cga	ttc	tta	cca	ctc	agg	gat	ctt	cgg	cag	gaa	ggt	gtc	1758	
Tyr	Lys	Thr	Arg	Phe	Leu	Pro	Leu	Arg	Asp	Leu	Arg	Gln	Glu	Gly	Val		
520					525					530					535		
cga	caa	gcc	cat	ggt	agc	tgg	ttc	cgt	ctc	tcc	ttt	gta	tac	aac	cac	1806	
Arg	Gln	Ala	His	Gly	Ser	Trp	Phe	Arg	Leu	Ser	Phe	Val	Tyr	Asn	His		
				540					545						550		
tat	ctc	ttc	ttt	gcc	tgt	atc	ctg	gtg	gtg	cta	ctg	gcc	atc	ttc	cta	1854	
Tyr	Leu	Phe	Phe	Ala	Cys	Ile	Leu	Val	Val	Leu	Leu	Ala	Ile	Phe	Leu		
				555				560							565		
tac	ctt	ctg	cgg	cta	cgc	cga	att	cac	cac	cga	caa	aca	cga	gcc	tca	1902	
Tyr	Leu	Leu	Arg	Leu	Arg	Arg	Ile	His	His	Arg	Gln	Thr	Arg	Ala	Ser		
				570				575							580		
gct	cca	ttg	gac	ttg	ctg	tgg	ctt	gaa	gag	gtg	gtg	ccc	atg	atg	gga	1950	
Ala	Pro	Leu	Asp	Leu	Leu	Trp	Leu	Glu	Glu	Val	Val	Pro	Met	Met	Gly		
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gta	cag	gtg	ggg	ccg	tga											1968	
Val	Gln	Val	Gly	Pro	*												
600					605												

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tttcaattag	ttactttttc	ttacaaggct	gggagaggga	gacagaacaa	tagaaaaata											180	
actggttgat	tcatatggag	gtcagagtgg	aagcaggtgt	gagagggtcc	cacagaagaa											240	
aacatggcag	ccaaagtgtt	tgagtccacg	gtaagtttgg	cttggcctta	gctgttgcag											300	
gagacctgtg	aactctgcct	tatataatgt	ggatgttggg	cacagagctg	tcatctttga											360	
ctgattccag	gacaaaaatg	acaggacatt	gtggtagggg	actcaatttc	tcatccc											417	
atg ggt aca	gaa acc aat	tat ctt tgc	ctt tct cca	cca cgt aat	gta											465	
Met Gly Thr	Glu Thr Asn	Tyr Leu Cys	Leu Ser Pro	Pro Arg Asn	Val												
1		5		10	15												

cca atc atc act ggt agc aaa gat tta cag aat gtc aat atc aca ctg	513
Pro Ile Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu	
20 25 30	
cgc atc atc ttc cag cct gtt gct agc cag ctt cct cgc atc ttc acc	561
Arg Ile Ile Phe Gln Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr	
35 40 45	
agc atc gga gag gac tat gat gag cct gtg ctg acg tac atc acg acc	609
Ser Ile Gly Glu Asp Tyr Asp Glu Pro Val Leu Thr Tyr Ile Thr Thr	
50 55 60	
gag atc ctc aag tca gtg gtg gct cgc ttt gat gct gga gaa gtt atc	657
Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly Glu Val Ile	
65 70 75 80	
act cag aga gag ctg gtc tcc agg cag gtg agc aac gac ctt acg gag	705
Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asn Asp Leu Thr Glu	
85 90 95	
caa gca gcc aca ttt ggg ctc atc ctg gac gac gtg tcc ttg aca tat	753
Gln Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr	
100 105 110	
ctg acc ttt gga aag gag ttc aca gaa gca gtg gaa gcc aaa cag gtg	801
Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val	
115 120 125	
gct cag cag gaa gca gag agg gcc aga ttt gtg aag gaa aag gct gag	849
Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Lys Glu Lys Ala Glu	
130 135 140	
cag cag aaa aag gct gag cag cag aaa aag gtt gag cag cag aaa aag	897
Gln Gln Lys Lys Ala Glu Gln Gln Lys Lys Val Glu Gln Gln Lys Lys	
145 150 155 160	
gca gcc gtg atc tct gct gag ggc gac tcc aag gca acc gag ctg att	945
Ala Ala Val Ile Ser Ala Glu Gly Asp Ser Lys Ala Thr Glu Leu Ile	
165 170 175	
gcc aac tca ctg gcc acc gcg ggg gac ggc ctg atg gag ctg tgc aag	993
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Met Glu Leu Cys Lys	
180 185 190	
ttg gaa gcc gcg gag gct ctc gga aca tga c ctacctgccg gcggggcagt	1044
Leu Glu Ala Ala Glu Ala Leu Gly Thr *	
195 200	
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ccacagcccc aatgattctt aacactgcct taccctcccta cccagaaat cactgaaatt	1164
tcataattgg cttaaagtga aggaaataaa agtaaaatca cttcagaact cttaaaaaaa	1224
aaaaa	1229

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 <213> Homo sapiens

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<400> 44

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ggagctgccca atcaaaagtg gcattac      atg aaa aat ata aaa gca ctt gtg      111
                                   Met Lys Asn Ile Lys Ala Leu Val
                                   1                               5

gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat      159
Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr
    10                               15                               20

gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa      207
Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln
    25                               30                               35                               40

cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc      255
Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu
                                45                               50                               55

tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa      303
Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln
                                60                               65                               70

ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag      351
Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln
    75                               80                               85

aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt      399
Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val
    90                               95                               100

gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca      447
Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala
   105                               110                               115                               120

cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac      495
Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His
    125                               130                               135

agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac      543
Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr
    140                               145                               150

aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca      591
Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr

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155	160	165	
ttc ccc atg ctt ctt aca gaa tgc acg gaa caa ctt ggg ctt gcc aga			639
Phe Pro Met Leu Leu Thr	Glu Cys Thr	Glu Gln Leu Gly Leu Ala Arg	
170	175	180	
gca gcc tcc aaa gta tat acc aaa gat gga acc cca atc ttt acc ttg			687
Ala Ala Ser Lys Val Tyr Thr Lys Asp Gly Thr Pro Ile Phe Thr Leu			
185	190	195	200
cgt gat ttg gtt tta tgg gct cta gat gaa tcc ttt ctc cag aga gac			735
Arg Asp Leu Val Leu Trp Ala Leu Asp	Glu Ser Phe Leu Gln Arg Asp		
205	210	215	
tct gag aaa caa aag caa gat gca gct cct gtt gga aaa gaa cag ata			783
Ser Glu Lys Gln Lys Gln Asp Ala Ala Pro Val Gly Lys Glu Gln Ile			
220	225	230	
att gtt gaa agt atg gaa gaa aat cca aga atg aaa gtg aaa aac aga			831
Ile Val Glu Ser Met Glu Glu Asn Pro Arg Met Lys Val Lys Asn Arg			
235	240	245	
tta ttt gca aaa tct gtg aca tcc gat agt ttg gat ggt ata gac aag			879
Leu Phe Ala Lys Ser Val Thr Ser Asp Ser Leu Asp Gly Ile Asp Lys			
250	255	260	
tct ttg ctt acc ctc atc ctc aga aat cct att gcc atc tgg gtg tct			927
Ser Leu Leu Thr Leu Ile Leu Arg Asn Pro Ile Ala Ile Trp Val Ser			
265	270	275	280
tgt ggt gaa cca ttt cta cct cca aat gct ttg cag aaa gca gaa aaa			975
Cys Gly Glu Pro Phe Leu Pro Pro Asn Ala Leu Gln Lys Ala Glu Lys			
285	290	295	
tta gag aaa cag aac tgg cta aaa aag gac aga att ttg gct gat cta			1023
Leu Glu Lys Gln Asn Trp Leu Lys Lys Asp Arg Ile Leu Ala Asp Leu			
300	305	310	
gat acc atg aga cac aaa atg aga cag tta aaa ggg cgg cga gta gcg			1071
Asp Thr Met Arg His Lys Met Arg Gln Leu Lys Gly Arg Arg Val Ala			
315	320	325	
gca tgt cag cca gcc acc atg gtt cct acc aag agc cct gtg cag ccc			1119
Ala Cys Gln Pro Ala Thr Met Val Pro Thr Lys Ser Pro Val Gln Pro			
330	335	340	
gtg gtg gtt gaa gga ggc tgg acc gaa cag act caa cag gaa att aaa			1167
Val Val Val Glu Gly Gly Trp Thr Glu Gln Thr Gln Gln Glu Ile Lys			
345	350	355	360
ctc atg gaa ctt ata aga cat aca gag gca cac ctt tct gaa atc caa			1215
Leu Met Glu Leu Ile Arg His Thr Glu Ala His Leu Ser Glu Ile Gln			
365	370	375	
gaa atg gaa tcc aaa ata aat ttt cca att gca acc aaa cgt ata gca			1263
Glu Met Glu Ser Lys Ile Asn Phe Pro Ile Ala Thr Lys Arg Ile Ala			
380	385	390	

gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg 1311
Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp
395 400 405

att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc 1359
Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly
410 415 420

aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg 1407
Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met
425 430 435 440

acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag 1455
Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln
445 450 455

tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga 1503
Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly
460 465 470

cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga 1551
His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg
475 480 485

gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac 1599
Ala Asn Tyr Ala Arg Ile Arg Arg Gln Gln Gly Pro Gln Ala Thr Asp
490 495 500

att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac 1647
Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His
505 510 515 520

aat taa ctctatcag aaccatcgga ttttctgctg tatttttctg gaaagaaaac 1703
Asn *

tttctttacc cacttataaa cagaagactg tgacaagaag gccattatt tccatcgctg 1763

aagactctaa atttggaata tcttctaaat aacaatcctg catagtattat taaaaaaaaat 1823

tagtcgtaaa atttatcctt caaaaatctg catttttaaata aaaccctgac agtgattttct 1883

caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt 1943

tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt 2003

gggacagata gtacaactga aataaaaagt ggaggcctct gcaaaaaata aaaaataaaa 2063

aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctatttttt aagaatgaac 2123

attgaaaaat gagacaatat atccataaat tcatagtatg acataccata 2173

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<220>
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agctgtaaca tgtaaatcag aactacctgg catcttctctg aacaagactt tcaatagggg      180
ccagt      atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag      227
           Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
           1             5             10

ata ctg aag tac tct ttc cca gtg gga cta aga acc agc aga aca gat      275
Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
   15             20             25             30

ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca      323
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
           35             40             45

agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag      371
Arg Pro Trp Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
           50             55             60

tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca      419
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
           65             70             75

ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
           80             85             90

aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct      515
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
           95             100             105             110

cca cca ctg gtc atg ctg atg aca aaa act tat att ccc ata tta gct      563
Pro Pro Leu Val Met Leu Met Thr Lys Thr Tyr Ile Pro Ile Leu Ala
           115             120             125

ttt act cag atg gct tat gga gcc agt ttc cta tct ttc ttg ggt ggg      611
Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
           130             135             140

atc aga tgg ggt ttt gct cta cca gaa ggt agt cca gcc aaa cca gac      659

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Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp	
145 150 155	
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Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe	
160 165 170	
gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata	755
Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile	
175 180 185 190	
atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat	803
Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His	
195 200 205	
tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc	851
Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala	
210 215 220	
act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa	899
Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu	
225 230 235	
aaa gga cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag	950
Lys Gly His Lys Arg Pro Gly Gln Val *	
240 245	
tgaggagcac ctctgccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg	1010
ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca	1070
cgtgtgaagt gacagccttg tgtgtgatct tttctgtctt cccaagtgtt gcattttcga	1130
cattaaagtt tacttttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan	1190
aacatgtgtn tgccagctac acctttctcn atttctgttt ggcttttttt cccacacca	1250
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acttgagcaa aagcttgaaa atccctgaca agtacttntc atctcatagt atattagttt	1370
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gc	1432

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 <222> (269) .. (1372)

<400> 46

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cctctctcag tccaaaagcg gcttttgggt cggcgagag agaccgggg gtctagcttt	180
tcctcgaaaa gcgcgcgcct gcccttggcc ccgagaacag acaaagagca ccgcagggcc	240
gatcacgtg ggggcgctga ggccggcc atg gtc atg gaa gtg ggc acc ctg	292
Met Val Met Glu Val Gly Thr Leu	
1 5	
gac gct gga ggc ctg cgg gcg ctg ctg ggg gag cga gcg gcg caa tgc	340
Asp Ala Gly Gly Leu Arg Ala Leu Leu Gly Glu Arg Ala Ala Gln Cys	
10 15 20	
ctg ctg ctg gac tgc cgc tcc ttc ttc gct ttc aac gcc ggc cac atc	388
Leu Leu Leu Asp Cys Arg Ser Phe Phe Ala Phe Asn Ala Gly His Ile	
25 30 35 40	
gcc ggc tct gtc aac gtg cgc ttc agc acc atc gtg cgg cgc cgg gcc	436
Ala Gly Ser Val Asn Val Arg Phe Ser Thr Ile Val Arg Arg Arg Ala	
45 50 55	
aag ggc gcc atg ggc ctg gag cac atc gtg ccc aac gcc gag ctc cgc	484
Lys Gly Ala Met Gly Leu Glu His Ile Val Pro Asn Ala Glu Leu Arg	
60 65 70	
ggc cgc ctg ctg gcc ggc gcc tac cac gcc gtg gtg ttg ctg gac gag	532
Gly Arg Leu Leu Ala Gly Ala Tyr His Ala Val Val Leu Leu Asp Glu	
75 80 85	
cgc agc gcc gcc ctg gac ggc gcc aag cgc gac ggc acc ctg gcc ctg	580
Arg Ser Ala Ala Leu Asp Gly Ala Lys Arg Asp Gly Thr Leu Ala Leu	
90 95 100	
gcg gcc ggc gcg ctc tgc cgc gag gcg cgc gcc gcg caa gtc ttc ttc	628
Ala Ala Gly Ala Leu Cys Arg Glu Ala Arg Ala Ala Gln Val Phe Phe	
105 110 115 120	
ctc aaa gga gga tac gaa gcg ttt tcg gct tcc tgc ccg gag ctg tgc	676
Leu Lys Gly Gly Tyr Glu Ala Phe Ser Ala Ser Cys Pro Glu Leu Cys	
125 130 135	
agc aaa cag tcg acc ccc atg ggg ctc agc ctt ccc ctg agt act agc	724
Ser Lys Gln Ser Thr Pro Met Gly Leu Ser Leu Pro Leu Ser Thr Ser	
140 145 150	
gtc cct gac agc gcg gaa tct ggg tgc agt tcc tgc agt acc cca ctc	772
Val Pro Asp Ser Ala Glu Ser Gly Cys Ser Ser Cys Ser Thr Pro Leu	
155 160 165	
tac gat cag ggt ggc ccg gtg gaa atc ctg ccc ttt ctg tac ctg ggc	820
Tyr Asp Gln Gly Gly Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly	
170 175 180	

agt gcg tat cac gct tcc cgc aag gac atg ctg gat gcc ttg ggc ata	868
Ser Ala Tyr His Ala Ser Arg Lys Asp Met Leu Asp Ala Leu Gly Ile	
185 190 195 200	
act gcc ttg atc aac gtc tca gcc aat tgt ccc aac cat ttt gag ggt	916
Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro Asn His Phe Glu Gly	
205 210 215	
cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac	964
His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp	
220 225 230	
atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag	1012
Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys	
235 240 245	
aat gct gga gga agg gtg ttt gtc cac tgc cag gca ggc att tcc cgg	1060
Asn Ala Gly Gly Arg Val Phe Val His Cys Gln Ala Gly Ile Ser Arg	
250 255 260	
tca gcc acc atc tgc ctt gct tac ctt atg agg act aat cga gtc aag	1108
Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg Thr Asn Arg Val Lys	
265 270 275 280	
ctg gac gag gcc ttt gag ttt gtg aag cag agg cga agc atc atc tct	1156
Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg Arg Ser Ile Ile Ser	
285 290 295	
ccc aac ttc agc ttc atg ggc cag ctg ctg cag ttt gag tcc cag gtg	1204
Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln Phe Glu Ser Gln Val	
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ctg gct ccg cac tgt tgc gca gag gct ggg agc ccc gcc atg gct gtg	1252
Leu Ala Pro His Cys Ser Ala Glu Ala Gly Ser Pro Ala Met Ala Val	
315 320 325	
ctc gac cga ggc acc tcc acc acc acc gtg ttc aac ttc ccc gtc tcc	1300
Leu Asp Arg Gly Thr Ser Thr Thr Val Phe Asn Phe Pro Val Ser	
330 335 340	
atc cct gtc cac tcc acg aac agt gcg ctg agc tac ctt cag agc ccc	1348
Ile Pro Val His Ser Thr Asn Ser Ala Leu Ser Tyr Leu Gln Ser Pro	
345 350 355 360	
att acg acc tct ccc agc tgc tga aaggccacgg gaggtgagggc tcttcacatc	1402
Ile Thr Thr Ser Pro Ser Cys *	
365	
ccattggggac tccatgctcc ttgagaggag aaatgcaata actctgggag gggctcgaga	1462
gggctgggtcc ttatttatatt aacttcaccc gagttcctct gggtttctaa gcagttatgg	1522
tgatgactta gcgtcaagac atttgctgaa ctgagcatat tcgggaccaa tatatagtgg	1582
gtacatcaag tccatctgac aaaatggggc agaagagaaa ggactcagtg tgtgatccgg	1642
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 ctgccttcac aaatgtcatt gtctactcct agaagaacca aatacctcaa tttttgtttt 1822
 tgagtactgt actatcctgt aaatatatct taagcaggtt tgttttcagc actgatggaa 1882
 aataccagtg ttgggttttt ttttagttgc caacagttgt atgtttgctg attatttatg 1942
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 cattatgatg tgtttatgtt cacagaaatt tttgtaattt ctctatggta acaacttttt 180
 atgccttaag agtgtctctg aggcaggatt ctaagagatt ctctttgact caatcccaga 240
 tagaggataa atctcctggc aaagcccaga atg acc aca gcc ctg gaa cct 291
 Met Thr Thr Ala Leu Glu Pro
 1 5
 gag gac caa aaa gga ctt ctg ata att aag gca gag gac cat tac tgg 339
 Glu Asp Gln Lys Gly Leu Leu Ile Ile Lys Ala Glu Asp His Tyr Trp
 10 15 20
 gga cag gat tcc agc tca caa aag tgc agt cct cac agg agg gaa ctc 387
 Gly Gln Asp Ser Ser Ser Gln Lys Cys Ser Pro His Arg Arg Glu Leu
 25 30 35
 tat aga caa cac ttc agg aag ctc tgc tat cag gat gca cct gga ccc 435
 Tyr Arg Gln His Phe Arg Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro
 40 45 50 55
 cgt gaa gct ctt acc cag ctg tgg gag ctc tgc cgt cag tgg ctg agg 483
 Arg Glu Ala Leu Thr Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg
 60 65 70
 cca gaa tgc cac acc aag gag cag att tta gac ctg ctg gtg cta gaa 531
 Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu
 75 80 85

cag ttc ctg agc att ctt cct aaa gac ctg caa gca tgg gtg cgt gca Gln Phe Leu Ser Ile Leu Pro Lys Asp Leu Gln Ala Trp Val Arg Ala 90 95 100	579
cac cat cca gag act gga gag gag gca gtg acg gta ctg gag gat ctg His His Pro Glu Thr Gly Glu Glu Ala Val Thr Val Leu Glu Asp Leu 105 110 115	627
gag aga gag ctt gat gaa cct gga aag cag gtc cca ggc aat tca gaa Glu Arg Glu Leu Asp Glu Pro Gly Lys Gln Val Pro Gly Asn Ser Glu 120 125 130 135	675
aga cgg gac ata ctc atg gac aag ttg gcc ccc ttg gga agg cca tat Arg Arg Asp Ile Leu Met Asp Lys Leu Ala Pro Leu Gly Arg Pro Tyr 140 145 150	723
gaa tca ctg act gtc cag ctc cat ccc aaa aag acc cag ctg gag cag Glu Ser Leu Thr Val Gln Leu His Pro Lys Lys Thr Gln Leu Glu Gln 155 160 165	771
gaa gct ggg aaa cca caa agg aat ggt gat aaa act agg act aag aat Glu Ala Gly Lys Pro Gln Arg Asn Gly Asp Lys Thr Arg Thr Lys Asn 170 175 180	819
gaa gag ttg ttc cag aag gaa gat atg ccc aaa gac aag gaa ttc ctt Glu Glu Leu Phe Gln Lys Glu Asp Met Pro Lys Asp Lys Glu Phe Leu 185 190 195	867
ggg gag ata aat gac aga ctg aac aaa gat act cct cag cat cct aag Gly Glu Ile Asn Asp Arg Leu Asn Lys Asp Thr Pro Gln His Pro Lys 200 205 210 215	915
tcc aaa gat att att gaa aat gag ggc aga tca gaa tgg caa cag agg Ser Lys Asp Ile Ile Glu Asn Glu Gly Arg Ser Glu Trp Gln Gln Arg 220 225 230	963
gaa aga aga cga tat aaa tgt gat gaa tgt ggg aaa agt ttc agt cat Glu Arg Arg Arg Tyr Lys Cys Asp Glu Cys Gly Lys Ser Phe Ser His 235 240 245	1011
agc tca gac ctt agt aaa cac agg aga act cac acg gga gag aag ccc Ser Ser Asp Leu Ser Lys His Arg Arg Thr His Thr Gly Glu Lys Pro 250 255 260	1059
tat aaa tgt gat gag tgt gga aaa gcc ttc att cag cgc tca cat ctc Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Ile Gln Arg Ser His Leu 265 270 275	1107
att gga cat cat aga gta cac acg gga gta aaa ccc tat aaa tgt aaa Ile Gly His His Arg Val His Thr Gly Val Lys Pro Tyr Lys Cys Lys 280 285 290 295	1155
gaa tgt ggg aaa gac ttc agt ggg cgc aca ggt ctt att cag cat cag Glu Cys Gly Lys Asp Phe Ser Gly Arg Thr Gly Leu Ile Gln His Gln 300 305 310	1203

gaa aaa ctg aag gtg caa gtt act gat acc aac cga agg ttt caa gat	535
Glu Lys Leu Lys Val Gln Val Thr Asp Thr Asn Arg Arg Phe Gln Asp	
70 75 80	
gct gga aaa gag gtg ata gtc cac aca gaa gat atc att cga tgt aga	583
Ala Gly Lys Glu Val Ile Val His Thr Glu Asp Ile Ile Arg Cys Arg	
85 90 95	
att cag cag aga aat att aca act gta gta gaa aaa ttg cag tta tgc	631
Ile Gln Gln Arg Asn Ile Thr Thr Val Val Glu Lys Leu Gln Leu Cys	
100 105 110	
ctt cct gtg cta gaa atg tac agt aag ctg aaa gaa cag atg agt gcc	679
Leu Pro Val Leu Glu Met Tyr Ser Lys Leu Lys Glu Gln Met Ser Ala	
115 120 125 130	
aaa agg tac tat tct gcc cta aaa act atg gaa caa tta gag aat gtg	727
Lys Arg Tyr Tyr Ser Ala Leu Lys Thr Met Glu Gln Leu Glu Asn Val	
135 140 145	
tac ttt ccc tgg gtt agt caa tac cgg ttt tgt cag ctc atg ata gaa	775
Tyr Phe Pro Trp Val Ser Gln Tyr Arg Phe Cys Gln Leu Met Ile Glu	
150 155 160	
aat ctt ccc aaa ctc cgt gag gat att aaa gaa atc tcc atg tct gat	823
Asn Leu Pro Lys Leu Arg Glu Asp Ile Lys Glu Ile Ser Met Ser Asp	
165 170 175	
ctc aaa gac ttt ttg gaa agt att cga aaa cat tct gac aaa ata ggt	871
Leu Lys Asp Phe Leu Glu Ser Ile Arg Lys His Ser Asp Lys Ile Gly	
180 185 190	
gaa aca gca atg aaa cag gca cag cat cag aaa acc ttc agt gtt tct	919
Glu Thr Ala Met Lys Gln Ala Gln His Gln Lys Thr Phe Ser Val Ser	
195 200 205 210	
ctg cag aaa caa aat aaa atg aaa ttt ggg aaa aat atg tat ata aat	967
Leu Gln Lys Gln Asn Lys Met Lys Phe Gly Lys Asn Met Tyr Ile Asn	
215 220 225	
cgt gat aga att cca gag gaa agg aat gaa act gta ttg aaa cat tca	1015
Arg Asp Arg Ile Pro Glu Glu Arg Asn Glu Thr Val Leu Lys His Ser	
230 235 240	
ctt gaa gaa gag gat gag aat gaa gaa gag atc tta act gtt cag gat	1063
Leu Glu Glu Glu Asp Glu Asn Glu Glu Glu Ile Leu Thr Val Gln Asp	
245 250 255	
ctt gtt gat ttt tcc cct gtt tat cga tgt ttg cac att tat tct gtt	1111
Leu Val Asp Phe Ser Pro Val Tyr Arg Cys Leu His Ile Tyr Ser Val	
260 265 270	
ttg ggt gac gag gaa aca ttt gaa aac tat tat cga aaa caa aga aag	1159
Leu Gly Asp Glu Glu Thr Phe Glu Asn Tyr Tyr Arg Lys Gln Arg Lys	
275 280 285 290	
aaa caa gca aga ctg gta ttg caa ccc cag tcg aat atg cat gaa aca	1207

Lys	Gln	Ala	Arg	Leu	Val	Leu	Gln	Pro	Gln	Ser	Asn	Met	His	Glu	Thr		
				295					300					305			
gtt	gat	ggc	tat	aga	aga	tat	ttc	act	caa	att	gta	ggg	ttc	ttt	gtg	1255	
Val	Asp	Gly	Tyr	Arg	Arg	Tyr	Phe	Thr	Gln	Ile	Val	Gly	Phe	Phe	Val		
			310					315					320				
gta	gaa	gat	cac	att	tta	cat	gtg	acc	caa	gga	tta	gta	acc	agg	gca	1303	
Val	Glu	Asp	His	Ile	Leu	His	Val	Thr	Gln	Gly	Leu	Val	Thr	Arg	Ala		
			325				330					335					
tac	act	gat	gaa	ctt	tgg	aac	atg	gcc	ctc	tca	aag	ata	att	gct	gtc	1351	
Tyr	Thr	Asp	Glu	Leu	Trp	Asn	Met	Ala	Leu	Ser	Lys	Ile	Ile	Ala	Val		
	340					345					350						
ctt	aga	gct	cat	tca	tcc	tat	tgc	act	gat	cct	gat	ctt	gtt	ctg	gag	1399	
Leu	Arg	Ala	His	Ser	Ser	Tyr	Cys	Thr	Asp	Pro	Asp	Leu	Val	Leu	Glu		
355					360					365				370			
ctg	aag	aat	ctt	act	gta	ata	ttt	gca	gat	act	tta	cag	ggt	tat	ggt	1447	
Leu	Lys	Asn	Leu	Thr	Val	Ile	Phe	Ala	Asp	Thr	Leu	Gln	Gly	Tyr	Gly		
			375					380						385			
ttt	cca	gtg	aac	cga	ctt	ttt	gac	ctt	tta	ttt	gaa	ata	aga	gac	caa	1495	
Phe	Pro	Val	Asn	Arg	Leu	Phe	Asp	Leu	Leu	Phe	Glu	Ile	Arg	Asp	Gln		
			390				395					400					
tac	aat	gaa	aca	ctg	ctt	aag	aaa	tgg	gct	gga	gtt	ttc	agg	gac	att	1543	
Tyr	Asn	Glu	Thr	Leu	Leu	Lys	Lys	Trp	Ala	Gly	Val	Phe	Arg	Asp	Ile		
	405					410						415					
ttt	gaa	gaa	gat	aat	tac	agc	ccc	atc	cct	gtt	gtc	aat	gaa	gaa	gaa	1591	
Phe	Glu	Glu	Asp	Asn	Tyr	Ser	Pro	Ile	Pro	Val	Val	Asn	Glu	Glu	Glu		
	420				425					430							
tat	aaa	att	gtc	atc	agc	aaa	ttt	ccc	ttt	caa	gat	cca	gac	ctt	gaa	1639	
Tyr	Lys	Ile	Val	Ile	Ser	Lys	Phe	Pro	Phe	Gln	Asp	Pro	Asp	Leu	Glu		
435				440					445					450			
aag	cag	tct	ttc	cca	aag	aaa	ttc	ccc	atg	tct	cag	tca	gtg	cct	cat	1687	
Lys	Gln	Ser	Phe	Pro	Lys	Lys	Phe	Pro	Met	Ser	Gln	Ser	Val	Pro	His		
			455					460					465				
att	tac	att	caa	gtt	aaa	gaa	ttt	att	tat	gcc	agc	ctt	aaa	ttt	tca	1735	
Ile	Tyr	Ile	Gln	Val	Lys	Glu	Phe	Ile	Tyr	Ala	Ser	Leu	Lys	Phe	Ser		
			470					475					480				
gag	tca	cta	cac	cgg	agc	tca	aca	gaa	ata	gac	gat	atg	ctt	aga	aaa	1783	
Glu	Ser	Leu	His	Arg	Ser	Ser	Thr	Glu	Ile	Asp	Asp	Met	Leu	Arg	Lys		
			485				490					495					
tca	aca	aat	ctg	ctg	ctg	acc	aga	act	ttg	agt	agc	tgt	tta	ctg	aac	1831	
Ser	Thr	Asn	Leu	Leu	Leu	Thr	Arg	Thr	Leu	Ser	Ser	Cys	Leu	Leu	Asn		
	500					505					510						
ctt	att	aga	aaa	cct	cat	ata	ggt	ttg	aca	gag	ctg	gta	caa	atc	atc	1879	
Leu	Ile	Arg	Lys	Pro	His	Ile	Gly	Leu	Thr	Glu	Leu	Val	Gln	Ile	Ile		

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ata aac aca aca cac ctg gag caa gct tgt aaa tat ctt gag gac ttt				1927
Ile Asn Thr Thr His Leu Glu Gln Ala Cys Lys Tyr Leu Glu Asp Phe	535	540	545	
ata act aac att aca aat att tcc caa gaa act gtt cat act aca aga				1975
Ile Thr Asn Ile Thr Asn Ile Ser Gln Glu Thr Val His Thr Thr Arg	550	555	560	
ctt tat gga ctt tct act ttc aag gat gct cga cat gca gca gaa gga				2023
Leu Tyr Gly Leu Ser Thr Phe Lys Asp Ala Arg His Ala Ala Glu Gly	565	570	575	
gaa ata tat acc aaa ctg aat caa aaa att gat gaa ttt gtt cag ctt				2071
Glu Ile Tyr Thr Lys Leu Asn Gln Lys Ile Asp Glu Phe Val Gln Leu	580	585	590	
gct gat tat gac tgg aca atg tct gag cca gat gga aga gct agt ggt				2119
Ala Asp Tyr Asp Trp Thr Met Ser Glu Pro Asp Gly Arg Ala Ser Gly	595	600	605	610
tat tta atg gac ctt ata aat ttt ttg aga agc atc ttt caa gtg ttt				2167
Tyr Leu Met Asp Leu Ile Asn Phe Leu Arg Ser Ile Phe Gln Val Phe	615	620	625	
act cat ttg cct ggg aaa gtt gct cag aca gct tgc atg tca gcc tgc				2215
Thr His Leu Pro Gly Lys Val Ala Gln Thr Ala Cys Met Ser Ala Cys	630	635	640	
cag cat ctg tca aca tcc tta atg cag atg cta ctg gac agt gag tta				2263
Gln His Leu Ser Thr Ser Leu Met Gln Met Leu Leu Asp Ser Glu Leu	645	650	655	
aaa caa ata agc atg gga gct gtt cag cag ttt aac tta gat gtc ata				2311
Lys Gln Ile Ser Met Gly Ala Val Gln Gln Phe Asn Leu Asp Val Ile	660	665	670	
cag tgt gaa ttg ttt gcc agc tct gag cct gtg cca gga ttc cag ggg				2359
Gln Cys Glu Leu Phe Ala Ser Ser Glu Pro Val Pro Gly Phe Gln Gly	675	680	685	690
gat acc ctg cag cta gca ttc att gac ctc aga caa ctc ctt gac ctg				2407
Asp Thr Leu Gln Leu Ala Phe Ile Asp Leu Arg Gln Leu Leu Asp Leu	695	700	705	
ttt atg gtt tgg gat tgg tct act tac cta gct gat tat ggg cag cca				2455
Phe Met Val Trp Asp Trp Ser Thr Tyr Leu Ala Asp Tyr Gly Gln Pro	710	715	720	
gct tct aag tac ctt cgg gtg aat cca aac aca gcc ctt act ctt ttg				2503
Ala Ser Lys Tyr Leu Arg Val Asn Pro Asn Thr Ala Leu Thr Leu Leu	725	730	735	
gag aag atg aag gat act agc aaa aag aac aat ata ttt gct cag ttc				2551
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Lys	Lys	Glu	Ala	Pro	Ala	Pro	Pro	Lys	Ala	Glu	Ala	Lys	Ala	Lys	Ala	
				10					15					20		

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Leu	Gln	Gly	Gln	Glu	Gly	Ser	Val	Glu	Arg	Cys	Pro	Gln	Pro	Gln	Lys	
			25						30				35			

aaa	caa	gat	cca	cat	gtc	acc	cac	ctt	ccg	gcg	gcc	caa	gac	act	gtg	199
Lys	Gln	Asp	Pro	His	Val	Thr	His	Leu	Pro	Ala	Ala	Gln	Asp	Thr	Val	
		40					45					50				

act	ccg	gag	gca	gcc	caa	ata	tcc	ttg	gaa	gag	cac	ccc	cag	gag	aaa	247
Thr	Pro	Glu	Ala	Ala	Gln	Ile	Ser	Leu	Glu	Glu	His	Pro	Gln	Glu	Lys	
		55				60					65					

taa	gctt	gaccaccatg	ttatcatcaa	gtttccgctg	accactgagt	aggctgtgaa	304
*							
70							

gaagatagaa	aacaacagcc	tacttgtgtt	cactgtggat	gttaaagcca	acaagcacca	364
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gatcaaacag	gctgtgaaga	agtttgtgac	attgatgtgg	ccaaagtcaa	cactctgatt	424
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cagtctgatg	gagagaggaa	ggcatatggt	cgactggctc	ctgactacga	tgcttttggt	484
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gttgccacca	aaattgggat	cacctaaact	gagtcaagct	ggctaattcc	aaatatatgt	544
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<220>

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cggccccgga	gccctcggc	ggcgccacc	atg	tac	tcg	gga	gcc	ggc	ccc	gca	173
			Met	Tyr	Ser	Gly	Ala	Gly	Pro	Ala	
			1				5				

ctt gca cct cct gcg ccg ccg ccc ccc atc caa gga tat gcc ttc aag	221
Leu Ala Pro Pro Ala Pro Pro Pro Ile Gln Gly Tyr Ala Phe Lys	
10 15 20	
cct cca cct aga ccc gac ttt ggg acc tcc ggg aga aca atc aaa tta	269
Pro Pro Pro Arg Pro Asp Phe Gly Thr Ser Gly Arg Thr Ile Lys Leu	
25 30 35 40	
cag gcc aat ttc ttc gaa atg gac atc ccc aaa att gac atc tat cat	317
Gln Ala Asn Phe Phe Glu Met Asp Ile Pro Lys Ile Asp Ile Tyr His	
45 50 55	
tat gaa ttg gat atc aag cca gag aag tgc ccg agg aga gtt aac agg	365
Tyr Glu Leu Asp Ile Lys Pro Glu Lys Cys Pro Arg Arg Val Asn Arg	
60 65 70	
gaa atc gtg gaa cac atg gtc cag cac ttt aaa aca cag atc ttt ggg	413
Glu Ile Val Glu His Met Val Gln His Phe Lys Thr Gln Ile Phe Gly	
75 80 85	
gat cgg aag ccc gtg ttt gac ggc agg aag aat cta tac aca gcc atg	461
Asp Arg Lys Pro Val Phe Asp Gly Arg Lys Asn Leu Tyr Thr Ala Met	
90 95 100	
ccc ctt ccg att ggg agg gac aag gtg gag ctg gag gtc acg ctg cca	509
Pro Leu Pro Ile Gly Arg Asp Lys Val Glu Leu Glu Val Thr Leu Pro	
105 110 115 120	
gga gaa ggc aag gat cgc atc ttc aag gtg tcc atc aag tgg gtg tcc	557
Gly Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Val Ser	
125 130 135	
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Cys Val Ser Leu Gln Ala Leu His Asp Ala Leu Ser Gly Arg Leu Pro	
140 145 150	
agc gtc cct ttt gag acg atc cag gcc ctg gac gtg gtc atg agg cac	653
Ser Val Pro Phe Glu Thr Ile Gln Ala Leu Asp Val Val Met Arg His	
155 160 165	
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Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Thr Ala	
170 175 180	
tcc gaa ggc tgc tct aac cct ctt ggc ggg ggc cga gaa gtg tgg ttt	749
Ser Glu Gly Cys Ser Asn Pro Leu Gly Gly Gly Arg Glu Val Trp Phe	
185 190 195 200	
ggc ttc cat cag tcc gtc ccg cct tct ctc tgg aaa atg atg ctg aat	797
Gly Phe His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn	
205 210 215	
att gat gtg tca gca aca gcg ttt tac aag gca cag cca gta atc gag	845
Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu	
220 225 230	

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Phe Val Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys	
235 240 245	
cct ctg aca gat tcc caa agg gta aag ttt acc aaa gaa att aaa ggt	941
Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly	
250 255 260	
cta aag gtg gag ata acg cac tgt ggg cag atg aag agg aag tac cgt	989
Leu Lys Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg	
265 270 275 280	
gtc tgc aat gtg acc cgg cgg ccc gcc agt cac caa aca ttc ccg ctg	1037
Val Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu	
285 290 295	
cag cag gag agc ggg cag acg gtg gag tgc acg gtg gcc cag tat ttc	1085
Gln Gln Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe	
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Lys Asp Arg His Lys Leu Val Leu Arg Tyr Pro His Leu Pro Cys Leu	
315 320 325	
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Gln Val Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys	
330 335 340	
aac att gtg gca gga caa aga tgt att aaa aaa tta acg gac aat cag	1229
Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln	
345 350 355 360	
acc tca acc atg atc aga gcg act gct agg tgc gcg ccc gat cgg caa	1277
Thr Ser Thr Met Ile Arg Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln	
365 370 375	
gaa gag att agc aaa ttg atg cga agt gca agt ttc aac aca gat cca	1325
Glu Glu Ile Ser Lys Leu Met Arg Ser Ala Ser Phe Asn Thr Asp Pro	
380 385 390	
tac gtc cgt gaa ttt gga atc atg gtc aaa gat gag atg aca gac gtg	1373
Tyr Val Arg Glu Phe Gly Ile Met Val Lys Asp Glu Met Thr Asp Val	
395 400 405	
act ggg cgg gtg ctg cag ccg ccc tcc atc ctc tac ggg ggc agg aat	1421
Thr Gly Arg Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg Asn	
410 415 420	
aaa gct att gcg acc cct gtc cag ggc gtc tgg gac atg cgg aac aag	1469
Lys Ala Ile Ala Thr Pro Val Gln Gly Val Trp Asp Met Arg Asn Lys	
425 430 435 440	
cag ttc cac acg ggc atc gag atc aag gtg tgg gcc att gcg tgc ttc	1517
Gln Phe His Thr Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe	
445 450 455	
gcc ccc cag cgc cag tgc acg gaa gtc cat ctg aag tcc ttc aca gag	1565

Ala	Pro	Gln	Arg	Gln	Cys	Thr	Glu	Val	His	Leu	Lys	Ser	Phe	Thr	Glu		
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cag	ctc	aga	aag	atc	tcg	aga	gac	gcc	ggc	atg	ccc	atc	cag	ggc	cag	1613	
Gln	Leu	Arg	Lys	Ile	Ser	Arg	Asp	Ala	Gly	Met	Pro	Ile	Gln	Gly	Gln		
		475					480					485					
ccg	tgc	ttc	tgc	aaa	tac	gcg	cag	ggg	gcg	gac	agc	gtg	gag	ccc	atg	1661	
Pro	Cys	Phe	Cys	Lys	Tyr	Ala	Gln	Gly	Ala	Asp	Ser	Val	Glu	Pro	Met		
	490					495					500						
ttc	cgg	cac	ctg	aag	aac	acg	tat	gcg	ggc	ctg	cag	ctg	gtg	gtg	gtc	1709	
Phe	Arg	His	Leu	Lys	Asn	Thr	Tyr	Ala	Gly	Leu	Gln	Leu	Val	Val	Val		
505					510					515					520		
atc	ctg	ccc	ggc	aag	acg	ccc	gtg	tac	gcc	gag	gtc	aag	cgc	gtg	gga	1757	
Ile	Leu	Pro	Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly		
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gac	acg	gtg	ctg	ggg	atg	gcc	acg	cag	tgc	gtg	cag	atg	aag	aac	gtg	1805	
Asp	Thr	Val	Leu	Gly	Met	Ala	Thr	Gln	Cys	Val	Gln	Met	Lys	Asn	Val		
			540					545					550				
cag	agg	acc	acg	cca	cag	acc	ctg	tcc	aac	ctc	tgc	ctg	aag	atc	aac	1853	
Gln	Arg	Thr	Thr	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Ile	Asn		
		555					560					565					
gtc	aag	ctg	gga	ggc	gtg	aac	aac	atc	ctg	ctg	ccc	cag	ggc	agg	ccg	1901	
Val	Lys	Leu	Gly	Gly	Val	Asn	Asn	Ile	Leu	Leu	Pro	Gln	Gly	Arg	Pro		
	570					575					580						
ccg	gtg	ttc	cag	cag	ccc	gtc	atc	ttt	ctg	gga	gca	gac	gtc	act	cac	1949	
Pro	Val	Phe	Gln	Gln	Pro	Val	Ile	Phe	Leu	Gly	Ala	Asp	Val	Thr	His		
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ccc	ccc	gcc	ggg	gat	ggg	aag	aag	ccc	tcc	att	gcc	gcc	gtg	gtg	ggc	1997	
Pro	Pro	Ala	Gly	Asp	Gly	Lys	Lys	Pro	Ser	Ile	Ala	Ala	Val	Val	Gly		
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agc	atg	gac	gcc	cac	ccc	aat	cgc	tac	tgc	gcc	acc	gtg	cgt	gtg	cag	2045	
Ser	Met	Asp	Ala	His	Pro	Asn	Arg	Tyr	Cys	Ala	Thr	Val	Arg	Val	Gln		
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cag	cac	cgg	cag	gag	atc	ata	caa	gac	ctg	gcc	gcc	atg	gtc	cgc	gag	2093	
Gln	His	Arg	Gln	Glu	Ile	Ile	Gln	Asp	Leu	Ala	Ala	Met	Val	Arg	Glu		
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ctc	ctc	atc	cag	ttc	tac	aag	tcc	acg	cgc	ttc	aag	ccc	acc	cgc	atc	2141	
Leu	Leu	Ile	Gln	Phe	Tyr	Lys	Ser	Thr	Arg	Phe	Lys	Pro	Thr	Arg	Ile		
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atc	ttc	tac	cgc	gac	ggc	gtc	tct	gaa	ggc	cag	ttc	cag	cag	gtt	ctc	2189	
Ile	Phe	Tyr	Arg	Asp	Gly	Val	Ser	Glu	Gly	Gln	Phe	Gln	Gln	Val	Leu		
665					670				675					680			
cac	cac	gag	ttg	ctg	gcc	atc	cgt	gag	gcc	tgt	atc	aag	cta	gaa	aaa	2237	
His	His	Glu	Leu	Leu	Ala	Ile	Arg	Glu	Ala	Cys	Ile	Lys	Leu	Glu	Lys		

685	690	695	
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acc cgg ctc ttc tgc act gac aag aac gag cgg gtt ggg aaa agt gga Thr Arg Leu Phe Cys Thr Asp Lys Asn Glu Arg Val Gly Lys Ser Gly 715 720 725			2333
aac att cca gca ggc acg act gtg gac acg aaa atc acc cac ccc acc Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Lys Ile Thr His Pro Thr 730 735 740			2381
gag ttc gac ttc tac ctg tgt agt cac gct ggc atc cag ggg aca agc Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser 745 750 755 760			2429
agg cct tcg cac tat cac gtc ctc tgg gac gac aat cgt ttc tcc tct Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn Arg Phe Ser Ser 765 770 775			2477
gat gag ctg cag atc cta acc tac cag ctg tgt cac acc tac gtg cgc Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg 780 785 790			2525
tgc aca cgc tcc gtg tcc atc cca gcg cca gca tac tac gct cac ctg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu 795 800 805			2573
gtg gcc ttc cgg gcc agg tac cac ctg gtg gat aag gaa cat gac agt Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser 810 815 820			2621
gct gaa gga agc cat acc tct ggg cag agt aac ggg cga gac cac caa Ala Glu Gly Ser His Thr Ser Gly Gln Ser Asn Gly Arg Asp His Gln 825 830 835 840			2669
gca ctg gcc aag gcg gtc cag gtt cac caa gac act ctg cgc acc atg Ala Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met 845 850 855			2717
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agaccagcta cactcagacc aacagatggc cagcccttcc gtgacagcca gcatcgaaca			2832
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                                   Met Val His Phe Ile
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Leu Gly Arg Leu Tyr Asn Phe Gln Pro Phe Leu Thr Arg Thr Glu Val
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tac aaa act ggt gtc aca cat tat ttt agc tta gag aaa gcc aag aaa      749
Tyr Lys Thr Gly Val Thr His Tyr Phe Ser Leu Glu Lys Ala Lys Lys
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gag cta ggt tat aag gct cag cca ttt gac ctc cag gaa gca gtg gaa      797
Glu Leu Gly Tyr Lys Ala Gln Pro Phe Asp Leu Gln Glu Ala Val Glu
                                   40                               45                               50

tgg ttt aaa gcc cat ggt cat ggc aga agt tct gga agt cgt gac tcg      845
Trp Phe Lys Ala His Gly His Gly Arg Ser Ser Gly Ser Arg Asp Ser
                                   55                               60                               65

gag tgt ttt gtt tgg gat ggg cta ttg gtc ttc ctc ctg att ata gca      893
Glu Cys Phe Val Trp Asp Gly Leu Leu Val Phe Leu Leu Ile Ile Ala
                                   70                               75                               80                               85

gtt ctc atg tgg ctg cct tct tct gtg att ctg tca ctg tga aggaggg      942
Val Leu Met Trp Leu Pro Ser Ser Val Ile Leu Ser Leu *
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Ile	Lys	Tyr	Ser	Cys	Pro	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser		
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Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asn	Thr	Val	Ile	Trp	Asp	Asn	Lys	Thr		
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Pro	Val	Cys	Asp	Ser	Glu	Leu	Lys	Tyr	Ala	Phe	Leu	Phe	Leu	Leu	Pro		
			155						160					165			
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						Met											
						1											
gtg	ggg	aga	tcc	cgg	cgg	cgc	gga	gca	gct	aag	tgg	gca	gct	gtg	cga	224	
Val	Gly	Arg	Ser	Arg	Arg	Arg	Gly	Ala	Ala	Lys	Trp	Ala	Ala	Val	Arg		
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Ala	Lys	Ala	Gly	Pro	Thr	Leu	Thr	Asp	Glu	Asn	Gly	Asp	Asp	Leu	Gly		
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ttg	cca	ccc	tca	cca	ggg	gac	acc	agc	tac	tac	caa	gat	cag	gta	gat	320	
Leu	Pro	Pro	Ser	Pro	Gly	Asp	Thr	Ser	Tyr	Tyr	Gln	Asp	Gln	Val	Asp		
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gac	ttt	cat	gag	gca	cga	tcc	cgg	gcc	gcc	tta	gct	aag	ggc	tgg	aat	368	
Asp	Phe	His	Glu	Ala	Arg	Ser	Arg	Ala	Ala	Leu	Ala	Lys	Gly	Trp	Asn		
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gaa	gta	cag	agt	gga	gac	gag	gag	gat	ggc	gag	gag	gag	gag	gag	gag	416	
Glu	Val	Gln	Ser	Gly	Asp	Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Glu	Glu		
				70					75						80		

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Val Leu Ala Leu Asp Met Asp Asp Glu Asp Asp Glu Asp Gly Gly Asn	
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Ala Gly Glu Glu Glu Glu Glu Glu Asn Ala Asp Asp Asp Gly Gly Ser	
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Ser Val Gln Ser Glu Ala Glu Ala Ser Val Asp Pro Ser Leu Ser Trp	
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Gly Gln Arg Lys Lys Leu Tyr Tyr Asp Thr Asp Tyr Gly Ser Lys Ser	
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Arg Gly Arg Gln Ser Gln Gln Glu Ala Glu Glu Glu Glu Arg Glu Glu	
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Glu Glu Glu Ala Gln Ile Ile Gln Arg Arg Leu Ala Gln Ala Leu Gln	
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Leu Leu Glu Leu Ile Glu Asp Leu Lys Val Lys Leu Thr Glu Val Lys	
230 235 240	
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Asp Glu Leu Glu Pro Leu Leu Glu Leu Val Glu Gln Gly Ile Ile Pro	
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Pro Gly Lys Gly Ser Gln Tyr Leu Arg Thr Lys Tyr Asn Leu Tyr Leu	
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Asn Tyr Cys Ser Asn Ile Ser Phe Tyr Leu Ile Leu Lys Ala Arg Arg	
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Val Pro Ala His Gly His Pro Val Ile Glu Arg Leu Val Thr Tyr Arg	
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Asn Leu Ile Asn Lys Leu Ser Val Val Asp Gln Lys Leu Ser Ser Glu	
310 315 320	
att cgt cat ctg ttg aca ctt aag gat gat gct gta aag aaa gaa ctg	1184
Ile Arg His Leu Leu Thr Leu Lys Asp Asp Ala Val Lys Lys Glu Leu	
325 330 335	
att cca aaa gca aaa tcc acc aag ccc aaa cca aag tct gtt tca aag	1232
Ile Pro Lys Ala Lys Ser Thr Lys Pro Lys Pro Lys Ser Val Ser Lys	
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Thr Ser Ala Ala Ala Cys Ala Val Thr Asp Leu Ser Asp Asp Ser Asp	
355 360 365	
ttt gat gaa aaa gca aaa ctg aag tac tat aaa gaa ata gaa gac agg	1328
Phe Asp Glu Lys Ala Lys Leu Lys Tyr Tyr Lys Glu Ile Glu Asp Arg	
370 375 380 385	
caa aag cta aag aga aag aaa gaa gaa aat agc act gaa gaa cag gct	1376
Gln Lys Leu Lys Arg Lys Lys Glu Glu Asn Ser Thr Glu Glu Gln Ala	
390 395 400	
ctt gaa gat caa aat gca aag aga gct att acc tat caa att gct aaa	1424
Leu Glu Asp Gln Asn Ala Lys Arg Ala Ile Thr Tyr Gln Ile Ala Lys	
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Asn Arg Gly Leu Thr Pro Arg Arg Lys Lys Ile Asp Arg Asn Pro Arg	
420 425 430	
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Val Lys His Arg Glu Lys Phe Arg Arg Ala Lys Ile Arg Arg Arg Gly	
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Gln Val Arg Glu Val Arg Lys Glu Glu Gln Arg Tyr Ser Gly Glu Leu	
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Ser Gly Ile Arg Ala Gly Val Lys Lys Ser Ile Lys Leu Lys *	
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Cys Asp Val Asp Ile Tyr Phe Ser Ala Glu Phe Leu Asn Ser Cys Arg	
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Leu Asn Ala Glu Pro Gly Lys Lys Val Phe Tyr Pro Val Val Phe Ser	
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Leu Tyr Asn Pro Ala Ile Val Tyr Ala Asn Gln Glu Val Pro Pro Pro	
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Val Glu Gln Gln Leu Val His Lys Lys Asp Ser Gly Phe Trp Arg Asp	
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Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Leu Thr Ile	
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Gly Gly Phe Asp Met Glu Val Lys Gly Trp Gly Gly Glu Asp Val His	
85 90 95	
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Leu Tyr Arg Lys Tyr Leu His Gly Asp Leu Ile Val Ile Arg Thr Pro	
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Val Pro Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Ala Asp Glu	
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Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
155 160 165 170	
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Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
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Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
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Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu	
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tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag	1012
Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys	
315 320 325 330	
aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa	1060
Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys	
335 340 345	
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Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp	
350 355 360	
gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca	1156

Glu	Asn	Pro	Leu	Asp	Asp	Asn	Ser	Glu	Glu	Glu	Met	Glu	Asp	Ala	Pro		
		365					370					375					
aaa	caa	aag	ctt	tct	aaa	aaa	cag	aag	aca	caa	gaa	aca	gta	aac	cag	1204	
Lys	Gln	Lys	Leu	Ser	Lys	Lys	Gln	Lys	Thr	Gln	Glu	Thr	Val	Asn	Gln		
	380					385					390						
cac	agg	atg	tac	ctg	gca	aag	att	cat	atc	tgc	ctg	cag	ctc	act	ttc	1252	
His	Arg	Met	Tyr	Leu	Ala	Lys	Ile	His	Ile	Cys	Leu	Gln	Leu	Thr	Phe		
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aga	tgg	ctt	ggg	gaa	aaa	agt	gtg	tgt	agg	gag	aga	gaa	gag	atg	gag	1300	
Arg	Trp	Leu	Gly	Glu	Lys	Ser	Val	Cys	Arg	Glu	Arg	Glu	Glu	Met	Glu		
			415						420					425			
aga	gcg	agc	aca	aat	gtg	cca	aaa	tgt	tgc	ttg	aaa	aca	gac	aga	att	1348	
Arg	Ala	Ser	Thr	Asn	Val	Pro	Lys	Cys	Cys	Leu	Lys	Thr	Asp	Arg	Ile		
			430					435					440				
atg	atg	acc	att	tca	atg	taa	at	ggac	ctggac	gaaggag	taa	aggtt	gatcc			1401	
Met	Met	Thr	Ile	Ser	Met	*											
			445														
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atgtc	agtg	cacag	atgat	cattac	acca	tgtgat	gatk	caaaa	agtga	agctaaa	agg					1521	
taagt	caaag	ttgcat	atta	tttgtaa	aatt	actga	atatt	gatag	taagg	atgtag	cttt					1581	
tcatat	atca	aataaaa	tct	tctttcc	cat	gactg	accag	gtaatt	taga	tgtat	ctgta					1641	
catat	ttatg	tatagat	aca	cacacac	ata	tgtata	caga	tgaag	agcgt	tgaga	agagg					1701	
atgct	agagg	aatgtg	ccca	cacacat	ctc	agcag	catgg	ccaaa	atcag	aaagat	gtca					1761	
ctttg	atcca	gttctc	gttt	accttat	cct	gctgtg	ggcg	tgatct	cgtc	gtggat	catt					1821	
aacact	tgac	actcac	atga	gaaca	agact	cctgct	gcgt	ccctgg	agtg	tcacta	agca					1881	
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Arg Arg Asp Ala Ser Glu Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu	
15 20 25	
gcc ctg aaa tgg cac ccg gat aaa aat ctg gat aat gcc gca gaa gca	148
Ala Leu Lys Trp His Pro Asp Lys Asn Leu Asp Asn Ala Ala Glu Ala	
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gct gaa caa ttt aaa tta atc caa gca gca tat gat gtg ttg agt gac	196
Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp	
45 50 55	
cct cag gaa aga gca tgg tat gat aat cat aga gag gcc cta ctt aaa	244
Pro Gln Glu Arg Ala Trp Tyr Asp Asn His Arg Glu Ala Leu Leu Lys	
60 65 70	
ggg ggg ttt gat ggc gaa tat caa gat gac agc tta gat ttg cta cgc	292
Gly Gly Phe Asp Gly Glu Tyr Gln Asp Asp Ser Leu Asp Leu Leu Arg	
75 80 85 90	
tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga	340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly	
95 100 105	
ttt tac acg gtg tat cgt aat gtt ttt gaa atg att gcc aag gaa gaa	388
Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu	
110 115 120	
cta gaa tct gtg tta gag gaa gag gtt gat gat ttc cca act ttt gga	436
Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly	
125 130 135	
gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat	484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr	
140 145 150	
tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat	532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
155 160 165 170	
gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa	580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
175 180 185	
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt	628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
190 195 200	
gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag	676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln	
205 210 215	
gcg cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa	724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys	

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gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val 235 240 245 250			772
gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys 255 260 265			820
gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly 270 275 280			868
tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp 285 290 295			916
ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu 300 305 310			964
tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys 315 320 325 330			1012
aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys 335 340 345			1060
caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp 350 355 360			1108
gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro 365 370 375			1156
aaa caa aag ctt tct aaa aaa cag aag aaa aag aaa cag aaa cca gca Lys Gln Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala 380 385 390			1204
cag aat tat gat gac aat ttc aat gta aat gga cct gga gaa gga gta Gln Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val 395 400 405 410			1252
aag gtt gat cca gaa gat act aac tta aat caa gac agt gcc aaa gaa Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys Glu 415 420 425			1300
ttg gaa gat agt ccc cag gaa aat gtc agt gtc aca gag atc att aaa Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile Ile Lys 430 435 440			1348
cca tgt gat gat cca aaa agt gaa gct aaa agt gtt cct aaa ccc aaa Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro Lys Pro Lys 445 450 455			1396

gga aag aaa acc aaa gat atg aaa aaa cct gtc aga gta cct gct gaa	1444
Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu	
460 465 470	
cca caa aca atg agt gtt ctt atc agc tgt aca acc tgc cat agt gaa	1492
Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu	
475 480 485 490	
ttt cca tct cgg aat aaa ctt ttt gac cat cta aag gcc aca ggt cat	1540
Phe Pro Ser Arg Asn Lys Leu Phe Asp His Leu Lys Ala Thr Gly His	
495 500 505	
gca aga gca cct tca tca tcg tct tta aac agc gca aca agt agt caa	1588
Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln	
510 515 520	
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Ser Lys Lys Glu Lys Arg Lys Asn Arg *	
525 530	
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tgtatttttt ttctcaagaa cagtgatagg tagaaactaa ttgaacattt ggtagtcttt	2179
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tttacatggc atgtcctccc taggcacagt gacagctgta aagtatgacg gaacaaggta	2359
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Gly Gly Pro Glu Ala Phe Ala Ala Phe Leu Arg Arg Glu Arg Leu Ala
45 50 55

cgt ttc ctg aac ccc gat gag gtg cac gcc att ctg cgc gcg gcg gag 245
Arg Phe Leu Asn Pro Asp Glu Val His Ala Ile Leu Arg Ala Ala Glu
60 65 70

agg ccg gga gag gag ggc gcg gcg gcg gcg gcg gcc gag gac tcg 293
Arg Pro Gly Glu Glu Gly Ala Ala Ala Ala Ala Ala Ala Glu Asp Ser
75 80 85

ttc ggc tcc tcg cac gac tgc tct tcg ggc acc tac ttc ccc gag cag 341
Phe Gly Ser Ser His Asp Cys Ser Ser Gly Thr Tyr Phe Pro Glu Gln
90 95 100 105

tcg gac ctg gag cca ccg ctg ttg gag ctt ggc tgg ccc gcc ttc tac 389
Ser Asp Leu Glu Pro Pro Leu Leu Glu Leu Gly Trp Pro Ala Phe Tyr
110 115 120

cag ggc gcc tac cgc ggc gcc acg cgt gtc gag acg cac ttc cag ccc 437
Gln Gly Ala Tyr Arg Gly Ala Thr Arg Val Glu Thr His Phe Gln Pro
125 130 135

cgc ggc gct ggc gaa ggt ggc ccc tac ggc tgc aag gac gct ctg cgc 485
 Arg Gly Ala Gly Glu Gly Gly Pro Tyr Gly Cys Lys Asp Ala Leu Arg
 140 145 150

cag cag ctc cgc tcg gcg cga gag gtg att gca gtg gtc atg gac gtg 533
Gln Gln Leu Arg Ser Ala Arg Glu Val Ile Ala Val Val Met Asp Val
155 160 165

ttc aca gac atc gac atc ttc aga gac ctg caa gaa ata tgc agg aaa 581
Phe Thr Asp Ile Asp Ile Phe Arg Asp Leu Gln Glu Ile Cys Arg Lys
170 175 180 185

cag gga gtt gct gtg tat atc ctt ctg gac cag gct ctc ctc tct caa 629
Gln Gly Val Ala Val Tyr Ile Leu Leu Asp Gln Ala Leu Leu Ser Gln
190 195 200

ttt ctg gat atg tgc atg gat ctg aaa gtt cat cct gaa cag gaa aag Phe Leu Asp Met Cys Met Asp Leu Lys Val His Pro Glu Gln Glu Lys 205 210 215	677
tta atg aca gtt cgg act atc aca gga aat atc tac tat gca agg tca Leu Met Thr Val Arg Thr Ile Thr Gly Asn Ile Tyr Tyr Ala Arg Ser 220 225 230	725
gga act aag att att ggg aag gtt cac gaa aag ttc acg ttg att gat Gly Thr Lys Ile Ile Gly Lys Val His Glu Lys Phe Thr Leu Ile Asp 235 240 245	773
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cac ttt gat ctg gag ttc cga atc ctg tat gcc cag tcc aag ccc atc His Phe Asp Leu Glu Phe Arg Ile Leu Tyr Ala Gln Ser Lys Pro Ile 285 290 295	917
agc ccc aaa ctc ctg tct cac ttc cag agc agc aac aag ttt gat cac Ser Pro Lys Leu Leu Ser His Phe Gln Ser Ser Asn Lys Phe Asp His 300 305 310	965
ctc acc aac cga aaa cca cag tcc aag gag ctc acc ctg ggc aac ctg Leu Thr Asn Arg Lys Pro Gln Ser Lys Glu Leu Thr Leu Gly Asn Leu 315 320 325	1013
ctg cgg atg cgg ctg gct agg ctg tca agt act ccc agg aag gcg gac Leu Arg Met Arg Leu Ala Arg Leu Ser Ser Thr Pro Arg Lys Ala Asp 330 335 340 345	1061
ctg gac cca gag atg ccc gca gag ggc aag gca gag cgc aag ccc cat Leu Asp Pro Glu Met Pro Ala Glu Gly Lys Ala Glu Arg Lys Pro His 350 355 360	1109
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gag cca gga gag gag atg cca ggg ctg agt gtg agt gag gtg gga aca Glu Pro Gly Glu Glu Met Pro Gly Leu Ser Val Ser Glu Val Gly Thr 395 400 405	1253
caa acc agc atc acc aca gca tgt gct ggt acc cag act gca gtc atc Gln Thr Ser Ile Thr Thr Ala Cys Ala Gly Thr Gln Thr Ala Val Ile 410 415 420 425	1301
acc agg ata gca agc tct caa acc acg att tgg tcc aga tcg acc act	1349

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Ser Ser Ser Ser Ser Ser Pro Thr Ser Gly Ser Pro Arg Gly Ser His			
75	80	85	
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Ser Ser Ala Leu Glu Arg Leu Glu Thr Lys Leu His Leu Leu Arg Gln			
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gag atg gtt aac ctc aga gcc aca gac gtc agg ctc atg cgc cag ttg			1047
Glu Met Val Asn Leu Arg Ala Thr Asp Val Arg Leu Met Arg Gln Leu			
110	115	120	
ctt gta atc aat gag agc atc gag tcc atc aag tgg atg atc gaa gaa			1095
Leu Val Ile Asn Glu Ser Ile Glu Ser Ile Lys Trp Met Ile Glu Glu			
125	130	135	
aaa gcc acc att acc agc aga ggc agc agc ctc agt ggc agc ctg tgc			1143
Lys Ala Thr Ile Thr Ser Arg Gly Ser Ser Leu Ser Gly Ser Leu Cys			
140	145	150	
agt ttg ttg gag agt cag agc acc tcc tta cgt ggc agc tac aac agc			1191
Ser Leu Leu Glu Ser Gln Ser Thr Ser Leu Arg Gly Ser Tyr Asn Ser			
155	160	165	
cta cac gat ggc agt gat ggg ctg gat ggc att tcc gtg gga agt tat			1239
Leu His Asp Gly Ser Asp Gly Leu Asp Gly Ile Ser Val Gly Ser Tyr			
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Leu Asp Thr Leu Ala Asp Asp Val Pro Gly His Gln Thr Pro Ser Asp			
190	195	200	
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Leu Asp Gln Phe Ser Asp Ser Ser Leu Ile Glu Asp Ser Gln Ala Leu			
205	210	215	
cac aag cgt cct aaa ttg gat tct gaa tac tac tgc ttt ggc tag tga			1383
His Lys Arg Pro Lys Leu Asp Ser Glu Tyr Tyr Cys Phe Gly *			
220	225	230	
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						Met
						1
aag gcc ttt ggt cct cca cat gag ggc ccc ctc caa gga ctc gtg gcc	166					
Lys Ala Phe Gly Pro Pro His Glu Gly Pro Leu Gln Gly Leu Val Ala						
5 10 15						
tcc cgc att gag act tat ggg ggc cgg cat cga gcc tct gct cag agc	214					
Ser Arg Ile Glu Thr Tyr Gly Gly Arg His Arg Ala Ser Ala Gln Ser						
20 25 30						
act act ggc aga ctc tat ccc cga gga tac cct gtg ctg gat ccc agt	262					
Thr Thr Gly Arg Leu Tyr Pro Arg Gly Tyr Pro Val Leu Asp Pro Ser						
35 40 45						
cgc cga cgc ctc cag cag tat gtc ccc ttt gcc agg ggt tct ggc cag	310					
Arg Arg Arg Leu Gln Gln Tyr Val Pro Phe Ala Arg Gly Ser Gly Gln						
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gcc cga ggc ctg tca ccc atg aga ctg cga gat cca gag ccc gag aag	358					
Ala Arg Gly Leu Ser Pro Met Arg Leu Arg Asp Pro Glu Pro Glu Lys						
70 75 80						
agg cac ggg ggc cat gtg ggg gct ggc ctg ctt cac tcc ccc aaa ctc	406					
Arg His Gly Gly His Val Gly Ala Gly Leu Leu His Ser Pro Lys Leu						
85 90 95						
aag gaa ctc acc aag gcc cat gag ctg gag gtg agg ctg cac act ttc	454					
Lys Glu Leu Thr Lys Ala His Glu Leu Glu Val Arg Leu His Thr Phe						
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Ser Met Phe Gly Met Pro Arg Leu Pro Pro Glu Asp Arg Arg His Trp						
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Glu Ile Gly Glu Gly Gly Asp Ser Gly Leu Thr Ile Glu Lys Ser Trp						
130 135 140 145						
agg gag ctg gtg cct ggg cac aag gag atg agc cag gag ctc tgc cac	598					
Arg Glu Leu Val Pro Gly His Lys Glu Met Ser Gln Glu Leu Cys His						
150 155 160						

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ctg cag cga gtg gga ctg ctg atg gaa gtg tca gct gag acc ctg ttt Leu Gln Arg Val Gly Leu Leu Met Glu Val Ser Ala Glu Thr Leu Phe 195 200 205	742
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ctt atc aag ccc cac cag cgc atc acc aag tac cca ctg ctg ctc cat Leu Ile Lys Pro His Gln Arg Ile Thr Lys Tyr Pro Leu Leu Leu His 310 315 320	1078
gct gtg ctc aag agg agc ccc gag gca cga gcc caa gag gcc ctg aat Ala Val Leu Lys Arg Ser Pro Glu Ala Arg Ala Gln Glu Ala Leu Asn 325 330 335	1126
gcc atg att gaa gcc gtg gag tca ttc ctg cga cat atc aat ggg cag Ala Met Ile Glu Ala Val Glu Ser Phe Leu Arg His Ile Asn Gly Gln 340 345 350	1174
gtc cgc cag ggc gaa gag caa gag agc ttg gcg gct gca gca caa cgc Val Arg Gln Gly Glu Glu Gln Glu Ser Leu Ala Ala Ala Ala Gln Arg 355 360 365	1222
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tct gat gtg ctc ctt gtg acc aag ccc cag cgc aag gcg gac aaa gcc Ser Asp Val Leu Leu Val Thr Lys Pro Gln Arg Lys Ala Asp Lys Ala 435 440 445	1462
aag gtc atc cga ccc cct ctc atg ctg gag aag ctc gtg tgc caa ccc Lys Val Ile Arg Pro Pro Leu Met Leu Glu Lys Leu Val Cys Gln Pro 450 455 460 465	1510
ctg cga gac ccc aac agc ttc ctg ctg atc cac ctc act gaa ttc cag Leu Arg Asp Pro Asn Ser Phe Leu Leu Ile His Leu Thr Glu Phe Gln 470 475 480	1558
tgt gtc tcc agc gcc ctc ctt gtg cac tgt ccc agt cct aca gac cgt Cys Val Ser Ser Ala Leu Leu Val His Cys Pro Ser Pro Thr Asp Arg 485 490 495	1606
gcc cag tgg ctg gag aag acc cag cag gcc cag gcc gcc cta cag aag Ala Gln Trp Leu Glu Lys Thr Gln Gln Ala Gln Ala Ala Leu Gln Lys 500 505 510	1654
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tcg acc att atc ccc cac ctg gtg gtg aca gaa gac aca gat gaa gat Ser Thr Ile Ile Pro His Leu Val Val Thr Glu Asp Thr Asp Glu Asp 565 570 575	1846
gct ccc ctt gtg cca gat gat acc tca gac tct ggc tac ggc act ttg Ala Pro Leu Val Pro Asp Asp Thr Ser Asp Ser Gly Tyr Gly Thr Leu 580 585 590	1894
atc cca ggc acc ccc acg ggg tcc cgc tcc cca ctg agc cgt cta cgc Ile Pro Gly Thr Pro Thr Gly Ser Arg Ser Pro Leu Ser Arg Leu Arg 595 600 605	1942
caa aga gcc ctt cgg cgg gac cct cgc ctc acc ttc tcc acc ctg gaa	1990

Gln Arg Ala Leu Arg Arg Asp Pro Arg Leu Thr Phe Ser Thr Leu Glu	
610 615 620 625	
ctc cgg gac atc cct ctg cgt ccc cac cct ccc gac ccc caa gct cct	2038
Leu Arg Asp Ile Pro Leu Arg Pro His Pro Pro Asp Pro Gln Ala Pro	
630 635 640	
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Gln Arg Arg Ser Ala Pro Glu Leu Pro Glu Gly Ile Leu Lys Gly Gly	
645 650 655	
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Ser Leu Pro Gln Glu Asp Pro Pro Thr Trp Ser Glu Glu Glu Asp Gly	
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Ala Ser Glu Arg Gly Asn Val Val Val Glu Thr Leu His Arg Ala Arg	
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Leu Arg Gly Gln Leu Pro Ser Ser Pro Thr His Ala Asp Ser Ala Gly	
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Glu Ser Pro Trp Glu Ser Ser Gly Glu Glu Glu Glu Gly Pro Leu	
710 715 720	
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Phe Leu Lys Ala Gly His Thr Ser Leu Arg Pro Met Arg Ala Glu Asp	
725 730 735	
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Met Leu Arg Glu Ile Arg Glu Glu Leu Ala Ser Gln Arg Ile Glu Gly	
740 745 750	
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Ala Glu Glu Pro Arg Asp Ser Arg Pro Arg Lys Leu Thr Arg Ala Gln	
755 760 765	
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Leu Gln Arg Met Arg Gly Pro His Ile Ile Gln Leu Asp Thr Pro Leu	
770 775 780 785	
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Ser Ala Ser Glu Val *	
790	
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2860

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cacgtgcata tgatcaactt tggacttctt ttgagattgc caggcgtttg ca atg	175
	Met
	1
gct gct act gtg aac ttg gaa ctt gat ccc att ttt ttg aaa gca cta	223
Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu	
5 10 15	
ggt ttc ttg cat tca aag agt aaa gat tct gct gaa aag cta aaa gca	271
Gly Phe Leu His Ser Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala	
20 25 30	
ctg ctt gat gaa tct ttg gct cgg ggc att gat tcc agt tac cgt cca	319
Leu Leu Asp Glu Ser Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro	
35 40 45	
tct caa aag gat gtg gag cca ccc aaa att tca agc aca aaa aac att	367
Ser Gln Lys Asp Val Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile	
50 55 60 65	
tcc att aag caa gag ccc aaa ata tca tcc agt ctt cct tct ggt aat	415
Ser Ile Lys Gln Glu Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn	
70 75 80	
aat aat ggc aag gtc ctc aca act gaa aag gta aag aag gaa gct gaa	463
Asn Asn Gly Lys Val Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu	
85 90 95	
aag aga cct gct gat aaa atg aaa tca gac atc act gaa gga gtt gat	511
Lys Arg Pro Ala Asp Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp	
100 105 110	
att cca aag aaa cct aga ttg gag aaa cca gaa aca cag tca tct ccc	559
Ile Pro Lys Lys Pro Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro	
115 120 125	
att act gtc caa agt agc aag gat tta cct atg gct gac ctt tcc agt	607
Ile Thr Val Gln Ser Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser	

130	135	140	145	
ttt gag gag acc agt gct gat gat ttt gcc atg gag atg gga ttg gcc				655
Phe Glu Glu Thr Ser Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala	150	155	160	
tgc gtt gtt tgt agg caa atg atg gtg gca tct ggc aat caa tta gta				703
Cys Val Val Cys Arg Gln Met Met Val Ala Ser Gly Asn Gln Leu Val	165	170	175	
gaa tgt cag gag tgc cat aat ctc tac cac cga gat tgt cat aaa ccc				751
Glu Cys Gln Glu Cys His Asn Leu Tyr His Arg Asp Cys His Lys Pro	180	185	190	
cag gtg aca gac aag gaa gcg aat gac cct cgc ctg gtg tgg tat tgt				799
Gln Val Thr Asp Lys Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys	195	200	205	
gcc cga tgt acc aga caa atg aaa aga atg gct caa aaa act cag aaa				847
Ala Arg Cys Thr Arg Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys	210	215	220	225
cca ccg cag aaa cca gcc cct gca gtt gtt tct gta act cca gct gtc				895
Pro Pro Gln Lys Pro Ala Pro Ala Val Val Ser Val Thr Pro Ala Val	230	235	240	
aaa gat cca ttg gtt aag aaa cca gaa act aaa ctg aaa caa gag aca				943
Lys Asp Pro Leu Val Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr	245	250	255	
act ttt cta gcg ttt aag aga aca gaa gtc aag aca tcc aca gtt att				991
Thr Phe Leu Ala Phe Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile	260	265	270	
tca gga aat tct tct agt gcc agc gtt tcc tcg tca gta act agt ggc				1039
Ser Gly Asn Ser Ser Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly	275	280	285	
tta act gga tgg gca gct ttt gca gcc aaa act tcc tct gct ggt cct				1087
Leu Thr Gly Trp Ala Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro	290	295	300	305
tca aca gca aaa ttg agt tca aca aca caa aac aat act ggg aaa cct				1135
Ser Thr Ala Lys Leu Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro	310	315	320	
gct act tcg tca gct aac cag aaa cct gtg ggt ttg act ggt ctg gca				1183
Ala Thr Ser Ser Ala Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala	325	330	335	
aca tca tcc aaa ggt gga ata ggt tcc aaa ata ggt tcc aat aac agc				1231
Thr Ser Ser Lys Gly Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser	340	345	350	
act acg ccc act gta cct tta aaa cca cct cca cct cta acc ttg ggt				1279
Thr Thr Pro Thr Val Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly	355	360	365	

aaa act ggc ctt agt cgc tca gtt agt tgt gac aat gtc agc aaa gta	1327
Lys Thr Gly Leu Ser Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val	
370 375 380 385	
ggg ctt cct agt cca agt agt tta gtt cca gga agc agc agc caa cta	1375
Gly Leu Pro Ser Pro Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu	
390 395 400	
agt ggg aat gga aat agt gga aca tca gga cct agt gga agt act acc	1423
Ser Gly Asn Gly Asn Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr	
405 410 415	
agc aaa act act tca gaa tcc agc agc tct ccc tca gca tcc ctt aaa	1471
Ser Lys Thr Thr Ser Glu Ser Ser Ser Pro Ser Ala Ser Leu Lys	
420 425 430	
ggc cca act tca caa gaa tca cag ctc aat gct atg aag cga tta cag	1519
Gly Pro Thr Ser Gln Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln	
435 440 445	
atg gtc aag aag aaa gct gcc caa aag aaa ctc aag aag taa tgtggcc	1568
Met Val Lys Lys Lys Ala Ala Gln Lys Lys Leu Lys Lys *	
450 455 460	
aagtagggttt ttgtatcata ttagcctaaa gatgaaaggc ttattattat gatataatct	1628
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tcgccagcga gggatgcgga gacgcccctg aacgacc atg gca tgc gcc gac gag	175
Met Ala Ser Ala Asp Glu	
1 5	
ctg acc ttc cat gaa ttc gag gag gcc act aat ctt ctg gct gac acc	223
Leu Thr Phe His Glu Phe Glu Glu Ala Thr Asn Leu Leu Ala Asp Thr	
10 15 20	
cca gat gca gcc acc acc agc aga agc gat cag ctg acc cca caa ggg	271
Pro Asp Ala Ala Thr Thr Ser Arg Ser Asp Gln Leu Thr Pro Gln Gly	
25 30 35	

cac gtg gct gtg gcc gtg ggc tca ggt ggc agc tat gga gcc gag gat	319
His Val Ala Val Ala Val Gly Ser Gly Gly Ser Tyr Gly Ala Glu Asp	
40 45 50	
gag gtg gag gag gag agt gac aag gcc gcg ctc ctg cag gag cag cag	367
Glu Val Glu Glu Glu Ser Asp Lys Ala Ala Leu Leu Gln Glu Gln Gln	
55 60 65 70	
cag cag cag cag ccg gga ttc tgg acc ttc agc tac tat cag agc ttc	415
Gln Gln Gln Gln Pro Gly Phe Trp Thr Phe Ser Tyr Tyr Gln Ser Phe	
75 80 85	
ttt gac gtg gac acc tca cag gtc ctg gac cgg atc aaa ggc tca ctg	463
Phe Asp Val Asp Thr Ser Gln Val Leu Asp Arg Ile Lys Gly Ser Leu	
90 95 100	
ctg ccc cgg cct ggc cac aac ttt gtg cgg cac cat ctg cgg aat cgg	511
Leu Pro Arg Pro Gly His Asn Phe Val Arg His His Leu Arg Asn Arg	
105 110 115	
ccg gat ctg tat ggc ccc ttc tgg atc tgt gcc acg ttg gcc ttt gtc	559
Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala Thr Leu Ala Phe Val	
120 125 130	
ctg gcc gtc act ggc aac ctg acg ctg gtg ctg gcc cag agg agg gac	607
Leu Ala Val Thr Gly Asn Leu Thr Leu Val Leu Ala Gln Arg Arg Asp	
135 140 145 150	
ccc tcc atc cac tac agc ccc cag ttc cac aag gtg acc gtg gca ggc	655
Pro Ser Ile His Tyr Ser Pro Gln Phe His Lys Val Thr Val Ala Gly	
155 160 165	
atc agc atc tac tgc tat gcg tgg ctg gtg ccc ctg gcc ctg tgg ggc	703
Ile Ser Ile Tyr Cys Tyr Ala Trp Leu Val Pro Leu Ala Leu Trp Gly	
170 175 180	
ttc ctg cgg tgg cgc aag ggt gtc cag gag cgc atg ggg ccc tac acc	751
Phe Leu Arg Trp Arg Lys Gly Val Gln Glu Arg Met Gly Pro Tyr Thr	
185 190 195	
ttc ctg gag act gtg tgc atc tac ggc tac tcc ctc ttt gtc ttc atc	799
Phe Leu Glu Thr Val Cys Ile Tyr Gly Tyr Ser Leu Phe Val Phe Ile	
200 205 210	
ccc atg gtg gtc ctg tgg ctc atc cct gtg cct tgg ctg cag tgg ctc	847
Pro Met Val Val Leu Trp Leu Ile Pro Val Pro Trp Leu Gln Trp Leu	
215 220 225 230	
ttt ggg gcg ctg gcc ctg ggc ctg tca gcc gcc ggg ctg gta ttc acc	895
Phe Gly Ala Leu Ala Leu Gly Leu Ser Ala Ala Gly Leu Val Phe Thr	
235 240 245	
ctc tgg ccc gtg gtc cgt gag gac acc agg ctg gtg gcc aca gtg ctg	943
Leu Trp Pro Val Val Arg Glu Asp Thr Arg Leu Val Ala Thr Val Leu	
250 255 260	

ctg tcc gtg gtc gtg ctg ctc cag gcc ctc ctg gcc atg ggc tgt gaa 991
 Leu Ser Val Val Val Leu Leu Gln Ala Leu Leu Ala Met Gly Cys Glu
 265 270 275

gtt gga ctt ctt ccg gtg tgc ctc ggg gac gtg gtc ctc ccc cca ttc 1039
 Val Gly Leu Leu Pro Val Cys Leu Gly Asp Val Val Leu Pro Pro Phe
 280 285 290

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 Ile Leu Pro *
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 Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser Trp Val
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cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg gcc gtg 152
 Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala Ala Val
 20 25 30

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 Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu Ser Arg
 35 40 45 50

gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat cac tgg 248
 Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp His Trp
 55 60 65

gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc tgg tca 296
 Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg Trp Ser
 70 75 80

gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc ttt ggc 344
 Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala Phe Gly
 85 90 95

ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg gaa gcc 392
 Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu Glu Ala

100	105	110	
cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc ggg gcc			440
Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys Gly Ala			
115	120	125	130
acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg ctg gtg			488
Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg Leu Val			
	135	140	145
cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag ccg gcc			536
His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu Pro Gly			
	150	155	160
tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc cat gag			584
Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser His Glu			
	165	170	175
atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cag att ccc cgg			632
Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Gln Ile Pro Arg			
	180	185	190
ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc atg ggg			680
Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly Met Gly			
	195	200	205
cca ggg gag tct gga cag ccg ccc cca gcc tgc tga cccc cagctttcta			730
Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *			
	215	220	
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gctgcttgct ggggccggga tttgcagggg aaccaggat ggcaactggcc catagggagc			850
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agagaaaatt atatcagaca atggcattct gctgtgggta ttcagggtgc atataaagga     1020

atg aaa gca aga caa ctt tta agg gaa aaa cac aaa gct tct atc gta      1068
Met Lys Ala Arg Gln Leu Leu Arg Glu Lys His Lys Ala Ser Ile Val
  1             5             10            15

ata caa agc acc tac aga atg tat agg cag tat tgt ttc tac caa aag      1116
Ile Gln Ser Thr Tyr Arg Met Tyr Arg Gln Tyr Cys Phe Tyr Gln Lys
             20             25             30

ctt cag tgg gct aca aaa atc ata caa gaa aaa tat aga gca aat aaa      1164
Leu Gln Trp Ala Thr Lys Ile Ile Gln Glu Lys Tyr Arg Ala Asn Lys
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aag aaa cag aaa gta ttt caa cac aat gaa ctt aag aaa gag act tgt      1212

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275	280	285	
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cag atg gct gtg tat cgg aga aga ttt gtt cag cag aaa aga gct gct Gln Met Ala Val Tyr Arg Arg Arg Phe Val Gln Gln Lys Arg Ala Ala 305 310 315 320			1980
atc act tta cag cat tat ttt agg acg tgg caa acc aga aaa cag ttt Ile Thr Leu Gln His Tyr Phe Arg Thr Trp Gln Thr Arg Lys Gln Phe 325 330 335			2028
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ttt ctg tct gca aaa cat caa aga caa gtc tat tta cag atc aga agc Phe Leu Ser Ala Lys His Gln Arg Gln Val Tyr Leu Gln Ile Arg Ser 355 360 365			2124
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aag ttt cag gaa att aaa aat agc acc ata aaa att cag gct atg tgg Lys Phe Gln Glu Ile Lys Asn Ser Thr Ile Lys Ile Gln Ala Met Trp 385 390 395 400			2220
agg aga tat aga gcc aag aaa tat tta tgt aaa gtg aaa gct gcc tgc Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala Cys 405 410 415			2268
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cag aga aaa tgg aga gct ata ctt cct gca aag ata gct cat gaa cac Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys Ile Ala His Glu His 465 470 475 480			2460
ttc tta atg ata aaa aga cat cga gct gct tgt ttg atc caa gca cat Phe Leu Met Ile Lys Arg His Arg Ala Ala Cys Leu Ile Gln Ala His 485 490 495			2508
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Ala Leu Ile Ile Gln Lys Tyr Ile Arg Ala Arg Glu Ala Gly Lys His	
515 520 525	
gaa agg ata aaa tat att gaa ttt aaa aaa tct aca gtt atc cta caa	2652
Glu Arg Ile Lys Tyr Ile Glu Phe Lys Lys Ser Thr Val Ile Leu Gln	
530 535 540	
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Ala Leu Val Arg Gly Trp Leu Val Arg Lys Arg Phe Leu Glu Gln Arg	
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Ala Lys Ile Arg Leu Leu His Phe Thr Ala Ala Ala Tyr Tyr His Leu	
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Asn Ala Val Arg Ile Gln Arg Ala Tyr Lys Leu Tyr Leu Ala Val Lys	
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Asn Ala Asn Lys Gln Val Asn Ser Val Ile Cys Ile Gln Arg Trp Phe	
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cga gca aga tta caa gaa aag aga ttt att cag aaa tat cat agc atc	2892
Arg Ala Arg Leu Gln Glu Lys Arg Phe Ile Gln Lys Tyr His Ser Ile	
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Lys Lys Ile Glu His Glu Gly Gln Glu Cys Leu Ser Gln Arg Asn Arg	
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Ala Ala Ser Val Ile Gln Lys Ala Val Arg His Phe Leu Leu Arg Lys	
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Arg Gly Tyr Ser Trp Arg Lys Lys Asn Asp Cys Thr Lys Ile Lys Ala	
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Ile Arg Leu Ser Leu Gln Val Val Asn Arg Glu Ile Arg Glu Glu Asn	
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Lys His Leu Ser Ala Ile Leu Glu Ala Leu Lys His Leu Glu Val Val	
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Ile Ser Lys Ile Phe Val Leu Ile Arg Ser Cys Asn Arg Ser Ile Pro	
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Cys Met Glu Val Ile Arg Tyr Ala Val Gln Val Leu Leu Asn Val Ser	
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Asp Ile Leu Leu Glu Leu Leu Gln Ile Tyr Arg Glu Lys Pro Gly Asn	
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Arg Ser Lys Val Val Asp Arg Ile Tyr Ser Leu Tyr Lys Leu Thr Ala	
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His Lys His Lys Met Asn Thr Glu Arg Ile Leu Tyr Lys Gln Lys Lys	
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Asn Ser Ser Ile Ser Ile Pro Phe Ile Pro Glu Thr Pro Val Arg Thr	
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Arg Ile Val Ser Arg Leu Lys Pro Asp Trp Val Leu Arg Arg Asp Asn	
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Thr Leu Gly Ile Pro Tyr *	
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Met Phe His Gln Met Lys Met Met Ser Gln Lys Met Asn Lys Ile Pro		
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Met Met Asn Asn Lys Tyr Lys Met Ile His Lys Thr His Lys Asn Ile		
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Ser Phe Cys Val Asp Glu Glu Glu Ser Cys Lys Gly Gln Ser Ser Glu		
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Glu Glu Val Cys Val Asp Phe Asn Leu Ile Thr Asp Asp Cys Phe Ala		
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Leu Pro Asp Asp Ser Ser Glu Glu Glu Asn Asn Val Asn Asp Lys Arg		
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Glu Ser Asn Thr Ala Val Asn Pro Ser Thr Val Lys Lys Asn Lys Gln		
	175 180 185	
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Gln Asp His Cys Leu Asn Ser Val Pro Ser Gly Ser Ser Ala Gln Ser		
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Lys Val Arg Ser Thr Pro Arg Val Asn Pro Leu Ala Lys Gln Ser Lys		
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Gln Thr Leu Leu Asn Leu Lys Asp Thr Ile Ser Glu Val Ser Asp Phe	
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Lys Pro Gln Asn His Asn Glu Val Gln Ser Thr Thr Pro Pro Phe Thr	
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Thr Val Asp Ser Gln Lys Asp Cys Arg Lys Phe Pro Val Pro Gln Lys	
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Arg Phe Gly His Leu Ala Leu Met Phe Pro Met Pro Ser Ala Ser Ala	
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Lys Arg Gly Ala His Gly Pro Gln Asp Leu Ala Asp Tyr Phe Gly Lys	
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Glu Ser Trp Asp Gly Ser Ala Leu Glu Asp Ser Ser Thr Ser Gly Ala	
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Ser Cys Ser Lys Ser Arg Pro His Leu Ala Gly Thr His Thr Ser Leu	
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Arg Leu Pro Gln Glu Gly Lys Gly Thr Cys Ile Leu Val Gly Gly His	
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Gly Leu Gln Val Glu Val Cys Pro Leu Asn Gly Cys Asp Tyr Ile Val	
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Ser Asn Arg Met Val Val Glu Arg Arg Ser Gln Ser Glu Met Leu Asn	
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Ser Val Asn Lys Asn Lys Phe Ile Glu Gln Ile Gln His Leu Gln Ser	
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Met Phe Glu Arg Ile Cys Val Ile Val Glu Lys Asp Arg Glu Lys Thr	
415 420 425	
gga gac aca tca agg atg ttt agg aga aca aag agc tat gac agc ctg	2666
Gly Asp Thr Ser Arg Met Phe Arg Arg Thr Lys Ser Tyr Asp Ser Leu	
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Gln Glu Glu Thr Ala Asp Leu Leu Lys Glu Leu Ser Leu Val Glu Gln
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aga aag aat gtt ggt att cat gtt cca aca gtg gtg aat agt aat aaa      2810
Arg Lys Asn Val Gly Ile His Val Pro Thr Val Val Asn Ser Asn Lys
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agt gag gca ctc cag ttt tat tta agt att ccc aat ata agt tat ata      2858
Ser Glu Ala Leu Gln Phe Tyr Leu Ser Ile Pro Asn Ile Ser Tyr Ile
                      495                      500                      505

act gca tta aat atg tgt cac cag ttt tca tct gtg aaa agg atg gct      2906
Thr Ala Leu Asn Met Cys His Gln Phe Ser Ser Val Lys Arg Met Ala
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aac agg tat gtc tgt tgt aat att ttt aaa tga ttactttt aaaagattcg      2957
Asn Arg Tyr Val Cys Cys Asn Ile Phe Lys *
525                      530                      535

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tttcctctca gccaggaagg attttgatat tcatcagaaa tacctccaga agattcaagg      300

agctgtagag gtgaagtaag cctgtgaagg accagc atg gga atc cta tac tct      354
Met Gly Ile Leu Tyr Ser
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gag ccc atc tgc caa gca gcc tat cag aat gac ttt gga caa gtg tgg      402

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Arg	Trp	Val	Lys	Glu	Asp	Ser	Ser	Tyr	Ala	Asn	Val	Gln	Asp	Gly	Phe	
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aat	gga	gac	acg	ccc	ctg	atc	tgt	gct	tgc	agg	cga	ggg	cat	gtg	aga	498
Asn	Gly	Asp	Thr	Pro	Leu	Ile	Cys	Ala	Cys	Arg	Arg	Gly	His	Val	Arg	
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Ile	Val	Ser	Phe	Leu	Leu	Arg	Arg	Asn	Ala	Asn	Val	Asn	Leu	Lys	Asn	
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Gln	Lys	Glu	Arg	Thr	Cys	Leu	His	Tyr	Ala	Val	Lys	Lys	Lys	Phe	Thr	
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Phe	Ile	Asp	Tyr	Leu	Leu	Ile	Ile	Leu	Leu	Met	Pro	Val	Leu	Leu	Ile	
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Gly	Tyr	Phe	Leu	Met	Val	Ser	Lys	Thr	Lys	Gln	Asn	Glu	Ala	Leu	Val	
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Arg	Met	Leu	Leu	Asp	Ala	Gly	Val	Glu	Val	Asn	Ala	Thr	Asp	Cys	Tyr	
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Gly	Cys	Thr	Ala	Leu	His	Tyr	Ala	Cys	Glu	Met	Lys	Asn	Gln	Ser	Leu	
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Ile	Pro	Leu	Leu	Glu	Ala	Arg	Ala	Asp	Pro	Thr	Ile	Lys	Asn	Lys		
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His	Gly	Glu	Ser	Ser	Leu	Asp	Ile	Ala	Arg	Arg	Leu	Lys	Phe	Ser	Gln	
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att	gaa	tta	atg	cta	agg	aaa	gca	ttg	taa	t	cctt	gtgacc	acacc	gatgg		933
Ile	Glu	Leu	Met	Leu	Arg	Lys	Ala	Leu	*							
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cta aga tat aca cac atg aag act gct ggt ggt gca agg tgt gga gtc      328
Leu Arg Tyr Thr His Met Lys Thr Ala Gly Gly Ala Arg Cys Gly Val
   25               30               35               40

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Ile Gly Ala Val Ile Ala Val Cys Arg Ser Glu Leu Glu Ser Pro Glu
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Lys Gly Leu Cys Cys Gly Leu Lys   *
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Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp
90 95 100

cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga 448
Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg
105 110 115

caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag 496
Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu
120 125 130

tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga 544
Ser Ser Ser Glu Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg
135 140 145 150

cag tat cat gag agt gag gag gag agt gaa gag gag gag gca gcc tga 592
Gln Tyr His Glu Ser Glu Glu Glu Ser Glu Glu Glu Glu Ala Ala *
155 160 165

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<213> Homo sapiens

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Met Ala Glu Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys
1 5 10

ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg 155
Leu Val Gly Ser Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu
15 20 25 30

gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag 203

Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln	
35 40 45	
gct gga agc agt ggg cca ggg aat tct cag aac agc ttt cta gtt caa	251
Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln	
50 55 60	
gag gtg atg gaa gaa gag tgg aat gct ttg cag tca gtg gag aat tgt	299
Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys	
65 70 75	
cca gaa gac ttg gct cag ctg gag gag ctg ata gac atg gct gtg ctg	347
Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu	
80 85 90	
gag gaa att caa cag gag ctg atc aac caa gag cag tcc atc atc agc	395
Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser	
95 100 105 110	
gag tat gag aag agc ttg cag ttt gat gaa aag tgt ctc agc atc atg	443
Glu Tyr Glu Lys Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met	
115 120 125	
ctg gct gag tgg gag gca aac cca ctc atc tgt cct gta tgt aca aag	491
Leu Ala Glu Trp Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys	
130 135 140	
tac aac ctg aga atc aca agc ggt gtg gtg gtg tgt cag tgt ggc ctg	539
Tyr Asn Leu Arg Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu	
145 150 155	
tcc atc cca tct cat tct tct gag ttg aca gag cag aag ctt cgt gcc	587
Ser Ile Pro Ser His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala	
160 165 170	
tgt tta gag ggt agt ata aat gag cac agt gca cat tgt ccc cac aca	635
Cys Leu Glu Gly Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr	
175 180 185 190	
cct gaa ttt tca gtc act gga gga aca gaa gaa aag tcc agt ctt ctc	683
Pro Glu Phe Ser Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu	
195 200 205	
atg agc tgt ctg gcc tgt gat act tgg gct gtg atc ctc tag agccagc	732
Met Ser Cys Leu Ala Cys Asp Thr Trp Ala Val Ile Leu *	
210 215 220	
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aaaaaa	857

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<400> 71

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cgctgggacg tatgtgccga gggccgcggc gtctgacctc atggcgtaga gcctagcaac      180
agcgcaggct cccagccgag tccggtt atg gcc gct gcc gtc ccg aag agg atg      233
                Met Ala Ala Ala Val Pro Lys Arg Met
                  1                      5

agg ggg cca gca caa gcg aaa ctg ctg ccc ggg tcg gcc atc caa gcc      281
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
  10                      15                      20                      25

ctt gtg ggg ttg gcg cgg ccg ctg gtc ttg gcg ctc ctg ctt gtg tcc      329
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val Ser
                30                      35                      40

gcc gct cta tcc agt gtt gta tca cgg act gat tca ccg agc cca acc      377
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
                45                      50                      55

gta ctc aac tca cat att tct acc cca aat gtg aat gct tta aca cat      425
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His
                60                      65                      70

gaa aac caa acc aaa cct tct att tcc caa atc agc acc acc ctc cct      473
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro
  75                      80                      85

ccc acg acg agt acc aag aaa agt gga gga gca tct gtg gtc cct cat      521
Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro His
  90                      95                      100                      105

ccc tcg cct act cct ctg tct caa gag gaa gct gat aac aat gaa gat      569
Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu Asp
                110                      115                      120

cct agt ata gag gag gag gat ctt ctc atg ctg aac agt tct cca tcc      617
Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro Ser
                125                      130                      135

aca gcc aaa gac act cta gac aat ggc gat tat gga gaa cca gac tat      665
Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp Tyr
                140                      145                      150

gac tgg acc acg ggc ccc agg gac gac gac gag tct gat gac acc ttg      713
Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr Leu

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155	160	165	
gaa gaa aac agg ggt tac atg gaa att gaa cag tca gtg aaa tct ttt			761
Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser Phe			
170	175	180	185
aag atg cca tcc tca aat ata gaa gag gaa gac agc cat ttc ttt ttt			809
Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe Phe			
	190	195	200
cat ctt att att ttt gct ttt tgc att gct gtt gtt tac att aca tat			857
His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr Tyr			
	205	210	215
cac aac aaa agg aag att ttt ctt ctg gtt caa agc agg aaa tgg cgt			905
His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp Arg			
	220	225	230
gat ggc ctt tgt tcc aaa aca gtg gaa tac cat cgc cta gat cag aat			953
Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln Asn			
	235	240	245
gtt aat gag gca atg cct tct ttg aag att acc aat gat tat att ttt			1001
Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile Phe			
	250	255	260
taa			1004
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<210> 72
 <211> 1562
 <212> DNA
 <213> Homo sapiens

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aatagtaact ggcctgtttg gatactaaaa ttgaaaataa ctttttagcct cctccttatg	180
atagccgccca gagtaaattgt tgagcattac tacagaaaag ccacaaacca agaattctacc	240
tgtttggaag gatcttttgc atctctgaag gtgcttaaag catacttagt gccttttcctt	300
ttaactggga agataaaaga agtatctgtc caagatatta atatgtaaga taacattgta	360
gacatgttct tctgataata caagggttat tctatttgca ttaggatatt tgtggacatg	420

tccatctaata ataaaggaaa gttttttaaat cattgaggca ttaggggctg agttatataa 480
tgtagaaact tctaaagata attggatgag aatatacata ttgacctgta tattatgact 540
aatcatgact cagatcttaa tacagggatg atctcatagc atttagatat cagaaaaggt 600
tttgacctat atgtctttaa tattgtttga atacatgtat aatctttatc attcctcagt 660
gtttcatttc tcaaattctg taaaaggaat ataagaggaa agacaattca tatacaaaga 720
caacgagatt aaaaatatgc agtaggaaaa ataattactt aaggggagat tttttttaca 780
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attaaccaca gaattatagc aggtattcat aacttaagtt tgaaaatcaa tagcgtctgc 1080
aatggatta acagattaga gaatcaacag catcgaaaa taggttaatg catattgctt 1140
ctaacaagtg catgaagaaa tagaagaagc tatgtagctt tcagttctga cagaaaaggg 1200
tgaaggaggg tatcatttca agaaaaaaaa tagctatcac gca atg gtt atc tct 1255
Met Val Ile Ser
1
gaa aat att tgt att aag atg tgt ata cat ggc cag gca tgg tgg ctc 1303
Glu Asn Ile Cys Ile Lys Met Cys Ile His Gly Gln Ala Trp Trp Leu
5 10 15 20
atg cct gta atc cca gca ctt tgg gag gca ggt gga tca cga ggt cag 1351
Met Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Gly Ser Arg Gly Gln
25 30 35
gag atc aag acc atc ctg gcc aac atg gtg aaa cct cat ctc tac taa 1399
Glu Ile Lys Thr Ile Leu Ala Asn Met Val Lys Pro His Leu Tyr *
40 45 50
aaatacaaaa atgagcgggg tgtggtggcc catgcctgta gtcccagctg ctcgggagac 1459
tgaatctctt gagcctggga agcagaggtt gcagtgaact gagatcgct cactgcactc 1519
cagccccggg gacagagcga gattccatct caaaaaaaaa aaa 1562

<210> 73
<211> 2100
<212> DNA
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aacaagaaac aataattcta agttagccag ccaatcaaac tacttcagta aatgatcata	180
ctacagcctg gaatcactca aacaaaaaat tcttctagtt ctctttaaag atattttatcg	240
tttatttttt catgaaacca aagtaattga ttcaacaata ctaacagttc tagcatgcaa	300
caaaccatct actatctaata gtttaattctt cttaacatgt atattttcat tcctataaag	360
tttccataag aagcttgcaa tgacaataaa ggtaaataag tacagttgtc ccttggtatc	420
catgggggat tgggttcctgg accgtcccc caaccacag ataccaaaaa tccaagtata	480
ctcaagtccc ttacataaaa tgacatattt gtatataacc aacgcacatc cgctgtata	540
ctttatccct agactaatac ctaatgcaat gtaaatagcta tttaaataac tgttatactg	600
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cacagatgca gagtacatgg atacagaggg ccaactgttt tgttacaggt acttcaaata	720
gcactacagt acatctttga caaaattttt acaatattcc acctttcaat atgaaacagc	780
ttaaaaaggc atgggtcaaa aataaagtat agtagtatca cttacgcaaa taaagtctca	840
gaatcataca agcacaacac tgtaggact ctccctgttt aggctgggaa aaacattata	900
caaaacattt tcttcaaata aaattacata aattgcttag aaaaatgcca aaatcaataa	960
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tcttgcttgc actggaggaa catatctcaa ggaaacctaa gagaaagtg tctttaaagc	1140
atgtgattct cctgtttttg ctggatgtct gtatctacat aataaacagg cacacttcta	1200
catcactggg tattttactc agactgtc atg ttt cat ctc tgt aaa tta aac	1252
Met Phe His Leu Cys Lys Leu Asn	
1 5	
cca agt tac tta aaa atc acc tgt ggt aaa aga agc aag cag atc acc	1300
Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr	
10 15 20	

ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca	1348
Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser	
25 30 35 40	
ggt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata	1396
Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile	
45 50 55	
gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc	1446
Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly *	
60 65	
ctctttttcag cttagaaaca taacggttca ttccttttat tgctagagaa tgtcattcct	1506
gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt	1566
tgtagtaaag aatatttccc aaatcataac agttctatgt ggaatgatac ccacaactct	1626
acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca	1686
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ctagtcattg ccatttgatc aaacttagaa caggcttaaa taacagaacc actccattaa	1806
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tctagaatag tcttaagtct atgactactg ctatcattaa tgagcaaata aatgacttga	1926
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agaaaaatat tcttggttaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc	2046
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agcgaccttg gccgttgcc tgaccatctt agtgctgtct gtctgacta tcatcatctg	180
cttcacctgc tctgctgct gcctttacaa gacgtgccgc cgaccacgtc cggttgtcac	240
caccaccaca tccaccactg tgggtgc atg ccc ctt atc ctc agc ctc caa gtg	293

	Met	Pro	Leu	Ile	Leu	Ser	Leu	Gln	Val	
	1				5					
tgc cgc cca gct acc cgt gga cca agc tac cag gcc tac cac acc atg										341
Cys Arg Pro Ala Thr Arg Gly Pro Ser Tyr Gln Gly Tyr His Thr Met										
10 15 20 25										
ccg cct cag cca ggg atg cca gca gcc acc cta ccc aat gca ggg aag										389
Pro Pro Gln Pro Gly Met Pro Ala Ala Thr Leu Pro Asn Ala Gly Lys										
30 35 40										
atg gcg gac att cag act gag cgt gcc tac caa aag cag ccg acc atc										437
Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile										
45 50 55										
ttt caa aac aag aag agg gtc ctg ctg gga gaa act gcc aag gag aag										485
Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys										
60 65 70										
ctc ccg cgg tac tac aag aac atc ggt ctg gcc ttc aag aca ccc aag										533
Leu Pro Arg Tyr Tyr Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Lys										
75 80 85										
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Glu Ala Ile Glu Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe Thr Gly										
90 95 100 105										
aat gtg tcc att cga ggg cgg atc ctc tct gcc gtg gtg acc aag atg										629
Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr Lys Met										
110 115 120										
aag atg cag agg acc att gtc atc cgc cga gac tat ctg cac tac atc										677
Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr Ile										
125 130 135										
cgc aag tac aac cgc ttc gag aag cgc cac aag aac atg tct gta cac										725
Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val His										
140 145 150										
ctg tcc ccc tgc ttc agg gac gtc cag atc ggt gac atc gtc aca gtg										773
Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val										
155 160 165										
ggc gag tgc cgg cct ctg agc aag aca gtg cgc ttc aac gtg ctc aag										821
Gly Glu Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys										
170 175 180 185										
gtc acc aag gct gcc ggc acc aag aag cag ttc cag aag ttc tga ggc										869
Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe *										
190 195 200										
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aaaa										933

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 <222> (446)..(2956)

<400> 75

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cgtgctccac ctctggccct tcaccatcca cgacctgcgg gcactcgggtg ctaagaagtt      180
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tctgctgaag gtagcattgc tgctgggggt ggaaattcac tgggggtgtca ctttcactgg      300
cctccagccc cctcctagga aggggagtgg ctggcgtgcc cagctccaac ccaaccccc      360
tgcccagctg gccaaactatg aatttgacgt ctttatctcg gctgcaggag gtaaattcgt      420
ccctgaaggc ttcaaagtgc gagaa  atg cga ggc aaa ctg gcc att ggc atc      472
                               Met Arg Gly Lys Leu Ala Ile Gly Ile
                               1               5

aca gcc aac ttt gtg aat gga cgc acc gtg gag gag aca cag gtg ccg      520
Thr Ala Asn Phe Val Asn Gly Arg Thr Val Glu Glu Thr Gln Val Pro
 10               15               20               25

gag atc agt ggt gta gcc agg atc tac aac cag agc ttc ttc cag agc      568
Glu Ile Ser Gly Val Ala Arg Ile Tyr Asn Gln Ser Phe Phe Gln Ser
               30               35               40

ctt ctc aaa gcc aca ggc att gat ctg gag aac att gtg tac tac aag      616
Leu Leu Lys Ala Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys
               45               50               55

gac gac acc cac tac ttt gtg atg aca gcc aag aag cag tgc ctg ctg      664
Asp Asp Thr His Tyr Phe Val Met Thr Ala Lys Lys Gln Cys Leu Leu
 60               65               70

cgg ctg ggg gtg ctg cgc cag gac tgg cca gac acc aat cgg ctg ctg      712
Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
 75               80               85

ggc agt gcc aat gtg gtg ccc gag gct ctg cag cgc ttt acc cgg gca      760
Gly Ser Ala Asn Val Val Pro Glu Ala Leu Gln Arg Phe Thr Arg Ala
 90               95               100               105

gct gct gac ttt gcc acc cat ggc aag ctc ggg aaa cta gag ttt gcc      808
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
 110               115               120
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cag gat gcc cat ggg cag cct gat gtc tct gcc ttt gac ttc acg agc	856
Gln Asp Ala His Gly Gln Pro Asp Val Ser Ala Phe Asp Phe Thr Ser	
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Met Met Arg Ala Glu Ser Ser Ala Arg Val Gln Glu Lys His Gly Ala	
140 145 150	
cgc ctg ctg ctg gga ctg gtg ggg gac tgc ctg gtg gag ccc ttc tgg	952
Arg Leu Leu Leu Gly Leu Val Gly Asp Cys Leu Val Glu Pro Phe Trp	
155 160 165	
ccc ctg ggc act gga gtg gca cgg ggc ttc ctg gca gcc ttt gat gca	1000
Pro Leu Gly Thr Gly Val Ala Arg Gly Phe Leu Ala Ala Phe Asp Ala	
170 175 180 185	
gcc tgg atg gtg aag cgg tgg gca gag ggc gct gag tcc cta gag gtg	1048
Ala Trp Met Val Lys Arg Trp Ala Glu Gly Ala Glu Ser Leu Glu Val	
190 195 200	
ttg gct gag cgt gag agc ctg tac cag ctt ctg tca cag aca tcc cca	1096
Leu Ala Glu Arg Glu Ser Leu Tyr Gln Leu Leu Ser Gln Thr Ser Pro	
205 210 215	
gaa aac atg cat cgc aat gtg gcc cag tat ggg ctg gac cca gcc acc	1144
Glu Asn Met His Arg Asn Val Ala Gln Tyr Gly Leu Asp Pro Ala Thr	
220 225 230	
cgc tac ccc aac ctg aac ctc cgg gca gtg acc ccc aat cag gta cga	1192
Arg Tyr Pro Asn Leu Asn Leu Arg Ala Val Thr Pro Asn Gln Val Arg	
235 240 245	
gac ctg tat gat gtg cta gcc aag gag cct gtg cag agg aac aac gac	1240
Asp Leu Tyr Asp Val Leu Ala Lys Glu Pro Val Gln Arg Asn Asn Asp	
250 255 260 265	
aag aca gat aca ggg atg cca gcc acc ggg tcg gca ggc acc cag gag	1288
Lys Thr Asp Thr Gly Met Pro Ala Thr Gly Ser Ala Gly Thr Gln Glu	
270 275 280	
gag ctg cta cgc tgg tgc cag gag cag aca gct ggg tac ccg gga gtc	1336
Glu Leu Leu Arg Trp Cys Gln Glu Gln Thr Ala Gly Tyr Pro Gly Val	
285 290 295	
cac gtc tcc gat ttg tct tcc tcc tgg gct gat ggg cta gct ctg tgt	1384
His Val Ser Asp Leu Ser Ser Ser Trp Ala Asp Gly Leu Ala Leu Cys	
300 305 310	
gcc ctg gtg tac cgg ctg cag cct ggc ctg ctg gaa ccc tca gag ctg	1432
Ala Leu Val Tyr Arg Leu Gln Pro Gly Leu Leu Glu Pro Ser Glu Leu	
315 320 325	
cag ggg ctg gga gct ctg gaa gca act gct tgg gca cta aag gtg gca	1480
Gln Gly Leu Gly Ala Leu Glu Ala Thr Ala Trp Ala Leu Lys Val Ala	
330 335 340 345	
gag aat gag ctg ggc atc aca ccg gtg gtg tct gca cag gcc gtg gta	1528

Glu Asn Glu Leu Gly Ile Thr Pro Val Val Ser Ala Gln Ala Val Val	
350 355 360	
gca ggg agt gac cca ctg ggc ctc att gcc tac ctc agc cac ttc cac	1576
Ala Gly Ser Asp Pro Leu Gly Leu Ile Ala Tyr Leu Ser His Phe His	
365 370 375	
agt gcc ttc aag agc atg gcc cac agc cca ggc cct gtc agc cag gcc	1624
Ser Ala Phe Lys Ser Met Ala His Ser Pro Gly Pro Val Ser Gln Ala	
380 385 390	
tcc cca ggg acc tcc agt gct gta tta ttc ctt agt aaa ctt cag agg	1672
Ser Pro Gly Thr Ser Ser Ala Val Leu Phe Leu Ser Lys Leu Gln Arg	
395 400 405	
acc ctg cag cga tcc cgg gcc aag gaa aat gca gag gat gct ggt ggc	1720
Thr Leu Gln Arg Ser Arg Ala Lys Glu Asn Ala Glu Asp Ala Gly Gly	
410 415 420 425	
aag aag ctg cgc ttg gag atg gag gcc gag acc cca agt act gag gtg	1768
Lys Lys Leu Arg Leu Glu Met Glu Ala Glu Thr Pro Ser Thr Glu Val	
430 435 440	
cca cct gac cca gag cct ggt gta ccc ctg aca ccc cca tcc caa cac	1816
Pro Pro Asp Pro Glu Pro Gly Val Pro Leu Thr Pro Pro Ser Gln His	
445 450 455	
cag gag gcc ggt gct ggg gac ctg tgt gca ctt tgt ggg gaa cac ctc	1864
Gln Glu Ala Gly Ala Gly Asp Leu Cys Ala Leu Cys Gly Glu His Leu	
460 465 470	
tat gtc ctg gaa cgc ctc tgt gtc aac ggc cat ttc ttc cac cgg agc	1912
Tyr Val Leu Glu Arg Leu Cys Val Asn Gly His Phe Phe His Arg Ser	
475 480 485	
tgc ttc cgc tgc cat acc tgt gag gcc aca ctg tgg cca ggt ggc tac	1960
Cys Phe Arg Cys His Thr Cys Glu Ala Thr Leu Trp Pro Gly Gly Tyr	
490 495 500 505	
gag cag cac cca gga gat gga cat tcc tac tgc ctc cag cac ctg ccc	2008
Glu Gln His Pro Gly Asp Gly His Ser Tyr Cys Leu Gln His Leu Pro	
510 515 520	
cag aca gac cac aaa gag gaa ggc agc gat aga ggc cct gag agt ccg	2056
Gln Thr Asp His Lys Glu Glu Gly Ser Asp Arg Gly Pro Glu Ser Pro	
525 530 535	
gag ctc ccc aca cca agt gag aat agc atg cca cca ggc ctc tca act	2104
Glu Leu Pro Thr Pro Ser Glu Asn Ser Met Pro Pro Gly Leu Ser Thr	
540 545 550	
ccc aca gcc tcg cag gag ggg gcc ggt cct gtt cca gat ccc agc cag	2152
Pro Thr Ala Ser Gln Glu Gly Ala Gly Pro Val Pro Asp Pro Ser Gln	
555 560 565	
ccc acc cgt cgg cag atc cgc ctc tcc agc ccg gag cgc cag cgg ttg	2200
Pro Thr Arg Arg Gln Ile Arg Leu Ser Ser Pro Glu Arg Gln Arg Leu	

570	575	580	585	
tcc tcc ctt aac ctt acc cct gac ccg gaa atg gag cct cca ccc aag				2248
Ser Ser Leu Asn Leu Thr Pro Asp Pro Glu Met Glu Pro Pro Pro Lys	590	595	600	
cct ccc cgc agc tgc tcc gcc ttg gcc cgc cac gcc ctg gag agc agc				2296
Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala Leu Glu Ser Ser	605	610	615	
ttt gtg ggc tgg ggc ctg cca gtc cag agc cct caa gct ctt gtg gcc				2344
Phe Val Gly Trp Gly Leu Pro Val Gln Ser Pro Gln Ala Leu Val Ala	620	625	630	
atg gag aag gag gaa aaa gag agt ccc ttc tcc agt gaa gag gaa gaa				2392
Met Glu Lys Glu Glu Lys Glu Ser Pro Phe Ser Ser Glu Glu Glu Glu	635	640	645	
gaa gat gtg cct ttg gac tca gat gtg gaa cag gcc ctg cag acc ttt				2440
Glu Asp Val Pro Leu Asp Ser Asp Val Glu Gln Ala Leu Gln Thr Phe	650	655	660	665
gcc aag acc tca ggc acc atg aat aac tac cca aca tgg cgt cgg act				2488
Ala Lys Thr Ser Gly Thr Met Asn Asn Tyr Pro Thr Trp Arg Arg Thr	670	675	680	
ctg ctg cgc cgt gcg aag gag gag gag atg aag agg ttc tgc aag gcc				2536
Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg Phe Cys Lys Ala	685	690	695	
cag acc atc caa cgg cga cta aat gag att gag gct gcc ttg agg gag				2584
Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala Ala Leu Arg Glu	700	705	710	
cta gag gcc gag ggc gtg aag ctg gag ctg gcc ttg agg cgc cag agc				2632
Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu Arg Arg Gln Ser	715	720	725	
agt tcc cca gaa cag caa aag aaa cta tgg gta gga cag ctg cta cag				2680
Ser Ser Pro Glu Gln Gln Lys Lys Leu Trp Val Gly Gln Leu Leu Gln	730	735	740	745
ctc gtt gac aag aaa aac agc ctg gtg gct gag gag gcc gag ctc atg				2728
Leu Val Asp Lys Lys Asn Ser Leu Val Ala Glu Glu Ala Glu Leu Met	750	755	760	
atc acg gtg cag gaa ttg aat ctg gag gag aaa cag tgg cag ctg gac				2776
Ile Thr Val Gln Glu Leu Asn Leu Glu Glu Lys Gln Trp Gln Leu Asp	765	770	775	
cag gag cta cga ggc tac atg aac cgg gaa gaa aac cta aag aca gct				2824
Gln Glu Leu Arg Gly Tyr Met Asn Arg Glu Glu Asn Leu Lys Thr Ala	780	785	790	
gct gat cgg cag gct gag gac cag gtc ctg agg aag ctg gtg gat ttg				2872
Ala Asp Arg Gln Ala Glu Asp Gln Val Leu Arg Lys Leu Val Asp Leu	795	800	805	

gtc aac cag aga gat gcc ctc atc cgc ttc cag gag gag cgc agg ctc	2920
Val Asn Gln Arg Asp Ala Leu Ile Arg Phe Gln Glu Glu Arg Arg Leu	
810 815 820 825	
agc gag ctg gcc ttg ggg aca ggg gcc cag ggc tag acga ggggtgggccg	2970
Ser Glu Leu Ala Leu Gly Thr Gly Ala Gln Gly *	
830 835	
tctgcttttcg ttcccacaaa gaaagcacct caccacagca cagtgccacc cctgttcac	3030
tgggctgcct ggcagagagc cttgctgttt acaattaaaa tgtttctgcc aaaaaaaaa	3090
aaa	3093

<210> 76
 <211> 1110
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (179)..(961)

<400> 76	
gctggagaac aactatctat tcgatgatga agatacccca ccaaacccaa aaaaagagat	60
ctctcgagga tccgaattcg cggccgcgtc gacgtgggct tgtgggtctt tgagaccga	120
aaattgagag cgtttttcgca ctccagcggc tgctcctggc ggctctgcgg ccgtcacc	178
atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac	226
Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr	
1 5 10 15	
cgt ttg gat tac cat gag aaa aag aga aag aag gaa agt cga gag gct	274
Arg Leu Asp Tyr His Glu Lys Lys Arg Lys Lys Glu Ser Arg Glu Ala	
20 25 30	
cat gaa cgt tca aag aag gca aag aaa atg att ggt ctg aag gct aag	322
His Glu Arg Ser Lys Lys Ala Lys Lys Met Ile Gly Leu Lys Ala Lys	
35 40 45	
ctt tac cat aaa cag cgt cat gct gag aaa ata caa atg aaa aag act	370
Leu Tyr His Lys Gln Arg His Ala Glu Lys Ile Gln Met Lys Lys Thr	
50 55 60	
atc aag atg cat gaa aag aga aac acc aaa caa aag aat gat gaa aag	418
Ile Lys Met His Glu Lys Arg Asn Thr Lys Gln Lys Asn Asp Glu Lys	
65 70 75 80	
aca cca cag gga gca gta cct gcc tat ctg ctg gac aga gag gga caa	466
Thr Pro Gln Gly Ala Val Pro Ala Tyr Leu Leu Asp Arg Glu Gly Gln	
85 90 95	

tct cga gct aaa gta ctt tcc aat atg att aaa cag aaa aga aaa gag	514
Ser Arg Ala Lys Val Leu Ser Asn Met Ile Lys Gln Lys Arg Lys Glu	
100 105 110	
aag gcg gga aaa tgg gaa gtc cct ctg cct aaa gta cgt gcc cag gga	562
Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly	
115 120 125	
gaa aca gaa gta tta aaa gtt att cga aca gga aag aga aag aag aag	610
Glu Thr Glu Val Leu Lys Val Ile Arg Thr Gly Lys Arg Lys Lys Lys	
130 135 140	
gca tgg aag aga atg gtt act aaa gtg tgc ttt gtt gga gat ggc ttt	658
Ala Trp Lys Arg Met Val Thr Lys Val Cys Phe Val Gly Asp Gly Phe	
145 150 155 160	
aca aga aaa cca cct aaa tat gaa aga ttc atc agg cca atg ggc ttg	706
Thr Arg Lys Pro Pro Lys Tyr Glu Arg Phe Ile Arg Pro Met Gly Leu	
165 170 175	
cgt ttc aag aaa gcc cat gta aca cat cct gaa ctg aaa gcc acc ttt	754
Arg Phe Lys Lys Ala His Val Thr His Pro Glu Leu Lys Ala Thr Phe	
180 185 190	
tgc cta cca ata ctt ggt gta aag aag aat ccc tca tcc cca ctg tat	802
Cys Leu Pro Ile Leu Gly Val Lys Lys Asn Pro Ser Ser Pro Leu Tyr	
195 200 205	
aca act ttg ggt gtt att acc aaa ggt act gtc att gaa gta aat gtg	850
Thr Thr Leu Gly Val Ile Thr Lys Gly Thr Val Ile Glu Val Asn Val	
210 215 220	
agc gaa ttg ggc ctt gtg aca caa gga ggc aaa gtt att tgg gga aaa	898
Ser Glu Leu Gly Leu Val Thr Gln Gly Gly Lys Val Ile Trp Gly Lys	
225 230 235 240	
tat gcc cag gtt acc aac aat cct gaa aat gat gga tgt ata aat gca	946
Tyr Ala Gln Val Thr Asn Asn Pro Glu Asn Asp Gly Cys Ile Asn Ala	
245 250 255	
gtc tta ctg gtt tga cagcaatttc atatataatt attgaggact acacaccaat	1001
Val Leu Leu Val *	
260	
tgaagaaact gccattactg tgatgtttct gaatactacc aaacagccat acatgtctgc	1061
aatgaagaga tttattaaat tgtaaacatt aaagtggaaa aaaaaaaaaa	1110

<210> 77
 <211> 1835
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (29)..(1714)

<400> 77

acgagcctgc gttttccggc cagaggac	atg atg cag ggg gag gca cac cct	52
	Met Met Gln Gly Glu Ala His Pro	
	1 5	
agt gct tcc ctt att gac aga acc atc aag atg aga aaa gaa aca gag	100	
Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys Glu Thr Glu		
10 15 20		
gct agg aaa gtg gtc tta gcc tgg gga ctc cta aat gta tct atg gct	148	
Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val Ser Met Ala		
25 30 35 40		
gga atg ata tat act gaa atg act gga aaa ttg att agt tca tac tac	196	
Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr Tyr		
45 50 55		
aat gtg aca tac tgg ccc ctc tgg tat att gag ctt gcc ctt gca tct	244	
Asn Val Thr Tyr Trp Pro Leu Trp Tyr Ile Glu Leu Ala Leu Ala Ser		
60 65 70		
ctc ttc agc ctt aat gcc tta ttt gat ttt tgg aga tat ttc aaa tat	292	
Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg Tyr Phe Lys Tyr		
75 80 85		
act gtg gca cca aca agt ctg gtt gtt agt cct gga cag caa aca ctt	340	
Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly Gln Gln Thr Leu		
90 95 100		
tta ggg ttg aaa aca gct gtt gta cag act acg cct cca cat gat ctg	388	
Leu Gly Leu Lys Thr Ala Val Val Gln Thr Thr Pro Pro His Asp Leu		
105 110 115 120		
gca gca acc caa atc cct ccc gct cca cct tcc cct tca att cag ggt	436	
Ala Ala Thr Gln Ile Pro Pro Ala Pro Pro Ser Pro Ser Ile Gln Gly		
125 130 135		
cag agt gtg ttg agt tat agc cct tct cgt tcg ccc agt acc agt ccc	484	
Gln Ser Val Leu Ser Tyr Ser Pro Ser Arg Ser Pro Ser Thr Ser Pro		
140 145 150		
aag ttc acc acc agc tgt atg act ggt tac agc cct cag ctg caa ggt	532	
Lys Phe Thr Thr Ser Cys Met Thr Gly Tyr Ser Pro Gln Leu Gln Gly		
155 160 165		
ctg tcc tca ggt ggc agt ggt tct tat agc cct gga gtg acc tac tcg	580	
Leu Ser Ser Gly Gly Ser Gly Ser Tyr Ser Pro Gly Val Thr Tyr Ser		
170 175 180		
ccc gtc agt ggt tat aat aag ttg gcg agc ttt agc ccc tct cct cct	628	
Pro Val Ser Gly Tyr Asn Lys Leu Ala Ser Phe Ser Pro Ser Pro Pro		
185 190 195 200		
tct ccg tac cct acc act gtt gga cca gtg gag agc agt gga ttg aga	676	

Ser	Pro	Tyr	Pro	Thr	Thr	Val	Gly	Pro	Val	Glu	Ser	Ser	Gly	Leu	Arg		
				205					210					215			
tct	cgc	tac	cgt	tct	tca	cct	acc	gtc	tac	aac	tca	cct	act	gac	aaa		724
Ser	Arg	Tyr	Arg	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Pro	Thr	Asp	Lys		
			220					225					230				
gaa	gac	tac	atg	acc	gac	cta	cga	act	ttg	gat	act	ttt	ctc	aga	agt		772
Glu	Asp	Tyr	Met	Thr	Asp	Leu	Arg	Thr	Leu	Asp	Thr	Phe	Leu	Arg	Ser		
		235					240					245					
gaa	gag	gag	aaa	cag	cat	agg	ggt	aag	ctg	ggg	agc	cca	gat	tct	acc		820
Glu	Glu	Glu	Lys	Gln	His	Arg	Val	Lys	Leu	Gly	Ser	Pro	Asp	Ser	Thr		
	250					255					260						
tct	cct	tcc	agc	agt	cct	act	ttc	tgg	aac	tat	agt	cgt	tct	atg	ggg		868
Ser	Pro	Ser	Ser	Ser	Pro	Thr	Phe	Trp	Asn	Tyr	Ser	Arg	Ser	Met	Gly		
265					270				275						280		
gat	tat	gca	caa	act	tta	aag	aag	ttt	cag	tat	cag	ctt	gcc	tgt	agg		916
Asp	Tyr	Ala	Gln	Thr	Leu	Lys	Lys	Phe	Gln	Tyr	Gln	Leu	Ala	Cys	Arg		
				285				290						295			
tct	cag	gcc	cca	tgt	gct	aac	aaa	gat	gaa	gcc	gat	ctc	agc	tct	aaa		964
Ser	Gln	Ala	Pro	Cys	Ala	Asn	Lys	Asp	Glu	Ala	Asp	Leu	Ser	Ser	Lys		
			300					305					310				
caa	gcc	gca	gaa	gag	gtc	tgg	gca	aga	gtg	gct	atg	aat	aga	caa	ctt		1012
Gln	Ala	Ala	Glu	Glu	Val	Trp	Ala	Arg	Val	Ala	Met	Asn	Arg	Gln	Leu		
		315					320					325					
ctt	gat	cat	atg	gat	tca	tgg	aca	gct	aaa	ttt	aga	aat	tgg	atc	aat		1060
Leu	Asp	His	Met	Asp	Ser	Trp	Thr	Ala	Lys	Phe	Arg	Asn	Trp	Ile	Asn		
	330					335				340							
gag	aca	ata	tta	gtg	cca	ctt	ggt	caa	gag	att	gag	tct	gtc	agc	aca		1108
Glu	Thr	Ile	Leu	Val	Pro	Leu	Val	Gln	Glu	Ile	Glu	Ser	Val	Ser	Thr		
345				350					355						360		
cag	atg	aga	cga	atg	ggg	tgt	cca	gag	cta	cag	ata	gga	gag	gct	agt		1156
Gln	Met	Arg	Arg	Met	Gly	Cys	Pro	Glu	Leu	Gln	Ile	Gly	Glu	Ala	Ser		
				365				370						375			
att	act	agc	ttg	aaa	caa	gct	gcc	ctg	ggt	aaa	gcg	cct	ctc	att	ccg		1204
Ile	Thr	Ser	Leu	Lys	Gln	Ala	Ala	Leu	Val	Lys	Ala	Pro	Leu	Ile	Pro		
			380					385					390				
act	ttg	aac	aca	atc	ggt	cag	tat	cta	gac	ctt	act	cca	aat	cag	gaa		1252
Thr	Leu	Asn	Thr	Ile	Val	Gln	Tyr	Leu	Asp	Leu	Thr	Pro	Asn	Gln	Glu		
		395				400						405					
tac	ttg	ttt	gaa	agg	atc	aaa	gaa	cta	tct	cag	gga	ggt	tgt	atg	agc		1300
Tyr	Leu	Phe	Glu	Arg	Ile	Lys	Glu	Leu	Ser	Gln	Gly	Gly	Cys	Met	Ser		
	410					415					420						
tca	ttt	cga	tgg	aac	aga	ggg	ggc	gac	ttc	aaa	gga	cga	aag	tgg	gat		1348
Ser	Phe	Arg	Trp	Asn	Arg	Gly	Gly	Asp	Phe	Lys	Gly	Arg	Lys	Trp	Asp		

425	430	435	440	
aca gac ctg ccc acc gat tct gct atc atc atg cat gta ttt tgc acc				1396
Thr Asp Leu Pro Thr Asp Ser Ala Ile Ile Met His Val Phe Cys Thr	445	450	455	
tac ctt gat tcc aga tta cct cca cat ccg aag tat ccc gac gga aaa				1444
Tyr Leu Asp Ser Arg Leu Pro Pro His Pro Lys Tyr Pro Asp Gly Lys	460	465	470	
act ttt act tct cag cac ttt gtt cag aca cca aat aaa cca gat gtt				1492
Thr Phe Thr Ser Gln His Phe Val Gln Thr Pro Asn Lys Pro Asp Val	475	480	485	
aca aat gag aat gtt ttt tgc att tat cag agt gct atc aac cct ccc				1540
Thr Asn Glu Asn Val Phe Cys Ile Tyr Gln Ser Ala Ile Asn Pro Pro	490	495	500	
cat tat gag ctc atc tac cag cgt cat gta tac aac ctg cca aag ggc				1588
His Tyr Glu Leu Ile Tyr Gln Arg His Val Tyr Asn Leu Pro Lys Gly	505	510	515	520
aga aat aat atg ttt cat aca ttg ttg atg ttt ctc tac atc ata aag				1636
Arg Asn Asn Met Phe His Thr Leu Leu Met Phe Leu Tyr Ile Ile Lys	525	530	535	
acc aaa gag tca gga atg ctt ggg aga gtt aat ctt ggt cta tct ggt				1684
Thr Lys Glu Ser Gly Met Leu Gly Arg Val Asn Leu Gly Leu Ser Gly	540	545	550	
gtg aat ata ttg tgg atc ttt ggc gag tag c aagtcataata tttaattctg				1735
Val Asn Ile Leu Trp Ile Phe Gly Glu *	555	560		
acatttagac tatttcactg aaccagaagt cgaaactaaa catctctgag ccaactgactc				1795
ttctgaaata aaatacacat ggggtgtaaaa aaaaaaaaaa				1835

<210> 78
 <211> 1029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (428)..(817)

<400> 78	
ccctgattat aactggatat tgggtagcat ccagttaaag tatcagtaga gcttggatgt	60
atcaaagaaa atattttatt caagttccca aaacaaactt gaggagttat gctggggtttg	120
aattgaagaa aaaaggccaa gttaaaatag gaaaacaaat gggttttcatt tgggtggcagt	180

tgaaatcaaa gtatacatgt gtatacatc taatccgtca tctatcccat gtggcatttt	240
ccaagggtttt aagagtctac caggccaaac cctttgccac tttactgct tttgctttgc	300
ttttcccctt tcttttctct cgctttgcct tcagcctttt tctttgcctt tggttcatcc	360
atattgggta ctgtccatgc tggtcggcgt gagcgtgagg tgtgggtgtt cgtttctcag	420
gtaaaac atg gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt	469
Met Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg	
1 5 10	
gct gaa aag aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa	517
Ala Glu Lys Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys	
15 20 25 30	
agt att ctc aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag	565
Ser Ile Leu Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu	
35 40 45	
ata gca act gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg	613
Ile Ala Thr Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met	
50 55 60	
caa tgt gag gta aaa gat gaa aaa gat gac atg aaa atg gag act gat	661
Gln Cys Glu Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp	
65 70 75	
att aag aga aac aaa aag act ctt cta gac cag cat gga cag tac cca	709
Ile Lys Arg Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro	
80 85 90	
ata tgg atg aac caa agg caa aga aaa agg ctg aag gca aag cga gag	757
Ile Trp Met Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu	
95 100 105 110	
aaa aga aag ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt	805
Lys Arg Lys Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly	
115 120 125	
ttg gcc tgg tag act cttaaaacct tggaaaatgc cacatgggat agatgacgga	860
Leu Ala Trp *	
130	
ttagaatgta tacacatgta tactttgatt tcaactgcc acaaatgaaa accatttggt	920
ttcctatttt aacttggcct tttttcttca attcaaacc agcataactc ctcaagtttg	980
ttttgggaac ttgaataaaa tattttcttt gatacaaaaa aaaaaaaaa	1029

<210> 79

<211> 5476

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (188)..(5149)

<400> 79

ggccccctgct cggataaagg tgggaggctc aggtgtcaat gtcaatgcaa agggcttgga	60
cttgggtggc agaggagggg tccaagttcc agcagtggac atttcatctt ctcttggggg	120
tagggcagta gaggtacagg gcccatctct ggagagtggg gatcatggca aaattaaatt	180
tcccacc atg aaa gtg ccg aaa ttt ggt gtc tca aca ggg cgt gag ggc	229
Met Lys Val Pro Lys Phe Gly Val Ser Thr Gly Arg Glu Gly	
1 5 10	
cag aca cca aag gca ggg ctg agg gtt tct gca cct gaa gtc tct gtg	277
Gln Thr Pro Lys Ala Gly Leu Arg Val Ser Ala Pro Glu Val Ser Val	
15 20 25 30	
ggg cac aag ggc ggc aag cca ggc ttg act atc caa gcc cct cag ctg	325
Gly His Lys Gly Gly Lys Pro Gly Leu Thr Ile Gln Ala Pro Gln Leu	
35 40 45	
gaa gtc agt gtg ccc tct gcc aat att gag ggc ctt gag ggg aag ctg	373
Glu Val Ser Val Pro Ser Ala Asn Ile Glu Gly Leu Glu Gly Lys Leu	
50 55 60	
aag ggc ccc caa atc act ggg cca tca ctt gag ggt gac cta ggc ctg	421
Lys Gly Pro Gln Ile Thr Gly Pro Ser Leu Glu Gly Asp Leu Gly Leu	
65 70 75	
aaa ggt gcc aag cca cag ggg cac att ggg gtg gat gcc tct gct ccc	469
Lys Gly Ala Lys Pro Gln Gly His Ile Gly Val Asp Ala Ser Ala Pro	
80 85 90	
caa att ggg ggt agc atc act ggc ccc agt gtg gaa gtt cag gcc cct	517
Gln Ile Gly Gly Ser Ile Thr Gly Pro Ser Val Glu Val Gln Ala Pro	
95 100 105 110	
gac att gat gtt cag ggg cct ggg agc aaa ctg aat gtg ccc aag atg	565
Asp Ile Asp Val Gln Gly Pro Gly Ser Lys Leu Asn Val Pro Lys Met	
115 120 125	
aaa gtc ccc aag ttc tct gta tca ggt gca aag gga gag gaa act ggg	613
Lys Val Pro Lys Phe Ser Val Ser Gly Ala Lys Gly Glu Glu Thr Gly	
130 135 140	
att gat gtg aca ctg cct aca ggt gaa gtg act gtt cct ggg gtc tct	661
Ile Asp Val Thr Leu Pro Thr Gly Glu Val Thr Val Pro Gly Val Ser	
145 150 155	
ggg gat gtc agc ctg cct gag att gct act ggt ggg ctg gaa gga aag	709
Gly Asp Val Ser Leu Pro Glu Ile Ala Thr Gly Leu Glu Gly Lys	
160 165 170	
atg aaa ggt act aaa gtg aag act cct gaa atg att att cag aaa cct	757

400	405	410	
gaa gga gaa ctc aaa ggc cca aaa gtg gac att gat gcc cca gat gtg Glu Gly Glu Leu Lys Gly Pro Lys Val Asp Ile Asp Ala Pro Asp Val 415 420 425 430			1477
gat gtt cat ggc cca gac tgg cac ttg aag atg ccc aag atg aaa atg Asp Val His Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 435 440 445			1525
ccc aaa ttc agt gtg cca ggg ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Val Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 450 455 460			1573
gtg aac ctg ccc aag gct gat gtg gac att tcc ggg ccc aag ata gat Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Ile Asp 465 470 475			1621
gtt act gct cct gat gtg agc att gag gaa cca gaa ggg aaa ttg aaa Val Thr Ala Pro Asp Val Ser Ile Glu Glu Pro Glu Gly Lys Leu Lys 480 485 490			1669
ggg ccc aag ttt aag atg cct gag atg aac atc aaa gtc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Val Pro Lys Ile 495 500 505 510			1717
tcc atg cct gat gtg gac tta cat ctg aaa ggc cct aac gta aag gga Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Asn Val Lys Gly 515 520 525			1765
gaa tat gat gtc aca atg cca aag gtt gaa agt gag att aaa gtt cct Glu Tyr Asp Val Thr Met Pro Lys Val Glu Ser Glu Ile Lys Val Pro 530 535 540			1813
gat gtt gaa ctt aaa agt gcc aaa atg gac att gat gtc cca gat gtg Asp Val Glu Leu Lys Ser Ala Lys Met Asp Ile Asp Val Pro Asp Val 545 550 555			1861
gag gtt caa ggc cca gac tgg cac ctg aag atg ccc aag atg aaa atg Glu Val Gln Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 560 565 570			1909
ccc aag ttc agc atg cct ggc ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 575 580 585 590			1957
gtg aac ctg ccc aag gct gat gtg gac atc tca gga ccc aag gtg ggt Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Val Gly 595 600 605			2005
gtt gaa gtt cca gat gtg aat att gaa gga cct gaa gga aag ctg aag Val Glu Val Pro Asp Val Asn Ile Glu Gly Pro Glu Gly Lys Leu Lys 610 615 620			2053
ggc ccc aag ttc aag atg cca gag atg aat atc aag gcc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Ala Pro Lys Ile 625 630 635			2101

Phe Lys Gly Glu Gly Pro Glu Val Asp Val Lys Leu Pro Lys Ala Asp	
1090 1095 1100	
gtt gat gtc tca gga ccc aaa atg gat gct gaa gtt cca gat gtg aat	3541
Val Asp Val Ser Gly Pro Lys Met Asp Ala Glu Val Pro Asp Val Asn	
1105 1110 1115	
att gaa ggt cca gac gca aaa cta aaa ggt ccc aaa ttc aag atg cca	3589
Ile Glu Gly Pro Asp Ala Lys Leu Lys Gly Pro Lys Phe Lys Met Pro	
1120 1125 1130	
gaa atg agt ata aag cct cag aag ata tcc ata cca gat gtt ggt ttg	3637
Glu Met Ser Ile Lys Pro Gln Lys Ile Ser Ile Pro Asp Val Gly Leu	
1135 1140 1145 1150	
cat ttg aaa ggt cct aaa atg aaa gga gat tat gat gta aca gtt cca	3685
His Leu Lys Gly Pro Lys Met Lys Gly Asp Tyr Asp Val Thr Val Pro	
1155 1160 1165	
aaa gta gaa gga gag ata aaa gct cct gat gtt gac atc aaa ggc ccc	3733
Lys Val Glu Gly Glu Ile Lys Ala Pro Asp Val Asp Ile Lys Gly Pro	
1170 1175 1180	
aaa gtt gat att aat gca cca gat gtg gag gtt cat ggc cca gac tgg	3781
Lys Val Asp Ile Asn Ala Pro Asp Val Glu Val His Gly Pro Asp Trp	
1185 1190 1195	
cac ctg aag atg ccc aag gta aaa atg ccc aag ttc agc atg cct ggc	3829
His Leu Lys Met Pro Lys Val Lys Met Pro Lys Phe Ser Met Pro Gly	
1200 1205 1210	
ttt aaa gga gag ggc cca gag gtg gat atg aac ctg ccc aag gct gac	3877
Phe Lys Gly Glu Gly Pro Glu Val Asp Met Asn Leu Pro Lys Ala Asp	
1215 1220 1225 1230	
ctt ggt gtt tca gga ccc aag gtg gac att gat gtt cca gat gtg aat	3925
Leu Gly Val Ser Gly Pro Lys Val Asp Ile Asp Val Pro Asp Val Asn	
1235 1240 1245	
ctt gaa gct cca gag ggg aaa cta aaa ggc cct aag ttc aag atg cca	3973
Leu Glu Ala Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro	
1250 1255 1260	
agc atg aat ata cag acg cac aaa atc tct atg cct gat gtt gga ctt	4021
Ser Met Asn Ile Gln Thr His Lys Ile Ser Met Pro Asp Val Gly Leu	
1265 1270 1275	
aat ttg aaa gcc cct aaa ctg aaa act gat gta gat gtt tcc ctt ccc	4069
Asn Leu Lys Ala Pro Lys Leu Lys Thr Asp Val Asp Val Ser Leu Pro	
1280 1285 1290	
aaa gtg gaa gga gac ttg aag ggt cct gaa att gat gtg aaa gcc cct	4117
Lys Val Glu Gly Asp Leu Lys Gly Pro Glu Ile Asp Val Lys Ala Pro	
1295 1300 1305 1310	
aag atg gat gtg aat gtt ggt gat att gat att gaa ggt cca gaa ggg	4165
Lys Met Asp Val Asn Val Gly Asp Ile Asp Ile Glu Gly Pro Glu Gly	

1315	1320	1325	
aag ttg aag ggc ccc aag ttt aag atg cct gag atg cat ttc aag gcc			4213
Lys Leu Lys Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Ala			
1330	1335	1340	
ccc aag atc tcc atg ccc gat gtg gac tta cac ttg aaa ggc ccc aaa			4261
Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys			
1345	1350	1355	
gtc aaa ggg gat atg gat gtg tct gtg ccc aag gta gaa ggt gaa atg			4309
Val Lys Gly Asp Met Asp Val Ser Val Pro Lys Val Glu Gly Glu Met			
1360	1365	1370	
aaa gtg cca gat gtt gac att aaa ggg ccc aaa gtg gac att gat gcc			4357
Lys Val Pro Asp Val Asp Ile Lys Gly Pro Lys Val Asp Ile Asp Ala			
1375	1380	1385	1390
cca gat gtg gag gtt cac gac cca gat tgg cac ctg aaa atg ccc aag			4405
Pro Asp Val Glu Val His Asp Pro Asp Trp His Leu Lys Met Pro Lys			
1395	1400	1405	
atg aaa atg ccc aag ttc agt atg cct ggc ttc aaa gca gag ggc cct			4453
Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro			
1410	1415	1420	
gaa gtg gat gtg aat ctc cga aag gct gac att gat gtg tct gga ccc			4501
Glu Val Asp Val Asn Leu Arg Lys Ala Asp Ile Asp Val Ser Gly Pro			
1425	1430	1435	
agt gtg gac act gat gct cct gat ttg gat att gag gga cca gaa gga			4549
Ser Val Asp Thr Asp Ala Pro Asp Leu Asp Ile Glu Gly Pro Glu Gly			
1440	1445	1450	
aag ttg aaa ggc tcc aaa ttt aag atg ccc aag ttg aat ata aaa gct			4597
Lys Leu Lys Gly Ser Lys Phe Lys Met Pro Lys Leu Asn Ile Lys Ala			
1455	1460	1465	1470
ccc aag gtc tcc atg cca gat gtg gac ttg aat ttg aag gga ccc aaa			4645
Pro Lys Val Ser Met Pro Asp Val Asp Leu Asn Leu Lys Gly Pro Lys			
1475	1480	1485	
ctg aag gga gag ata gat gct tct gtg cca gaa ctg gaa ggt gat ctc			4693
Leu Lys Gly Glu Ile Asp Ala Ser Val Pro Glu Leu Glu Gly Asp Leu			
1490	1495	1500	
aga ggg ccg caa gtt gat gtc aaa ggt cct ctt gtg gaa gcg gag gtg			4741
Arg Gly Pro Gln Val Asp Val Lys Gly Pro Leu Val Glu Ala Glu Val			
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ccc gat gtt gat ctg gag tgt cct gat gca aag ctg aag ggc ccc aag			4789
Pro Asp Val Asp Leu Glu Cys Pro Asp Ala Lys Leu Lys Gly Pro Lys			
1520	1525	1530	
ctt aag atg cct gag atg cac ttc aag gcc ccc aag atc tcc atg cct			4837
Leu Lys Met Pro Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro			
1535	1540	1545	1550

gat gtg gac tta cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat	4885
Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp	
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gtg tct ttg cca aaa ttg gag gga gat tta aca ggc ccc agt gtg gat	4933
Val Ser Leu Pro Lys Leu Glu Gly Asp Leu Thr Gly Pro Ser Val Asp	
1570 1575 1580	
gtg gag gtg cct gat gtt gag ctg gag tgt cct gat gca aag ttg aaa	4981
Val Glu Val Pro Asp Val Glu Leu Glu Cys Pro Asp Ala Lys Leu Lys	
1585 1590 1595	
ggg ccc aag ttt aag atg cct gag atg cac ttc aag acc ccc aag atc	5029
Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Thr Pro Lys Ile	
1600 1605 1610	
tcc atg cct gat gtg aac tta aac ttg aaa ggc ccc aaa gtc aaa ggg	5077
Ser Met Pro Asp Val Asn Leu Asn Leu Lys Gly Pro Lys Val Lys Gly	
1615 1620 1625 1630	
gat atg gat gtg tct gtt ccc aaa att gga ggg aga ttt aac agg ccc	5125
Asp Met Asp Val Ser Val Pro Lys Ile Gly Gly Arg Phe Asn Arg Pro	
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cag tgt gga tgt gga ggt gcc tga tgttgagctg gctgtcgttg ttctgagggc	5179
Gln Cys Gly Cys Gly Gly Ala *	
1650	
ggcatcactc tgggggtcagt ctctcccctg tcctttgagg acatacagac ctcacctatt	5239
gtttaagtgt ttgaaccagc cccgaacca agcaacacca gagtcctcct tacatttctt	5299
cagtgagcaa accttacgca ccgtgaactt gggagtcaaa ccagctgtgc ccctcactag	5359
ccgggtaagc gcagggaggt atcgtgccac actgagcatc agttccccaa tccgaatcag	5419
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 <213> Homo sapiens

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Met Ala Val Lys Leu Gly	
1 5	

acc ctc ctg ctg gcc ctt gcc ctg ggc ctg gcc cag cca gcc tct gcc	160
Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu Ala Gln Pro Ala Ser Ala	
10 15 20	
cgc cgg aag ctg ctg gtg ttt ctg ctg gat ggt ttt cgc tca gac tac	208
Arg Arg Lys Leu Leu Val Phe Leu Leu Asp Gly Phe Arg Ser Asp Tyr	
25 30 35	
atc agt gat gag gcg ctg gag tca ttg cct ggt ttc aaa gag att gtg	256
Ile Ser Asp Glu Ala Leu Glu Ser Leu Pro Gly Phe Lys Glu Ile Val	
40 45 50	
agc agg gga gta aaa gtg gat tac ttg act cca gac ttc cct agt ctc	304
Ser Arg Gly Val Lys Val Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu	
55 60 65 70	
tcg tat ccc aat tat tat acc cta atg act ggc cgc cat tgt gaa gtc	352
Ser Tyr Pro Asn Tyr Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val	
75 80 85	
cat cag atg atc ggg aac tac atg tgg gac ccc acc acc aac aag tcc	400
His Gln Met Ile Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser	
90 95 100	
ttt gac att ggc gtc aac aaa gac agc cta atg cct ctc tgg tgg aat	448
Phe Asp Ile Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn	
105 110 115	
gga tca gaa cct ctg tgg gtc act ctg acc aag gcc aaa agg aag gtc	496
Gly Ser Glu Pro Leu Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val	
120 125 130	
tac atg tac tac tgg cca ggc tgt gag gtt gag att ctg ggt gtc aga	544
Tyr Met Tyr Tyr Trp Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg	
135 140 145 150	
ccc acc tac tgc cta gaa tat aaa aat gtc cca acg gat atc aat ttt	592
Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn Phe	
155 160 165	
gcc aat gca gtc agc gat gct ctt gac tcc ttc aag agt ggc cgg gcc	640
Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly Arg Ala	
170 175 180	
gac ctg gca gcc ata tac cat gag cgc att gac gtg gaa ggc cac cac	688
Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu Gly His His	
185 190 195	
tac ggg cct gca tct ccg cag agg aaa gat gcc ctc aag gct gta gac	736
Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu Lys Ala Val Asp	
200 205 210	
act gtc ctg aag tac atg acc aag tgg atc cag gag cgg ggc ctg cag	784
Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln Glu Arg Gly Leu Gln	
215 220 225 230	

gac cgc ctg aac gtc att att ttc tgc gat cac gga atg acc gac att	832
Asp Arg Leu Asn Val Ile Ile Phe Ser Asp His Gly Met Thr Asp Ile	
235 240 245	
ttc tgg atg gac aaa gtg att gag ctg aat aag tac atc agc ctg aat	880
Phe Trp Met Asp Lys Val Ile Glu Leu Asn Lys Tyr Ile Ser Leu Asn	
250 255 260	
gac ctg cag caa gtg aag gac cgc ggg cct gtt gtg agc ctt tgg ccg	928
Asp Leu Gln Gln Val Lys Asp Arg Gly Pro Val Val Ser Leu Trp Pro	
265 270 275	
gcc cct ggg aaa cac tct gag ata tat aac aaa ctg agc aca gtg gaa	976
Ala Pro Gly Lys His Ser Glu Ile Tyr Asn Lys Leu Ser Thr Val Glu	
280 285 290	
cac atg act gtc tac gag aaa gaa gcc atc cca agc agg ttc tat tac	1024
His Met Thr Val Tyr Glu Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr	
295 300 305 310	
aag aaa gga aag ttt gtc tct cct ttg act tta gtg gct gat gaa ggc	1072
Lys Lys Gly Lys Phe Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly	
315 320 325	
tgg ttc ata act gag aat cga gag atg ctt ccg ttt tgg atg aac agc	1120
Trp Phe Ile Thr Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser	
330 335 340	
acc ggc agg cgg gaa ggt tgg cag cgt gga tgg cac ggc tac gac aac	1168
Thr Gly Arg Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn	
345 350 355	
gag ctc atg gac atg cgg ggc atc ttc ctg gcc ttc gga cct ggt agg	1216
Glu Leu Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Gly Arg	
360 365 370	
cga gga aat gac cag atg ctc tca gac ccc att ccc aag gaa gtg tct	1264
Arg Gly Asn Asp Gln Met Leu Ser Asp Pro Ile Pro Lys Glu Val Ser	
375 380 385 390	
gta agg ggg gct acg ggt gcc agg aga ggc tgc agg gat ttc ctt aca	1312
Val Arg Gly Ala Thr Gly Ala Arg Arg Gly Cys Arg Asp Phe Leu Thr	
395 400 405	
gac cct ctt tat gag cca agc aga gca aac cca gcc ggt ctc cat gaa	1360
Asp Pro Leu Tyr Glu Pro Ser Arg Ala Asn Pro Ala Gly Leu His Glu	
410 415 420	
aca tct ttt gct ggc ttc ctt tca aat gct tct tgg gtt tgg caa atg	1408
Thr Ser Phe Ala Gly Phe Leu Ser Asn Ala Ser Trp Val Trp Gln Met	
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 <213> Homo sapiens

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 <222> (256)..(1002)

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caccctcaag cttcaggtga gctgagcttc taacactacc atcaaagcaa ctggaacccc	180
ttgaatttga tttctggaga cgcgagcata atccttttgc aaacatctca acgctggctc	240
tccaggtgga gcacc atg gaa ggc gac tgt ctg agc tgc atg aag tat ctg	291
Met Glu Gly Asp Cys Leu Ser Cys Met Lys Tyr Leu	
1 5 10	
atg ttt gta ttc aat ttc ttc ata ttt ctg ggc ggg gcc tgc ctg ctg	339
Met Phe Val Phe Asn Phe Phe Ile Phe Leu Gly Gly Ala Cys Leu Leu	
15 20 25	
gcc atc ggc atc tgg gtc atg gtg gac ccc acc ggc ttc cgg gag atc	387
Ala Ile Gly Ile Trp Val Met Val Asp Pro Thr Gly Phe Arg Glu Ile	
30 35 40	
gtg gct gcc aat cct ctg ctc ctc acg ggc gcc tac atc ctc ctg gcc	435
Val Ala Ala Asn Pro Leu Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala	
45 50 55 60	
atg ggg ggc ctg ctc ttt ctg ctc ggc ttc ctg ggc tgc tgc ggg gcc	483
Met Gly Gly Leu Leu Phe Leu Leu Gly Phe Leu Gly Cys Cys Gly Ala	
65 70 75	
gtc cgt gag aac aag tgt ctg ctg cta ttt ttc ttc ctg ttc atc ctg	531
Val Arg Glu Asn Lys Cys Leu Leu Leu Phe Phe Phe Leu Phe Ile Leu	
80 85 90	
atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc	579
Ile Ile Phe Leu Ala Glu Leu Ser Ala Ala Ile Leu Ala Phe Ile Phe	
95 100 105	
agg gaa aat ctc acc cga gaa ttc ttc acc aag gag ctc acc aag cac	627
Arg Glu Asn Leu Thr Arg Glu Phe Phe Thr Lys Glu Leu Thr Lys His	
110 115 120	
tac cag ggc aat aac gac aca gac gtc ttc tct gcc acc tgg aac tcg	675
Tyr Gln Gly Asn Asn Asp Thr Asp Val Phe Ser Ala Thr Trp Asn Ser	
125 130 135 140	

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gtc atg atc aca ttt ggt tgc tgc ggg gtc aac ggg cct gaa gac ttt      723
Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn Gly Pro Glu Asp Phe
                145                150                155

aag ttt gca tct gtg ttt cga ctc ctg acc ctg gat agt gaa gag gtg      771
Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu Asp Ser Glu Glu Val
                160                165                170

ccg gag gcc tgc tgc cgg agg gaa ccc caa agt cgg gac ggg gtc ctg      819
Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser Arg Asp Gly Val Leu
                175                180                185

ctg agc cgg gag gag tgc ctc ctg gga agg agc cta ttc cta aac aag      867
Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser Leu Phe Leu Asn Lys
                190                195                200

cag ggc tgt tac acg gtg atc ctc aac acc ttc gag acc tac gtc tac      915
Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr
                205                210                215                220

ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc atc gag ctt ttc gcc      963
Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala
                225                230                235

atg atc ttt gcc atg tgc ctc ttc cgg ggc atc cag tag agggatatggc     1012
Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln *
                240                245

ctgaagcctg aagactcgcc ccacccacca ctgcccagca cccaatgtcc tcccgtgccc     1072

ctccccgctg tcctcttggc ccagggggag aagatgaggc catcagagat ggccaggaga     1132

agggccaggg gaatagagct attttttttaa caaaacaaaa tgaagacaaa aatatggact     1192

gatgtatcct cgcttgact cagggcaggt gccgtgggtt ctccagagac ccagcacct     1252

ggcccaggat agcaaggctg ctctagagac aaaggaacac aaggccaggc cactatgggc     1312

agcaagaccc gggccttatt ctcatggcgt gactgtgcc aagtggggtt cggcaggggc     1372

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 <213> Homo sapiens

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 <222> (264)..(1508)

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tct tcc cga atg gtg gtg cca aag gca gcc att tac caa aca cag gcc Ser Ser Arg Met Val Val Pro Lys Ala Ala Ile Tyr Gln Thr Gln Ala 220 225 230			962
ttc tat gcc aaa ggg aaa atg aag gaa gta aaa cag ctt gtg gct aac Phe Tyr Ala Lys Gly Lys Met Lys Glu Val Lys Gln Leu Val Ala Asn 235 240 245			1010
ttg cgt ggg gaa tcc tta tca tct gga aag aca gag acg tgg aat ggc Leu Arg Gly Glu Ser Leu Ser Ser Gly Lys Thr Glu Thr Trp Asn Gly 250 255 260 265			1058
aag ttg ctg aaa att cca cca gtt tct ccc tct atc ctc gac tgt agt Lys Leu Leu Lys Ile Pro Pro Val Ser Pro Ser Ile Leu Asp Cys Ser 270 275 280			1106
ata atc cgc gtg gaa tat tca cta atg gta tat gtg gat att cct gga Ile Ile Arg Val Glu Tyr Ser Leu Met Val Tyr Val Asp Ile Pro Gly 285 290 295			1154
gct atg gat tta ttt ctt aat ttg cca ctt gtc atc ggt acc att cct Ala Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro 300 305 310			1202
cta cat cca ttt ggt agc aga acc tca agt gta agc agt cag tgt agc Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser 315 320 325			1250
atg aat atg aac tgg ctc agt tta tca ctt cct gaa aga cct gaa gca Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu Arg Pro Glu Ala 330 335 340 345			1298
cca ccc agc tat gca gaa gtg gta aca gag gaa caa agg cgg aac aat Pro Pro Ser Tyr Ala Glu Val Val Thr Glu Glu Gln Arg Arg Asn Asn 350 355 360			1346
ctt gca cca gtg agt gct tgt gat gac ttt gag aga gcc ctt caa gga Leu Ala Pro Val Ser Ala Cys Asp Asp Phe Glu Arg Ala Leu Gln Gly 365 370 375			1394
cca ctg ttt gca tat atc cag gag ttt cga ttc ttg cct cca cct ctt Pro Leu Phe Ala Tyr Ile Gln Glu Phe Arg Phe Leu Pro Pro Pro Leu 380 385 390			1442
tat tca gag att gat cca aat cct gat cag tca gca gat gat aga cca Tyr Ser Glu Ile Asp Pro Asn Pro Asp Gln Ser Ala Asp Asp Arg Pro 395 400 405			1490
tcc tgc ccc tct cgt tga aggaac acttggttga atcaagttga tgtgggttcc Ser Cys Pro Ser Arg * 410 415			1544

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 gaagcctaca gcaacattct gagactgctc caacatgctt gaagatctaa gcttttctct 1724
 tttaaaactg gcacatactc agagcagtct tcttagccta tggtcgtacg tgtcaagaca 1784
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 <213> Homo sapiens

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 <222> (509)..(685)

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 agtgtaacta tatccccacc tctgcttgct ttctttccct cccctccaat gataaagaaa 180
 atgataaatt ttctgttggt cattcaattc ttattttaaa taagactaag tataggcatt 240
 gtacctgaca ttgctacgtt tctaccagtg tttcaattta aagtgcctagt gtttaaaaac 300
 attttcaagg gataaggcct tctgtacttt gcttatttga agaatacagt gtaggagcag 360
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 ttattcaggt tctaaccctt tgctgtacac aagcagacag aaatgcctct gttacataaa 480
 tgagaaaaag ctattatgct gatggagc atg ctt ttt aaa tcc ttt aaa aac 532
 Met Leu Phe Lys Ser Phe Lys Asn
 1 5
 act cac cat ata aac ttg cat ttg agc ttg tgt gtt ctt ttg tta atg 580
 Thr His His Ile Asn Leu His Leu Ser Leu Cys Val Leu Leu Leu Met
 10 15 20
 tgt aga gtt ctc ctt tct cga aat tgc cag tgt gta ctt ggc tta act 628
 Cys Arg Val Leu Leu Ser Arg Asn Cys Gln Cys Val Leu Gly Leu Thr
 25 30 35 40
 caa gaa cag ttt ctt ctg gat tcc tta ttt gat tta ttt aac cta att 676
 Gln Glu Gln Phe Leu Leu Asp Ser Leu Phe Asp Leu Phe Asn Leu Ile
 45 50 55
 ata ttc taa tattgca aatattacca taagtgggta aaagtaaaat tcctcttctg 732

Ile Phe *

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Met Ile Tyr Lys
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tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg 644
Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met
5 10 15 20

cat cag aaa att cac aca gct gag aag ccc cat aaa tgt gac aag tgt 692
His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys
25 30 35

gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac 740
Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp
40 45 50

cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt 788
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe
55 60 65

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Ser Thr Thr Thr Lys Leu Asn Arg His Lys Lys Ile His Thr Val Glu	
70 75 80	
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Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe Asn Trp Ser Ser	
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His Leu Gln Ile His Met Arg Val His Thr Gly Glu Lys Pro Tyr Val	
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Cys Ser Glu Cys Gly Arg Gly Phe Ser Asn Ser Ser Asn Leu Cys Met	
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Gly Lys Ala Phe Arg His Thr Ser Ser Leu Cys Met His Gln Arg Val	
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Ser Gln Ser Ser Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu	
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Lys Pro Tyr Arg Cys Cys Gly Cys Gly Lys Ala Phe Ser Gln Ser Ser	
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Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys	
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Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Ser Leu Cys Ile	
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Ile *	
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Val Gly Tyr Gly Asp Ser Lys Asp Cys Ile Leu Glu Pro Leu Ser Leu
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cca gaa agt cca ggt ggc acc acc act tta gaa ggt tct cca tct gtg      203
Pro Glu Ser Pro Gly Gly Thr Thr Thr Leu Glu Gly Ser Pro Ser Val
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cct tgt att ttc tgt gaa gaa cat ttt cct gtg gct gaa caa gac aaa      251
Pro Cys Ile Phe Cys Glu Glu His Phe Pro Val Ala Glu Gln Asp Lys
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ctt ctg aag cac atg att att gag cat aag att gtc ata gct gat gtc      299
Leu Leu Lys His Met Ile Ile Glu His Lys Ile Val Ile Ala Asp Val
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aag ttg gtt gct gat ttc caa agg tac att tta tat tgg agg aaa agg      347
Lys Leu Val Ala Asp Phe Gln Arg Tyr Ile Leu Tyr Trp Arg Lys Arg
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ttc act gaa cag ccc atc aca gat ttt tgt agt gta ata aga att aat      395
Phe Thr Glu Gln Pro Ile Thr Asp Phe Cys Ser Val Ile Arg Ile Asn
           95              100              105              110

tcc act gct cca ttt gaa gaa caa gag aat tat ttt ttg tta tgt gac      443
Ser Thr Ala Pro Phe Glu Glu Gln Glu Asn Tyr Phe Leu Leu Cys Asp
           115              120              125

gtt tta cca gaa gat aga att ctt aga gaa gag ctt cag aaa cag aga      491
Val Leu Pro Glu Asp Arg Ile Leu Arg Glu Glu Leu Gln Lys Gln Arg
           130              135              140

ctg aga gaa att ctg gaa caa cag cag caa gaa cga aat gat acc aat      539
Leu Arg Glu Ile Leu Glu Gln Gln Gln Gln Glu Arg Asn Asp Thr Asn
           145              150              155

ttt cat ggc gtt tgt atg ttt tgc aat gaa gaa ttc ctt gga aac aga      587
Phe His Gly Val Cys Met Phe Cys Asn Glu Glu Phe Leu Gly Asn Arg
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tct gtt att ttg aac cac atg gcc aga gaa cat gct ttc aac att gga      635
Ser Val Ile Leu Asn His Met Ala Arg Glu His Ala Phe Asn Ile Gly
           175              180              185              190

ttg cca gac aac att gta aac tgc aat gaa ttt ttg tgt aca tta cag      683
Leu Pro Asp Asn Ile Val Asn Cys Asn Glu Phe Leu Cys Thr Leu Gln
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aaa aag ctt gac aat ttg cag tgc ttg tac tgt gag aag acc ttc agg      731

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Asp	Lys	Asn	Thr	Leu	Lys	Asp	His	Met	Arg	Lys	Lys	Gln	His	Arg	Lys	
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Ile	Asn	Pro	Lys	Asn	Arg	Glu	Tyr	Asp	Arg	Phe	Tyr	Val	Ile	Asn	Tyr	
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Glu	Leu	Leu	Asp	His	Gln	Glu	Asp	Asp	Trp	Ser	Asp	Trp	Glu	Glu	His	
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Pro	Ala	Ser	Ala	Val	Cys	Leu	Phe	Cys	Glu	Lys	Gln	Ala	Glu	Thr	Ile	
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Glu	Lys	Leu	Tyr	Val	His	Met	Glu	Asp	Ala	His	Glu	Phe	Asp	Leu	Leu	
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Lys	Ile	Lys	Ser	Glu	Leu	Gly	Leu	Asn	Phe	Tyr	Gln	Gln	Val	Lys	Leu	
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gtc	aat	ttt	att	cgg	agg	caa	gtt	cac	caa	tgc	aga	tgt	tat	ggc	tgc	1115
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Thr	Lys	His	Thr	Ser	Leu	Leu	Pro	Asp	Arg	Lys	Thr	Trp	Asp	Gln	Leu	
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Glu	Tyr	Tyr	Phe	Pro	Thr	Tyr	Glu	Asn	Asp	Thr	Leu	Leu	Cys	Thr	Leu	
		385					390					395				
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Ser	Asp	Ser	Glu	Ser	Asp	Leu	Thr	Ala	Gln	Glu	Gln	Asn	Glu	Asn	Val	
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ccc	atc	atc	agt	gaa	gat	aca	tct	aaa	ctg	tat	gct	ttg	aaa	caa	agc	1355
Pro	Ile	Ile	Ser	Glu	Asp	Thr	Ser	Lys	Leu	Tyr	Ala	Leu	Lys	Gln	Ser	
415					420				425					430		
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Ser	Ile	Leu	Asn	Gln	Leu	Leu	Leu	*								

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Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe
20 25 30
gag tct att gcc att gcc caa gaa aaa ttg gaa gct cca cca ccc acc 202
Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr
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cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata 250
Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile
50 55 60
ggg ttt ggc ttt ttg gat aat gca att atg att gtt gct gga acc cat 298
Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His
65 70 75 80
att gaa atg tct att gga att att ttg gga att tca act atg gca gct 346
Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala
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Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala
100 105 110
ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat 442
Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp
115 120 125

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 130 135 140

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 Leu Gly Lys Ala Val Gly Val Thr Ile Gly Cys Ile Leu Gly Met Phe
 145 150 155 160

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 Pro Leu Ile Phe Phe Gly Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr
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 Lys Ser *

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cta ctg gtc ttg tca ggt gcc tgg ggc atg caa atg tgg gtg acc ttc Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe 75 80 85	532
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 Ser Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val
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 Thr Val Thr Ile Gly Leu Leu Leu Ile Pro Lys Phe Ser His Ser Ser
 45 50 55

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 Asn Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu
 60 65 70 75

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 Asp Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala
 80 85 90

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 Trp Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys
 95 100 105

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 Lys Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr
 110 115 120

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 Asn Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly
 125 130 135

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Arg Ser Ile Met Arg Arg Ile Thr Glu Ile Pro Glu Thr Val Ser Arg	
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Gln Cys Ser Lys Glu Asp Lys Glu Gly Ala Asp His Gly Thr Ala Lys	
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Gly Thr Ala Leu Ile Arg Lys Asn Pro Pro Glu Ser Ser Gly Asn Thr	
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Gly Lys Ser Lys Glu Glu Thr Leu Lys Asn Arg Val Phe Ser Leu Lys	
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Lys Ser His Ser Thr Tyr Asp His Val Arg Asp Gln Thr Glu Glu Ser	
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Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2' and 'Study 3'. Each study involves a 'Pretest' and a 'Main Study'. The 'Main Study' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post) as factors. The 'Pretest' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post) as factors.

Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2' and 'Study 3'. Each study involves a 'Pretest' and a 'Main Study'. The 'Pretest' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post). The 'Main Study' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post). The 'Pretest' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post). The 'Main Study' for each study is a 2x2 factorial design with 'Condition' (Control, Experimental) and 'Time' (Pre, Post).

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Glu	Gly	Gly	Glu	Ile	Ile	His	Asn	Lys	His	Ala	Gly	*				
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caaaactatgg	agccttttaaa	ggctctttatt	tctaataaatc	tggtactcta	agatacat	ttt										1002
taagcttgat	tatcatatga	caaagatttt	aaaaccatct	cagtgtgccc	taatttttca											1062
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cagcgttaag	cctgtctgga	tcaatataaa	caagtagggt	gtaggcagtc	ctctatttgc											1182
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tctacaaatc	gctatgtaaa	taacagatat	gcttcatgat	tgtgaccagt	catgttattt											1422
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gaaagaactg	gtcaacaaag	atgaaagtgc	agcaaagcaa	tgaaaaatga	taaacactgga											1602
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tggtcttgct	gctgtgtatt	cataggagct	tagtgaaggc	aaacttacca	acacaaataa											1722
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aa																1784

<210> 92
 <211> 2559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (978)..(1451)

<400> 92

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agtaaaaaat atgctgggta taaaccttag gggactaccc attgaatatg tgggtccatcg      60
ttgacctaaa catcattatg tgggtgcatga ctgtccgtat atgcagatta aactaccaaa      120
cattttttcc agcaaagggtg gtttttgaaa gtaacctaat gaaaccctgg ctgccatggg      180
cattttaatt ctggactgag aagaagcgac tctgcgttgt gctgttggcc caggcctgca      240
tgcctgagga ctggtggccg ttacagttcc ttgctgtggt cgccggtctc tctgtattct      300
gccactgctc tcatgtggca tttggcagaa gtactacgta gatttctgtg ctactgaaaa      360
aaataaaaaac agtgggttcct tttaatagcc ctgatttgag acttaggaga ggggtcaagag      420
tccctacctg atttatgagg agagaagatt ttttaaaaac ctcatgtgat gctgtcatac      480
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aactagagaa gtttgtgttc tgttggaaacc ctctgtagaa cactttacac tcagttctga      600
tggacctttt caggggcgat tttttaaaaa ccgctctcga aagtagtctt aaaatgagag      660
cactttattg atggcttttc aggactgtgt tggatatttt catgcagtgt atttgtcagc      720
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ggcagtgaag cattttatag tttctcctcc ctcatgggtt ctgaattttg gtgacagggtg      960
tattttcttaa tgcagat   atg aaa aac agt agc tcc gta tcg aat aca ttg      1010
                        Met Lys Asn Ser Ser Ser Val Ser Asn Thr Leu
                        1           5           10

aca aat gga tgt gtc atc aat gga cat ttg gac ttc ccc tcc acg acc      1058
Thr Asn Gly Cys Val Ile Asn Gly His Leu Asp Phe Pro Ser Thr Thr
                        15           20           25

ccg ctc agt ggg atg gaa agc agg aat ggc cag tgc ttg aca gga act      1106
Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr Gly Thr
                        30           35           40

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aac gga att agc agt gga tta gcc cca gga cag ccg ttt ccg agt agc Asn Gly Ile Ser Ser Gly Leu Ala Pro Gly Gln Pro Phe Pro Ser Ser 45 50 55	1154
cag ggt tct ctc tgc att agt ggg act gag gag cca gag aag acc ctg Gln Gly Ser Leu Cys Ile Ser Gly Thr Glu Glu Pro Glu Lys Thr Leu 60 65 70 75	1202
aga gct aac cct gag ttg tgc ggt tct ctg cac ctg aac ggg agt cca Arg Ala Asn Pro Glu Leu Cys Gly Ser Leu His Leu Asn Gly Ser Pro 80 85 90	1250
agt agc tgc ata gcc agt agg cct tcc tgg gtg gaa gac att ggg gat Ser Ser Cys Ile Ala Ser Arg Pro Ser Trp Val Glu Asp Ile Gly Asp 95 100 105	1298
aac ctg tac tat gga cac tac cac ggg ttt ggg gac act gct gaa agc Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala Glu Ser 110 115 120	1346
atc cca gaa ctg aac agt gtg gtc gag cat tcc aag tcc gtg aag gtg Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val Lys Val 125 130 135	1394
cag gag cgg tac gac agt gcc gtg ctg ggc acc atg cac ctg cac cac Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu His His 140 145 150 155	1442
ggc tcc tag agacgct gacctggctc tcggaaacgc aggagtcctt cctggtagcc Gly Ser *	1498
agctcagaat acccatgtag cagcaacttg aacgaatgtc acaacttgta ctttttttat	1558
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ataccactat gtatatccag ttaactgaga gaattttgac tctcttaata aaactgcatt 2338
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atattgtaat gaatttttac ttttttgatt tttgtaataa aaattggtgc agataaaatg 2458
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cacaaattga ataaaaaact ctcacactca aaaaaaaaaa a 2559

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<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (286)..(759)

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tttactgcag tttcatcatg gggtttgttg atgtgcagtc catttattgc cctgtcttgc 180
ttaaatattc ttgttgagaa cagctggagg ctttgactgg gttcctagtt ctgttttctg 240
ggaaggcaac gtggattctg tttttagac attaatgagc tttaa atg gga att 294
Met Gly Ile
1
ggg gat gat gta tgt cta caa aaa aaa agt tgg agc ggc cgc caa 342
Gly Asp Asp Val Cys Leu Gln Lys Lys Lys Ser Trp Ser Gly Arg Gln
5 10 15
ctt agg ggc cac gtg agc cac ggc cac ggc cgc ata ggc aag cac cgg 390
Leu Arg Gly His Val Ser His Gly His Gly Arg Ile Gly Lys His Arg
20 25 30 35
aag cac ccc ggc ggc cgc ggt aat gct ggt ggt ctg cat cac cac cgg 438
Lys His Pro Gly Gly Arg Gly Asn Ala Gly Gly Leu His His His Arg
40 45 50
atc aac ttc gac aaa tac cac cca ggc tac ttt ggg aaa gtt ggt atg 486
Ile Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met
55 60 65
aag cat tac cac tta aag agg aac cag agc ttc tgc cca act gtc aac 534
Lys His Tyr His Leu Lys Arg Asn Gln Ser Phe Cys Pro Thr Val Asn
70 75 80
ctt gac aaa ttg tgg act ttg gtc agt gaa cag aca cgg gtg aat gct 582

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Leu Asp Lys Leu Trp Thr Leu Val Ser Glu Gln Thr Arg Val Asn Ala
  85                               90                               95

gct aaa aac aag act ggg gct gct ccc atc att gat gtg gtg cga tcg      630
Ala Lys Asn Lys Thr Gly Ala Ala Pro Ile Ile Asp Val Val Arg Ser
100                               105                               110                               115

ggc tac tat aaa gtt ctg gga aag gga aag ctc cca aag cag cct gtc      678
Gly Tyr Tyr Lys Val Leu Gly Lys Gly Lys Leu Pro Lys Gln Pro Val
                               120                               125                               130

atc gtg aag gcc aaa ttc ttc agc aga aga gct gag gag aag att aag      726
Ile Val Lys Ala Lys Phe Phe Ser Arg Arg Ala Glu Glu Lys Ile Lys
                               135                               140                               145

agt gtt ggg ggg gcc tgt gtc ctg gtg gct tga agccacat ggagggagtt      777
Ser Val Gly Gly Ala Cys Val Leu Val Ala *
                               150                               155

tcattaaatg ctaactactt tttcaaaaaa aaaaaa      813

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<210> 94
<211> 1686
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (737)..(1003)

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<400> 94
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atggatctaa aactttgttt ccttccaatt tacatagtaa agtcaactgc atacagttct      120
ttccatgtgt aagttttaca ttgtatttt ctacaattaa gtaaatctaa atgttaaatt      180
ttaacacata tatccaatta tgtacacaat tacaatgtca atttataagt caagcttact      240
taacaatcat aaattacaaa aaacgcacta tgaataatgt tgttctagaa gtatcacatc      300
aactcatatg atctaggtga acccaaaagt aaaaaataat gattataaat tatggtagtg      360
tctgtaaaac cctgttataa aggaggtatt cttttaaaat atgtacctta tatataaaag      420
ctcctgactc cttttaagga ccaaaattat tttcagtcta accattttca ttaaagcgct      480
tatttaaaaa gtatcacctt ataaaactga gtatataaaa tacaatgcag cccttgatag      540
ctaagaatct ttataaacgc caatgattta gtgacctgtt tatcaaacta tttctatgga      600
tgggttgatt ttttttcttc ctctaaatta agtggcccta gactaatata tttgttcagt      660
tattctgttt tcttccttac tgccatttca catctccatc agtgagttcc tcaggatttg      720

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cctttatggtt acaact	atg aaa gtc ttc aat cca att ccc tgc ttc cac	769
	Met Lys Val Phe Asn Pro Ile Pro Cys Phe His	
	1 5 10	
aca aag gac aaa gaa agc cta aac ttt cct ttt ttc tgg gct cca ata	817	
Thr Lys Asp Lys Glu Ser Leu Asn Phe Pro Phe Phe Trp Ala Pro Ile		
	15 20 25	
gga agc agc att tac aac gtg tct ggc ttg gtg gga gga aga ttg tca	865	
Gly Ser Ser Ile Tyr Asn Val Ser Gly Leu Val Gly Gly Arg Leu Ser		
	30 35 40	
att gag gta tca tgt gtg ttc acc tgc ctc tct tgc cct att tct ttg	913	
Ile Glu Val Ser Cys Val Phe Thr Cys Leu Ser Cys Pro Ile Ser Leu		
	45 50 55	
gtt gct ata aat ttc ctg ctt ctc aaa tat ctg gat ttt tgg cta cct	961	
Val Ala Ile Asn Phe Leu Leu Leu Lys Tyr Leu Asp Phe Trp Leu Pro		
	60 65 70 75	
att tgg ctt ccg tct ttg gtg ttt ata tct gtc tgg ttt tag caggtct	1010	
Ile Trp Leu Pro Ser Leu Val Phe Ile Ser Val Trp Phe *		
	80 85	
ctctgattcc tgaccacag ctccctcct tctctaatat tcaagtatgc tgcttccta	1070	
actcctcatt ccttctcctt gaatttcact ttacaattgc gctaggttct aacatcggtg	1130	
gccatagatt accacaaaac ataatttctt aaattctgca aatttctaata gtttctaatac	1190	
ttggtttcct acaagatcta acactaagct tgtgttatcc tgattacagt gtatataaaa	1250	
caatgcttgt ggaaaattaa cctaggagaa agcttatagg ggaaacctga tgatgaattt	1310	
tattaaatta ataaccctta taacaatttc aaatgtaata ctatctggat ttgaacttca	1370	
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ataacattat caggcttgta aaatacttta tcaaatcaat gcatcagtta aagcaggggt	1550	
ccccagccct gggctgtgtg tggcctgtta ggaatcgggc cacacagttg gtgagctgag	1610	
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<210> 95

<211> 1217

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (353)..(472)

<400> 95

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taagtttttg tattccacta ctttcagttc aataaaacct agagttgttt catctgcgcc      180
taaagtgtat ggcacaattt tcttaagaat taggggaacc aggtgcctac agttaaagga      240
acgtttcagt tcctttcatt cattcctggg tttttctttt attttctaag aaggttgaag      300
aaggatgagt gatagagaag aaagcaacac cattgatttt tttttttaag aa      atg      355
                                     Met
                                     1

ata tat ata tgt ata tgt ttg tgt gtg tgt gtg tgt gtg tgt gta ttc      403
Ile Tyr Ile Cys Ile Cys Leu Cys Val Cys Val Cys Val Cys Val Phe
                5                10                15

tgt gca tta ttt tgt cat gat ctc aat tct ctt ctt tcc acc aaa gtt      451
Cys Ala Leu Phe Cys His Asp Leu Asn Ser Leu Leu Ser Thr Lys Val
                20                25                30

tgt cgt aat att ttc tcc tga ag gtgcattctg gtccttttaa attagtcagt      504
Cys Arg Asn Ile Phe Ser      *
                35                40

gttatattgt aggagactgt catggaaaaa aggactcagt ttactttcgt cattttcaca      564
ggggaacctt ttaaaacaat cttttcagca gcagatacct ttaaccctaa taatctcagg      624
ccttgatgaa aatactatat tttgtagatt atgggttaaag ggggaaaatt actagttccg      684
taagataaat atgagctcca tttgacttct gatgtctggt ttagcattac ataatatggt      744
gatcttacac tctgcttttg tccaaataaa atgcaatagt atcaatatca atttcagaaa      804
aatggactga atatgctttt ttggtgatga aatctcatgt acgatattta tagtgatgtg      864
cttttatttt ctcatgagat actaaatatt aattgtgttg tacatttggt cttagcatat      924
attaaagttt tgaaccaaat gtgttaaagc ttacgctttg ccatgtaa atccccagaag      984
ttgttgagct caaatgtatc ctacatccag ctgtagaaat ttgtcagaaa ttgttttaat      1044
tttgatatata attgtactgt ttaattctag ccattgcgct gaacagtatt tgagttacca      1104
tataatatgg ctttacacaa ggaaatgtgt ggcttttggt ttgtatTTTT tcagtataga      1164
agttcctgtg tcttatttta ataaagttat tagtaaaaact gaaaaaaaaa aaa      1217

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<210> 96
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (691)..(1173)

<400> 96

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gcttgcaatt gaacatcacc ccccaactgg aagagcctca catcctggac gaatgaccaa	180
ggcgccagga gaaagactgt gttttctccc acgctacctg ccgcccgcctc ttctcttggc	240
tctctgcaaa cacctgaagc tgtgaccacc agaaagggca caggcttgct ttctcagac	300
tacaggatca tcaatggcaa aagtggaact caggacatcc agcctggccc tctttttaat	360
aataatgctg atggagtggc cacagatata acttctacca gatccttaaa ttacaaaagc	420
actagcagcg gtcacagaga aatatcatca cctaggattc aggatgctgg acctgcttcc	480
cgagatgtcc aggccactgg cagaatcgca gatgatgctg acccaagagt agcacttggt	540
aacgattctt tatctgatgt cacaagtacc acatcttcta ggggtggatga tcatgactca	600
gaggaaatth gtcttgacca tctgtgtaag ggttgctccgc ttaatggtag ctgcagcaaa	660
gtccacttcc atctgcctta ccggtggcag	
atg ctt att ggt aaa acc tgg	711
Met Leu Ile Gly Lys Thr Trp	
1 5	
acg gac ttt gag cac atg gag acg atc gag aaa ggc tac tgt aac ccc	759
Thr Asp Phe Glu His Met Glu Thr Ile Glu Lys Gly Tyr Cys Asn Pro	
10 15 20	
gga atc cac ctc tgt tct gta gga agt tat aca atc aat ttt cgg gta	807
Gly Ile His Leu Cys Ser Val Gly Ser Tyr Thr Ile Asn Phe Arg Val	
25 30 35	
atg agt tgt gat tcc ttt ccc atc cga cgc ctc tcc act cct tct tct	855
Met Ser Cys Asp Ser Phe Pro Ile Arg Arg Leu Ser Thr Pro Ser Ser	
40 45 50 55	
gtc acc aag cca gcc aat tct gtc ttc acc acc aaa tgg att tgg tat	903
Val Thr Lys Pro Ala Asn Ser Val Phe Thr Thr Lys Trp Ile Trp Tyr	
60 65 70	
tgg aag aat gaa tct ggc aca tgg att cag tat gga gaa gag aaa gac	951
Trp Lys Asn Glu Ser Gly Thr Trp Ile Gln Tyr Gly Glu Glu Lys Asp	
75 80 85	

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aaa cgg aaa aat tca aac gtc gac tct tca tac ctg gag tct ctc tat      999
Lys Arg Lys Asn Ser Asn Val Asp Ser Ser Tyr Leu Glu Ser Leu Tyr
          90                      95                      100

caa tcc tgt ccg agg gga gtt gtg cca ttt cag gcg ggc tca cgg aac      1047
Gln Ser Cys Pro Arg Gly Val Val Pro Phe Gln Ala Gly Ser Arg Asn
          105                      110                      115

tat gag ctg agt ttc caa ggg atg att cag aca aac ata gct tcc aaa      1095
Tyr Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys
          120                      125                      130                      135

act caa aag gat gtc atc aga aga cca aca ttt gtg cct cag tgg tat      1143
Thr Gln Lys Asp Val Ile Arg Arg Pro Thr Phe Val Pro Gln Trp Tyr
          140                      145                      150

gtg cag cag atg aag aga ggg cca gag taa g tgttctgaag cagctgtttg      1194
Val Gln Gln Met Lys Arg Gly Pro Glu *
          155                      160

ctgacagatg cttgagatgt tcatgccctg ggctcatcaa gtcactcgtg aatctggagc      1254

ctgttttcct gaaaagttcc tgtttgcatt actctgcagt ttccatttgc attatcgatg      1314

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<210> 97
<211> 1163
<212> DNA
<213> Homo sapiens

<220>
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<222> (469)..(600)

<400> 97
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gctctggtaa gccaaagactc cttgtgttta cctgttcac tctgcaatct aggggggtagc      180

attttgtcct gtgtccttac cggcaaaacg atgtataaat gaaagaaatt gagatgggtgc      240

acgatgcaca gttgaagtga acttgcgggg tttttcagta tctacgattc atagatctgg      300

aattcgcggc cgcgtcgacg aaatatctct ttcaataatg aaagaataag aaaaagaaat      360

agaagagctg gaaacaatag gtaaagttta ggctaggcct tagacttctc ctgcattgta      420

atccttctgg ttgccacat atgcatgctg tcaggaagtt gatgaggt atg tac agg      477
                               Met Tyr Arg

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aca atg att ttc cat ttt ttg cct tta ggc acc gac tca ttg gtc act 525
 Thr Met Ile Phe His Phe Leu Pro Leu Gly Thr Asp Ser Leu Val Thr
 5 10 15

cat ctg ctg aat gta tcc tct cag gca ata ctg ccc att gga gca cga 573
 His Leu Leu Asn Val Ser Ser Gln Ala Ile Leu Pro Ile Gly Ala Arg
 20 25 30 35

agc cgc caa ttt gtc aac gtg agt tga aatct ctttcccat tcacccacc 625
 Ser Arg Gln Phe Val Asn Val Ser *
 40

attgaatcct agagttgtcc tcctagaatt acaaagaatg gatctcatcc ctcttgga 685

tggtatcctt ctgatatttg aagaatctag tcatatcctt aaaatggctc acagcattcc 745

aaacttcgcg cttcacctag aaatgctttt ttttttctta tctcagtcta atgtatttta 805

aactagtctt tagctcattt aaccagcccc caatgtcctc ttctgttggg tgagcacctc 865

gcagtttgaa gagcattttg tttagtgaag tcaacaaata caaagtcagt gaaagaaacc 925

ccatatactc tctgcaagct cttagtatca catcagatat tcaagccatg cagctctttc 985

ttcctttctta ttctttgtct aaacaggatc atgccatctt ccctgtgagt tgtttggaag 1045

atgagctttc gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttggggt 1105

tggtggggta ttttcatcat cgaatagata gttatataca tcagcctatc aatcgccc 1163

<210> 98

<211> 3320

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (160)..(2202)

<400> 98

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gtcccgggcc cggagcgcta ggagcgcgcg gaaggagcc atg gct ctg gac ggg 174
 Met Ala Leu Asp Gly
 1 5

ata agg atg cca gat ggc tgc tac gcg gac ggg acg tgg gaa ctg agt 222
 Ile Arg Met Pro Asp Gly Cys Tyr Ala Asp Gly Thr Trp Glu Leu Ser
 10 15 20

gtc cat gtg acg gac ctg aac cgc gat gtc acc ctg aga gtg acc ggc Val His Val Thr Asp Leu Asn Arg Asp Val Thr Leu Arg Val Thr Gly 25 30 35	270
gag gtg cac att gga ggc gtg atg ctt aag ctg gtg gag aaa ctc gat Glu Val His Ile Gly Gly Val Met Leu Lys Leu Val Glu Lys Leu Asp 40 45 50	318
gta aaa aaa gat tgg tct gac cat gct ctc tgg tgg gaa aag aag aga Val Lys Lys Asp Trp Ser Asp His Ala Leu Trp Trp Glu Lys Lys Arg 55 60 65	366
act tgg ctt ctg aag aca cat tgg acc tta gat aag tat ggt att cag Thr Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr Gly Ile Gln 70 75 80 85	414
gca gat gct aag ctt cag ttc acc cct cag cac aaa ctg ctc cgc ctg Ala Asp Ala Lys Leu Gln Phe Thr Pro Gln His Lys Leu Leu Arg Leu 90 95 100	462
cag ctt ccc aac atg aag tat gtg aag gtg aaa gtg aat ttc tct gat Gln Leu Pro Asn Met Lys Tyr Val Lys Val Lys Val Asn Phe Ser Asp 105 110 115	510
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cca gaa atc ttg gca aaa atg ttc aag cct caa gct ctt ctt gat aaa Pro Glu Ile Leu Ala Lys Met Phe Lys Pro Gln Ala Leu Leu Asp Lys 230 235 240 245	894
gca aaa atc aac caa gga tgg ctt gat tcc tca aga tct ctc atg gaa	942

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Ile Gly Gly Ser Asn His Leu Ala Val Val Leu Asp Asp Ile Ile Leu
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gca gtt att gac tcc att ttt gtg tgg ttc att ttt att agt ttg gca 151
Ala Val Ile Asp Ser Ile Phe Val Trp Phe Ile Phe Ile Ser Leu Ala
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Gln Thr Met Lys Thr Leu Arg Leu Arg Lys Asn Thr Val Lys Phe Ser	
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tta tat aga cat ttt aaa aat act ctg atc ttt gct gtg ctg gct tct	247
Leu Tyr Arg His Phe Lys Asn Thr Leu Ile Phe Ala Val Leu Ala Ser	
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Ile Val Phe Met Gly Trp Thr Thr Lys Thr Phe Arg Ile Ala Lys Cys	
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Gln Ser Asp Trp Met Glu Arg Trp Val Asp Asp Ala Phe Trp Ser Phe	
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ctt ttt tcg ctt atc ctt att gta atc atg ttt ttg tgg aga cca tca	391
Leu Phe Ser Leu Ile Leu Ile Val Ile Met Phe Leu Trp Arg Pro Ser	
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gca aac aat cag aga tat gcc ttc atg ccc tta ata gat gat tct gat	439
Ala Asn Asn Gln Arg Tyr Ala Phe Met Pro Leu Ile Asp Asp Ser Asp	
120 125 130	
gat gaa att gag gaa ttc atg gta act tct gaa aat tta acc gaa gga	487
Asp Glu Ile Glu Glu Phe Met Val Thr Ser Glu Asn Leu Thr Glu Gly	
135 140 145	
ata aaa tta aga gcc tca aaa tca gtt tcc aat gga aca gct aag cct	535
Ile Lys Leu Arg Ala Ser Lys Ser Val Ser Asn Gly Thr Ala Lys Pro	
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gcc act tct gag aac ttt gat gaa gat ttg aag tgg gta gaa gaa aat	583
Ala Thr Ser Glu Asn Phe Asp Glu Asp Leu Lys Trp Val Glu Glu Asn	
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att ccc tct tca ttc aca gat gta gct ctt cca gtg tta gtg gat tca	631
Ile Pro Ser Ser Phe Thr Asp Val Ala Leu Pro Val Leu Val Asp Ser	
180 185 190 195	
gat gag gaa atc atg acc aga tct gaa atg gct gaa aaa atg ttc tct	679
Asp Glu Glu Ile Met Thr Arg Ser Glu Met Ala Glu Lys Met Phe Ser	
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Ser Glu Lys Ile Met *	
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 Met Glu Val Val Asp Glu
 1 5
 acg gag gcg ctg cag cgc ttc ttc gaa ggc cac gac atc aac ggt gcc 163
 Thr Glu Ala Leu Gln Arg Phe Phe Glu Gly His Asp Ile Asn Gly Ala
 10 15 20
 ctg gag ccc tcc aac ata gac acc agc atc ctg gag gag tac atc agc 211
 Leu Glu Pro Ser Asn Ile Asp Thr Ser Ile Leu Glu Glu Tyr Ile Ser
 25 30 35
 aag gag gat gcc tcc gac ctc tgc ttc cct gac atc tct gct cca gcc 259
 Lys Glu Asp Ala Ser Asp Leu Cys Phe Pro Asp Ile Ser Ala Pro Ala
 40 45 50
 agc tcg gcc tcc tac tcc cac ggg cag cct gcg atg cct ggc tcc agc 307
 Ser Ser Ala Ser Tyr Ser His Gly Gln Pro Ala Met Pro Gly Ser Ser
 55 60 65 70

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Gly Val His His Leu Ser Pro Pro Gly Gly Gly Pro Ser Pro Gly Arg	
75 80 85	
cat ggt ccc ctc cca ccc ccg ggc tac ggc acc ccg ctg aac tgc aac	403
His Gly Pro Leu Pro Pro Pro Gly Tyr Gly Thr Pro Leu Asn Cys Asn	
90 95 100	
aac aac aac ggc atg ggc gct gcc ccc aag ccc ttc ccg ggg ggc acc	451
Asn Asn Asn Gly Met Gly Ala Ala Pro Lys Pro Phe Pro Gly Gly Thr	
105 110 115	
ggg ccc ccc atc aag gct gag ccc aag gct ccc tat gcc cca ggc aca	499
Gly Pro Pro Ile Lys Ala Glu Pro Lys Ala Pro Tyr Ala Pro Gly Thr	
120 125 130	
ctg ccg gac tct ccc cca gac tcg ggc tcc gag gcc tac tcc ccc cag	547
Leu Pro Asp Ser Pro Pro Asp Ser Gly Ser Glu Ala Tyr Ser Pro Gln	
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Gln Val Asn Glu Pro His Leu Leu Arg Thr Ile Thr Pro Glu Thr Leu	
155 160 165	
tgc cac gtg gga gtg ccc tcc cgc ctg gag cat ccg ccc cca cct cca	643
Cys His Val Gly Val Pro Ser Arg Leu Glu His Pro Pro Pro Pro Pro	
170 175 180	
gcc cac ttg cca ggc ccc ccg cca ccc cca cca ccc cca cct cac tac	691
Ala His Leu Pro Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro His Tyr	
185 190 195	
cct gtc ctg cag cgg gat ctg tac atg aag gcc gag ccc ccg atc ccc	739
Pro Val Leu Gln Arg Asp Leu Tyr Met Lys Ala Glu Pro Pro Ile Pro	
200 205 210	
cac tac gct gcc atg ggg cag ggg ctg gtg ccc act gat ctt cac cac	787
His Tyr Ala Ala Met Gly Gln Gly Leu Val Pro Thr Asp Leu His His	
215 220 225 230	
acc cag cag tcc cag atg ctg cac cag ctc ctg cag cag cac gga gct	835
Thr Gln Gln Ser Gln Met Leu His Gln Leu Leu Gln Gln His Gly Ala	
235 240 245	
gag ctc cct aca cac ccc tcc aag aag agg aag cac tct gaa tcc ccc	883
Glu Leu Pro Thr His Pro Ser Lys Lys Arg Lys His Ser Glu Ser Pro	
250 255 260	
ccg agc acc ctc aat gcc cag atg ctg aat gga atg atc aaa cag gag	931
Pro Ser Thr Leu Asn Ala Gln Met Leu Asn Gly Met Ile Lys Gln Glu	
265 270 275	
cct ggg acc gtg aca gcc ctg cct ctg cac ccc act cga gcc cca tcg	979
Pro Gly Thr Val Thr Ala Leu Pro Leu His Pro Thr Arg Ala Pro Ser	
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cct	ctc	agc	att	gcc	cgt	gtc	cag	aca	ccg	cct	tgg	cac	ccg	cca	ggt	1075
Pro	Leu	Ser	Ile	Ala	Arg	Val	Gln	Thr	Pro	Pro	Trp	His	Pro	Pro	Gly	
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gcc	ccc	tcc	cca	ggc	ctc	ctg	cag	gac	agt	gac	agc	ctc	agt	ggc	tcc	1123
Ala	Pro	Ser	Pro	Gly	Leu	Leu	Gln	Asp	Ser	Asp	Ser	Leu	Ser	Gly	Ser	
			330					335					340			
tac	ctg	gac	ccc	aac	tac	cag	tcc	atc	aag	tgg	cag	cct	cat	cag	cag	1171
Tyr	Leu	Asp	Pro	Asn	Tyr	Gln	Ser	Ile	Lys	Trp	Gln	Pro	His	Gln	Gln	
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aac	aag	tgg	gcg	acc	ctg	tac	gat	gct	aac	tac	aag	gag	ctg	ccc	atg	1219
Asn	Lys	Trp	Ala	Thr	Leu	Tyr	Asp	Ala	Asn	Tyr	Lys	Glu	Leu	Pro	Met	
	360					365					370					
ctc	acc	tac	cgc	gtg	gat	gcg	gac	aag	ggc	ttc	aac	ttt	tcg	gtg	ggc	1267
Leu	Thr	Tyr	Arg	Val	Asp	Ala	Asp	Lys	Gly	Phe	Asn	Phe	Ser	Val	Gly	
375					380					385					390	
gac	gac	gcc	ttt	gtg	tgc	cag	aag	aag	aac	cac	ttc	cag	gtg	aca	gtg	1315
Asp	Asp	Ala	Phe	Val	Cys	Gln	Lys	Lys	Asn	His	Phe	Gln	Val	Thr	Val	
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tac	atc	ggc	atg	ctg	ggc	gag	ccc	aag	tac	gtc	aag	acg	ccc	gag	ggc	1363
Tyr	Ile	Gly	Met	Leu	Gly	Glu	Pro	Lys	Tyr	Val	Lys	Thr	Pro	Glu	Gly	
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ctc	aag	ccc	ctc	gac	tgc	ttc	tat	ctg	aag	ctg	cac	gga	gtg	aag	ctg	1411
Leu	Lys	Pro	Leu	Asp	Cys	Phe	Tyr	Leu	Lys	Leu	His	Gly	Val	Lys	Leu	
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gag	gcc	ctg	aac	cag	tcc	att	aac	atc	gag	cag	tcc	cag	tca	gac	cgg	1459
Glu	Ala	Leu	Asn	Gln	Ser	Ile	Asn	Ile	Glu	Gln	Ser	Gln	Ser	Asp	Arg	
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Ser	Lys	Arg	Pro	Phe	Asn	Pro	Val	Thr	Val	Asn	Leu	Pro	Pro	Glu	Gln	
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gtc	acg	aag	gtg	act	gtg	ggg	cgg	ctg	cac	ttc	agc	gag	acc	acc	gct	1555
Val	Thr	Lys	Val	Thr	Val	Gly	Arg	Leu	His	Phe	Ser	Glu	Thr	Thr	Ala	
				475					480					485		
aac	aac	atg	cgt	aag	aag	ggc	aag	ccc	aac	ccg	gac	cag	agg	tac	ttc	1603
Asn	Asn	Met	Arg	Lys	Lys	Gly	Lys	Pro	Asn	Pro	Asp	Gln	Arg	Tyr	Phe	
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atg	ctg	gtg	gtg	gcc	ctc	cag	gct	cat	gca	cag	aac	cag	aac	tac	acg	1651
Met	Leu	Val	Val	Ala	Leu	Gln	Ala	His	Ala	Gln	Asn	Gln	Asn	Tyr	Thr	
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ctg	gcc	gcc	cag	atc	tca	gag	cgc	atc	att	gtg	cgg	gcc	tcc	aac	cca	1699
Leu	Ala	Ala	Gln	Ile	Ser	Glu	Arg	Ile	Ile	Val	Arg	Ala	Ser	Asn	Pro	

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Gly Gln Phe Glu Ser Asp Ser Asp Val Leu Trp Gln Arg Ala Gln Val			
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Pro Asp Thr Val Phe His His Gly Arg Val Gly Ile Asn Thr Asp Arg			
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ccg gat gag gcg ctg gtt gtg cac ggg aat gtc aag gtc atg ggc tcg			1843
Pro Asp Glu Ala Leu Val Val His Gly Asn Val Lys Val Met Gly Ser			
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ctt atg cac ccc tcc gac ctg cgc gcc aag gaa cac gtg cag gag gtg			1891
Leu Met His Pro Ser Asp Leu Arg Ala Lys Glu His Val Gln Glu Val			
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gac acc acc gag caa ttg aag agg atc tcg cgc atg cgg ctg gtg cac			1939
Asp Thr Thr Glu Gln Leu Lys Arg Ile Ser Arg Met Arg Leu Val His			
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tac aga tac aag ccc gag ttc gcc gcc agc gcg ggc atc gag gcc acc			1987
Tyr Arg Tyr Lys Pro Glu Phe Ala Ala Ser Ala Gly Ile Glu Ala Thr			
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gcg cca gag aca ggt gtc atc gct cag gag gtg aag gag atc ttg cct			2035
Ala Pro Glu Thr Gly Val Ile Ala Gln Glu Val Lys Glu Ile Leu Pro			
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gag gct gtg aaa gac acc gga gac atg gtc ttt gcc aat ggg aaa acc			2083
Glu Ala Val Lys Asp Thr Gly Asp Met Val Phe Ala Asn Gly Lys Thr			
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Ile Glu Asn Phe Leu Val Val Asn Lys Glu Arg Ile Phe Met Glu Asn			
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gta ggg gcc gtg aag gag ctg tgc aag ctg aca gac aac ctg gag acg			2179
Val Gly Ala Val Lys Glu Leu Cys Lys Leu Thr Asp Asn Leu Glu Thr			
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cgc att gat gag ctg gag cgc tgg agc cac aag ctg gcc aag ctg cgg			2227
Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu Ala Lys Leu Arg			
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cgg ctc gac agc ctc aag tcc acc ggc agc tcg ggc gcc ttc agc cat			2275
Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly Ala Phe Ser His			
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gca ggg agc cag ttc agt cgg gcg ggc agc gtc ccc cac aag aag agg			2323
Ala Gly Ser Gln Phe Ser Arg Ala Gly Ser Val Pro His Lys Lys Arg			
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ccc ccc aag gtg gcc agc aag tca tcg tcc gtg gtt ccg gac cag gcc			2371
Pro Pro Lys Val Ala Ser Lys Ser Ser Ser Val Val Pro Asp Gln Ala			
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Cys Ile Ser Gln Arg Phe Leu Gln Gly Thr Ile Ile Ala Leu Val Val	
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gtc atg gcc ttc agc gtg gtg tcc atg tcc aca ctg tac gtg ctg agc	2467
Val Met Ala Phe Ser Val Val Ser Met Ser Thr Leu Tyr Val Leu Ser	
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ctg cgc aca gag gag gac ctg gta gac act gat gcc agg tcc agc cag	2515
Leu Arg Thr Glu Glu Asp Leu Val Asp Thr Asp Gly Arg Ser Ser Gln	
795 800 805	
agc ttt ggg acc acg cag ctc cga cag tcc ccc ttg acc acg ggg cta	2563
Ser Phe Gly Thr Thr Gln Leu Arg Gln Ser Pro Leu Thr Thr Gly Leu	
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Pro Gly Ile Gln Pro Ser Leu Leu Leu Val Thr Thr Ser Leu Thr Ser	
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Leu Pro Val Thr Asn Ile Arg Ala Lys Ser Trp Gly Leu Ser Val Asn	
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Val Gly Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Glu Pro Val	
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Pro Ser Leu Thr Ser Ile Gln Val Leu Glu Asn Ser Met Ser Ile Thr	
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Tyr His Ile Pro Val Ser Ser Gly Thr Pro Leu His Leu Ser Leu Thr	
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His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp Pro Ile Thr	
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Tyr His Phe His Phe Tyr Arg Leu Cys Asp *	
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 Met Leu Thr Gln Leu Lys
 1 5

gca aaa tca gag ggg aag ctt gca aaa cag att tgc aaa gtt gtg ttg 163
 Ala Lys Ser Glu Gly Lys Leu Ala Lys Gln Ile Cys Lys Val Val Leu
 10 15 20

gat cat ttt gaa aaa cag tat tcc aaa gaa ctc gga gat gcc tgg aat 211
 Asp His Phe Glu Lys Gln Tyr Ser Lys Glu Leu Gly Asp Ala Trp Asn
 25 30 35

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 Thr Val Arg Glu Ile Leu Thr Ser Pro Ser Cys Trp Gln Tyr Ala Val
 40 45 50

ctg ctt aac cga ttc aat tat cct ttt gaa ctg gaa aag gat tta cat 307
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 55 60 65 70

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 75 80 85

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 Lys Ser Val Lys Cys Tyr Leu Ser Arg Thr Pro Gly Arg Ile Pro Ser
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Arg Leu Arg Trp Leu Arg Gln Thr Leu Glu Ser Phe Ile Pro Gln Pro	
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Leu Ile Asn Val Ile Lys Val Ser Glu Leu Asp Gly Arg Lys Met Gly	
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gat gcc cag cct gaa atg ttt gac aag gtg tta gtg gat gct ccg tgt	739
Asp Ala Gln Pro Glu Met Phe Asp Lys Val Leu Val Asp Ala Pro Cys	
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Ser Asn Asp Arg Ser Trp Leu Phe Ser Ser Asp Ser Gln Lys Ala Ser	
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Cys Arg Ile Ser Gln Arg Arg Asn Leu Pro Leu Leu Gln Ile Glu Leu	
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tta agg tct gca att aag gcc tta cgt cct gga ggg ata ctt gta tac	883
Leu Arg Ser Ala Ile Lys Ala Leu Arg Pro Gly Gly Ile Leu Val Tyr	
250 255 260	
tct aca tgc acg ctt tcc aag gca gaa aat caa gat gtg atc agt gaa	931
Ser Thr Cys Thr Leu Ser Lys Ala Glu Asn Gln Asp Val Ile Ser Glu	
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Ile Leu Asn Ser His Gly Asn Ile Met Pro Met Asp Ile Lys Gly Ile	
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Ala Arg Thr Cys Ser His Asp Phe Thr Phe Ala Pro Thr Gly Gln Glu	
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Cys Gly Leu Leu Val Ile Pro Asp Lys Gly Lys Ala Trp Gly Pro Met	
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tat gta gcc aaa ttg aag aaa tca tgg agc aca gga aaa tgg tga cat	1123
Tyr Val Ala Lys Leu Lys Lys Ser Trp Ser Thr Gly Lys Trp *	
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 Met
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 cag ctc ttc aat gga gga tgc cca ccc cct cct cct gtc ctg aat ggt 163
 Gln Leu Phe Asn Gly Gly Cys Pro Pro Pro Pro Val Leu Asn Gly
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 Glu Asp Val Leu Pro Asp Leu Asn Leu Leu Pro Pro Leu Gln Pro Pro
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 Leu Pro Gly Leu Leu Pro Ser Glu Lys Glu Ala Pro Ala Pro Met Gly
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 Pro Pro Pro Gln Ala Pro Ala Glu Gly Pro Ser Val Gln Pro Gly Pro
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 Leu Arg Pro Met Glu Glu Glu Leu Pro Pro Pro Pro Ala Glu Pro Val
 85 90 95

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 Glu Lys Gly Ala Ser Thr Asp Ile Cys Ala Phe Cys His Lys Thr Val
 100 105 110

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 Phe Pro Arg Glu Leu Ala Val Glu Ala Met Lys Arg Gln Tyr His Ala
 115 120 125

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 Gln Cys Phe Thr Cys Arg Thr Cys Arg Arg Gln Leu Ala Gly Gln Ser
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Thr Leu Glu Arg Cys Gly Lys Cys Gly Glu Val Val Arg Asp His Ile
      165                      170                      175

atc agg gcc ctg ggc cag gcc ttc cac ccc tcc tgc ttc acg tgt gtg      691
Ile Arg Ala Leu Gly Gln Ala Phe His Pro Ser Cys Phe Thr Cys Val
      180                      185                      190

acc tgc gcc cgg tgc att ggg gat gag agc ttt gcc ctg ggc agc cag      739
Thr Cys Ala Arg Cys Ile Gly Asp Glu Ser Phe Ala Leu Gly Ser Gln
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aac gag gtg tac tgc ctg gac gac ttc tac agg aaa ttc gcc ccc gtc      787
Asn Glu Val Tyr Cys Leu Asp Asp Phe Tyr Arg Lys Phe Ala Pro Val
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tgc agc atc tgt gaa aat ccc atc atc cct cgg gat ggg aaa gat gcc      835
Cys Ser Ile Cys Glu Asn Pro Ile Ile Pro Arg Asp Gly Lys Asp Ala
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ttc aaa atc gaa tgc atg gga aga aac ttc cat gaa aat tgc tac agg      883
Phe Lys Ile Glu Cys Met Gly Arg Asn Phe His Glu Asn Cys Tyr Arg
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Cys Glu Asp Cys Arg Ile Leu Leu Ser Val Glu Pro Thr Asp Gln Gly
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Cys Tyr Pro Leu Asn Asn His Leu Phe Cys Lys Pro Cys His Val Lys
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Arg Ser Ala Ala Gly Cys Cys *
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Ile Lys Trp Gln Gln Glu Leu Ser Trp Glu Glu Ala Ala Arg Arg Leu			
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Glu Ala Phe Asp Arg Ala Lys Ala Glu Asn Lys Leu Val His Ser Ile			
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Gln Cys Leu Ala Ser Gln Ala Ala Ser Arg Asp Cys Phe Arg Arg
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gaa ccc acg ctt ctg acc tgt gct ctg tct ttg cag ttc tgc acg gag 154
Glu Pro Thr Leu Leu Thr Cys Ala Leu Ser Leu Gln Phe Cys Thr Glu
20 25 30
cta aac cag ccg acc ctg ccc aac atc cgc aag tgg aag ggg ccc cgg 202
Leu Asn Gln Pro Thr Leu Pro Asn Ile Arg Lys Trp Lys Gly Pro Arg
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Gly Cys Trp Lys Ala Val Val Ala Glu Lys Pro Ser Asn Gln Leu Gln
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Lys Val Pro Ser Ser Ala Lys Pro Gly Leu Ser Leu His Leu Ile Tyr

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Ile Pro Gly Ser Ile Leu Tyr Phe Cys Pro Ile Phe Lys Ser Leu Pro			
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Phe Ile Ser Lys Cys Pro Gly Phe Arg Phe Thr Phe Arg Leu Val Met			
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Asp Ser Cys Gln Glu Gly Asn Glu Ser Leu Arg Val Leu Gly Glu Arg			
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Arg Gly Glu Arg Gln Gln Met Gly Ile Ser Val Leu Cys Pro Ser Asn			
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Pro Phe Ala Thr Val Leu Ser Ser Ala Lys Phe Val Gln Ser Ser Leu			
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Leu Val Asp *			
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Glu Pro Ile Pro Cys Gly Leu Gly Glu His Val Thr Arg Pro Gly Leu	

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Leu Ser Pro Thr Ala Ser *			
75			
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Val Ser Tyr Val Arg Pro Ala Glu Pro Ala Phe Leu Ala Arg Phe Lys			
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Glu Arg Val Gly Tyr Arg Glu Gly Pro Thr Val Glu Thr Lys Arg Ile			
25 30 35			
cag cct cag ccc cca gat gaa gat ggg gat cac agt gac aaa gaa gat			199
Gln Pro Gln Pro Pro Asp Glu Asp Gly Asp His Ser Asp Lys Glu Asp			
40 45 50			
gaa cag cct caa gtg gtg gtt tta aaa aag gga gac ctg tca gtt gaa			247
Glu Gln Pro Gln Val Val Leu Lys Lys Gly Asp Leu Ser Val Glu			
55 60 65 70			
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Glu Val Met Lys Ile Lys Ala Glu Ile Lys Ala Ala Lys Ala Asp Glu			

75	80	85	
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Glu Pro Thr Pro Ala Asp Gly Arg Ile Ile Tyr Arg Lys Pro Val Lys			
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cat ccc tca gat gaa aaa tat tca ggt tta aca gca agc tca aaa aag			391
His Pro Ser Asp Glu Lys Tyr Ser Gly Leu Thr Ala Ser Ser Lys Lys			
105	110	115	
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Lys Lys Pro Asn Glu Asp Glu Val Asn Gln Asp Ser Val Lys Lys Asn			
120	125	130	
tca caa aaa caa att aaa aat agt agc ctc ctt tct ttt gac aac gaa			487
Ser Gln Lys Gln Ile Lys Asn Ser Ser Leu Leu Ser Phe Asp Asn Glu			
135	140	145	150
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Asp Glu Asn Glu *			
155			
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cgctgggaag ggacggccct cgcccgcggt g atg gtg gtt agc aag atg aac			172
Met Val Val Ser Lys Met Asn			
1	5		
aaa gat gcg cag atg aga gca gcg att aac caa aag ttg ata gaa act			220
Lys Asp Ala Gln Met Arg Ala Ala Ile Asn Gln Lys Leu Ile Glu Thr			
10	15	20	

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gga gaa aga gaa cgc ctc aaa gag ttg ctg aga gct aaa tta att gaa      268
Gly Glu Arg Glu Arg Leu Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu
    25                      30                      35

tgt ggc tgg aag gat cag ttg aag gca cac tgt aaa gag gta att aaa      316
Cys Gly Trp Lys Asp Gln Leu Lys Ala His Cys Lys Glu Val Ile Lys
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gaa aaa gga cta gaa cac gtt act gtt gat gac ttg gtg gct gaa atc      364
Glu Lys Gly Leu Glu His Val Thr Val Asp Asp Leu Val Ala Glu Ile
                60                      65                      70

act cca aaa ggc aga gcc ctg gta cct gac agt gta aag aag gag ctc      412
Thr Pro Lys Gly Arg Ala Leu Val Pro Asp Ser Val Lys Lys Glu Leu
                75                      80                      85

cta caa aga ata aga aca ttc ctt gct cag cat gcc agc ctt taa gat      460
Leu Gln Arg Ile Arg Thr Phe Leu Ala Gln His Ala Ser Leu *
                90                      95                      100

tgaattagat tgtgtttgttg tggtttttatt tctgaaagta aaacttgcca taaattagaa      520

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aattagaatc ttttcacatg agactacaga gaaagatttg tatttgtaac aaaaaattag      300
ctgggcatgg tggcaggtgc ctgtaatccc agctacttgg gaggctgagg caggagaatc      360
gcttgaaccc gggaggcgga ggttgagcaa ctacactgcg ctgcatcgga ctogacgccc      420

gctggtgacg cacacgctgc gccggaagtg tgaactgtct gcctccgggc tttgtc      476
atg gcg gct gct gct gca cgc tgg aac cat gtg tgg gtc ggc acc gag      524
Met Ala Ala Ala Ala Arg Trp Asn His Val Trp Val Gly Thr Glu
    1                      5                      10                      15

act ggg atc ttg aaa ggg gta aat ctt cag cga aaa cag gcg gcg aac      572

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Thr	Gly	Ile	Leu	Lys	Gly	Val	Asn	Leu	Gln	Arg	Lys	Gln	Ala	Ala	Asn		
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Phe	Thr	Ala	Gly	Gly	Gln	Pro	Arg	Arg	Glu	Glu	Ala	Val	Ser	Ala	Leu		
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tgt	tgg	ggc	acc	ggc	ggc	gag	acc	cag	atg	ctg	gtg	ggc	tgc	gcg	gac	668	
Cys	Trp	Gly	Thr	Gly	Gly	Glu	Thr	Gln	Met	Leu	Val	Gly	Cys	Ala	Asp		
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agg	acg	gtg	aag	cac	ttc	agc	acc	gag	gat	ggc	ata	ttc	cag	ggt	cag	716	
Arg	Thr	Val	Lys	His	Phe	Ser	Thr	Glu	Asp	Gly	Ile	Phe	Gln	Gly	Gln		
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aga	cac	tgc	ccg	ggc	ggg	gag	ggc	atg	ttc	cgt	ggc	ctc	gcc	cag	gcc	764	
Arg	His	Cys	Pro	Gly	Gly	Glu	Gly	Met	Phe	Arg	Gly	Leu	Ala	Gln	Ala		
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gac	ggc	acc	ctc	atc	aca	tgt	gtg	gat	tct	ggg	att	ctc	aga	gtc	tgg	812	
Asp	Gly	Thr	Leu	Ile	Thr	Cys	Val	Asp	Ser	Gly	Ile	Leu	Arg	Val	Trp		
			100					105					110				
cat	gac	aag	gac	aag	gac	aca	tcc	tct	gac	cca	ctc	ctg	gaa	ctg	aga	860	
His	Asp	Lys	Asp	Lys	Asp	Thr	Ser	Ser	Asp	Pro	Leu	Leu	Glu	Leu	Arg		
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Val	Gly	Pro	Gly	Val	Cys	Arg	Met	Arg	Gln	Asp	Pro	Ala	His	Pro	His		
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Val	Val	Ala	Thr	Gly	Gly	Lys	Glu	Asn	Ala	Leu	Lys	Ile	Trp	Asp	Leu		
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Gln	Gly	Ser	Glu	Glu	Pro	Val	Phe	Arg	Ala	Lys	Asn	Val	Arg	Asn	Asp		
				165					170					175			
tgg	ctg	gac	ttg	cgg	ggt	ccc	atc	tgg	gac	cag	gac	ata	cag	ttt	ctc	1052	
Trp	Leu	Asp	Leu	Arg	Val	Pro	Ile	Trp	Asp	Gln	Asp	Ile	Gln	Phe	Leu		
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cca	gga	tca	cag	aag	ctt	gtc	acc	tgc	aca	ggg	tac	cac	cag	gtc	cgt	1100	
Pro	Gly	Ser	Gln	Lys	Leu	Val	Thr	Cys	Thr	Gly	Tyr	His	Gln	Val	Arg		
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Val	Tyr	Asp	Pro	Ala	Ser	Pro	Gln	Arg	Arg	Pro	Val	Leu	Glu	Thr	Thr		
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Tyr	Gly	Glu	Tyr	Pro	Leu	Thr	Ala	Met	Thr	Leu	Thr	Pro	Gly	Gly	Asn		
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tca	gtg	att	gtg	gga	aac	act	cat	ggg	cag	ctg	gca	gaa	att	gac	ctt	1244	
Ser	Val	Ile	Val	Gly	Asn	Thr	His	Gly	Gln	Leu	Ala	Glu	Ile	Asp	Leu		

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Arg Gln Gly Arg Leu Leu Gly Cys Leu Lys Gly Leu Ala Gly Ser Val			
260	265	270	
cgt ggg ttg cag tgc cac cct tca aag cct cta cta gcc tcc tgt ggc			1340
Arg Gly Leu Gln Cys His Pro Ser Lys Pro Leu Leu Ala Ser Cys Gly			
275	280	285	
ttg gac aga gtc ttg agg ata cac agg atc cag aat cca cgg ggt ctg			1388
Leu Asp Arg Val Leu Arg Ile His Arg Ile Gln Asn Pro Arg Gly Leu			
290	295	300	
gag cat aag gtt tat ctc aag tct caa ttg aac tgc ctc ctc ttg tca			1436
Glu His Lys Val Tyr Leu Lys Ser Gln Leu Asn Cys Leu Leu Leu Ser			
305	310	315	320
ggc agg gac aac tgg gag gat gag ccc caa gag cct caa gaa ccc aac			1484
Gly Arg Asp Asn Trp Glu Asp Glu Pro Gln Glu Pro Gln Glu Pro Asn			
325	330	335	
aag gtg ccc cta gaa gac aca gag aca gat gaa ctt tgg gca tcc ttg			1532
Lys Val Pro Leu Glu Asp Thr Glu Thr Asp Glu Leu Trp Ala Ser Leu			
340	345	350	
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Glu Ala Ala Ala Lys Arg Lys Leu Ser Gly Leu Glu Gln Pro Gln Gly			
355	360	365	
gct ctc caa acg aga cgg aga aag aag aag cgg cct ggg tcc acc agc			1628
Ala Leu Gln Thr Arg Arg Arg Lys Lys Lys Arg Pro Gly Ser Thr Ser			
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Pro *			
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Met Leu Leu	

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 Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys Ser
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ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag gct ggc tta 213
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cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc acc aac aag 261
 Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn Lys
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cga aag gct tac tcg gag cgt aga atc atg ggg tac tca atg cag gag 309
 Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser Met Gln Glu
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 Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu Phe Val Pro
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 85 90 95

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 Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg Tyr Thr Ser
 100 105 110 115

gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt tgt act gat 501
 Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val Cys Thr Asp
 120 125 130

ggc aag ctc ttc aac cac tta gag act att tgg cga ttc agc cct ggt 549
 Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly
 135 140 145

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 Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser Ile Ser Phe
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gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg gca gcc acc 693
 Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg Ala Ala Thr
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aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg ttc cat gag 741
 Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met Phe His Glu
 200 205 210

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 Val His Gln Thr *
 215

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 Met Lys Leu Thr Phe Lys Lys
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 Lys Ala Val Ser Phe Ala Asp Ala Ala Ala Gln Gly Pro Leu Leu
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Pro Ala Met Val Asn Pro Thr Met Phe Phe His Ile Ala Val Asp Gly
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 Glu Pro Leu Gly Cys Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro
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 Lys Thr Ala Glu Asn Phe His Ala Leu Ser Thr Gly Glu Lys Gly Phe
 60 65 70

ggg tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt acg tgt 652
 Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Thr Cys
 75 80 85

cag agt ggt gac ttc aca cgc cat aca gca ttg gtg gca agt cca tct 700
 Gln Ser Gly Asp Phe Thr Arg His Thr Ala Leu Val Ala Ser Pro Ser
 90 95 100

gca ggg aga aat ttg atg aca aga act tca tcc tga agca tacgggtcct 750
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agttggcagc ggcaagcgcg ctgcggttcc ggtggcgcc atg tcg ttc tgc agc 174
 Met Ser Phe Cys Ser
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gtg tgt gcc aag tgt ggc tat gag ctg ttc tcc agc cgc tcg aag tat	270
Val Cys Ala Lys Cys Gly Tyr Glu Leu Phe Ser Ser Arg Ser Lys Tyr	
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Ala His Ser Ser Pro Trp Pro Ala Phe Thr Glu Thr Ile His Ala Asp	
40 45 50	
agc gtg gcc aag cgt ccg gag cac aat aga tct gaa gcc ttg aag gtg	366
Ser Val Ala Lys Arg Pro Glu His Asn Arg Ser Glu Ala Leu Lys Val	
55 60 65	
tcc tgt ggc aag tgt ggc aat ggg ttg ggc cac gag ttc ctg aac gac	414
Ser Cys Gly Lys Cys Gly Asn Gly Leu Gly His Glu Phe Leu Asn Asp	
70 75 80 85	
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 gac ttt tta tca gga att cag att gaa ttt aag cag tct tct cac cag 156
 Asp Phe Leu Ser Gly Ile Gln Ile Glu Phe Lys Gln Ser Ser His Gln
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 Arg Ser Leu Arg Ala Arg Leu Tyr Trp Leu Gln Val Asp Asn Gln Leu
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 Pro Gly Ala Met Phe Pro Val Val Phe His Pro Val Ala Pro Pro Lys
 50 55 60
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 Ser Ile Ala Leu Asp Ser Glu Pro Lys Pro Phe Ile Asp Val Ser Val
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 Ile Thr Arg Phe Asn Glu Tyr Ser Lys Val Leu Gln Phe Lys Tyr Phe
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 Met Val Leu Ile Gln Glu Met Ala Leu Lys Ile Asp Gln Gly Phe Leu
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 Gly Ala Ile Ile Ala Leu Phe Thr Pro Thr Thr Asp Pro Glu Ala Glu
 110 115 120 125
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 130 135 140
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 Glu Leu Met Glu Thr Ser Met Thr Asp Met Ser Ile Leu Ser Phe Phe
 145 150 155
 gaa cat ttc cat att tct cct gtg aag ttg cat ttg agt ttg tct ttg 588
 Glu His Phe His Ile Ser Pro Val Lys Leu His Leu Ser Leu Ser Leu
 160 165 170
 ggt tcc gga ggt gaa gaa tca gac aaa gaa aaa cag gaa atg ttt gca 636
 Gly Ser Gly Gly Glu Glu Ser Asp Lys Glu Lys Gln Glu Met Phe Ala

175	180	185	
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Val His Ser Val Asn Leu Leu Lys Ser Ile Gly Ala Thr Leu Thr			
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Asp Val Asp Asp Leu Ile Phe Lys Leu Ala Tyr Tyr Glu Ile Arg Tyr			
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cag ttc tac aag aga gat cag ctt ata tgg agt gtt gtt agg cat tac			780
Gln Phe Tyr Lys Arg Asp Gln Leu Ile Trp Ser Val Val Arg His Tyr			
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Ser Glu Gln Phe Leu Lys Gln Met Tyr Val Leu Val Leu Gly Leu Asp			
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gta ctt gga aac cca ttt gga tta att aga ggt ctg tct gaa gga gtt			876
Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Gly Leu Ser Glu Gly Val			
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Glu Ala Leu Phe Tyr Glu Pro Phe Gln Gly Ala Val Gln Gly Pro Glu			
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Glu Phe Ala Glu Gly Leu Val Ile Gly Val Arg Ser Leu Phe Gly His			
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Arg Arg Glu Glu Leu Ser Arg Gln Pro Arg Asp Phe Gly Asp Ser Leu			
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Ala Arg Gly Gly Lys Gly Phe Leu Arg Gly Val Val Gly Gly Val Thr			
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Gly Ile Ile Thr Lys Pro Val Glu Gly Ala Lys Lys Glu Gly Ala Ala			
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ggtatttggt taggatacct cagtattcta gagctatggg atttattttg ctttgaagtc      300

cagaggtatt tagctttatt ctaaaagcg  atg aag ttc ctc tta att aaa gac      353
                               Met Lys Phe Leu Leu Ile Lys Asp
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gct cct gga aaa aaa aaa agg aaa aat tta atg ctg tct ttt aaa agg      401
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Lys His Ala Lys Gly Gln Asp Leu Phe Asp Gln Ile Val Tyr His Leu
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gac ctt gtg gaa aca gat tac ttt ggc ctc cag ttc ctc gac tct gcc      497
Asp Leu Val Glu Thr Asp Tyr Phe Gly Leu Gln Phe Leu Asp Ser Ala
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cag gtt gcg cac tgg ctg gat cat gcc aaa ccc ata aaa aag cag atg      545
Gln Val Ala His Trp Leu Asp His Ala Lys Pro Ile Lys Lys Gln Met
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Lys Ile Gly Pro Ala Tyr Ala Leu His Phe Arg Val Lys Tyr Tyr Ser
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Ser Glu Pro Asn Asn Leu Arg Glu Glu Phe Thr Arg Tyr Leu Phe Val
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tta caa ctc agg cat gac att ctt tct gga aaa ttg aaa tgc cct tat      689
Leu Gln Leu Arg His Asp Ile Leu Ser Gly Lys Leu Lys Cys Pro Tyr
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Glu Thr Ala Val Glu Leu Ala Ala Leu Cys Leu Gln Ala Glu Leu Gly

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 Thr Pro Arg Lys His His Gln His His His Gln Gln Gln His His Gln
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 35 40 45
 cag gcc agc agc caa agt gtg tat atg cta gat gaa ggc ttg act att 432
 Gln Ala Ser Ser Gln Ser Val Tyr Met Leu Asp Glu Gly Leu Thr Ile
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Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro Ala		
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Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu Asp		
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165 170 175		

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 180 185 190

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 Ala Glu Asp Thr Thr Gln Leu Glu Arg Ala Gly Gln Leu Pro Pro Val
 195 200 205

ttc tga agctgccaca ggggaggagt ctcttctcag tgagggtctc cgaggagtccc 736
 Phe *
 210

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 Met Pro Arg Arg
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aag aaa aaa gtt aaa gaa gtc tcc gaa tct cgg aac ctg gag aag aag	223
Lys Lys Lys Val Lys Glu Val Ser Glu Ser Arg Asn Leu Glu Lys Lys	
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gat gtg gaa act acc agt tct gtc agt gtg aag agg aag cgt aga ctt	271
Asp Val Glu Thr Thr Ser Ser Val Ser Val Lys Arg Lys Arg Arg Leu	
25 30 35	
gag gat gca ttc att gtg ata tcc gat agt gat gga gag gaa cca aag	319
Glu Asp Ala Phe Ile Val Ile Ser Asp Ser Asp Gly Glu Glu Pro Lys	
40 45 50	
gag gaa aat ggg ttg cag aaa acg aag aca aaa cag tcg aat aga gca	367
Glu Glu Asn Gly Leu Gln Lys Thr Lys Thr Lys Gln Ser Asn Arg Ala	
55 60 65	
aag tgt ttg gcc aaa aga aaa att gca cag atg aca gaa gaa gaa cag	415
Lys Cys Leu Ala Lys Arg Lys Ile Ala Gln Met Thr Glu Glu Glu Gln	
70 75 80	
ttt gct ctg gct ctc aaa atg agt gag cag gaa gct agg gag gtg aac	463
Phe Ala Leu Ala Leu Lys Met Ser Glu Gln Glu Ala Arg Glu Val Asn	
85 90 95 100	
agc cag gag gag gaa gaa gag gag ctc ttg agg aaa gcc att gct gaa	511
Ser Gln Glu Glu Glu Glu Glu Glu Leu Leu Arg Lys Ala Ile Ala Glu	
105 110 115	
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Ser Leu Asn Ser Cys Arg Pro Ser Asp Ala Ser Ala Thr Arg Ser Arg	
120 125 130	
cct ctg gcc act gga ccg tct tcc cag tcc cat caa gag aaa acc aca	607
Pro Leu Ala Thr Gly Pro Ser Ser Gln Ser His Gln Glu Lys Thr Thr	
135 140 145	
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Asp Ser Gly Leu Thr Glu Gly Ile Trp Gln Leu Val Pro Pro Ser Leu	
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Phe Lys Gly Ser His Ile Ser Gln Gly Asn Glu Ala Glu Glu Arg Glu	
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Glu Pro Trp Asp His Thr Glu Lys Thr Glu Glu Glu Pro Val Ser Gly	
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Ser Ser Gly Ser Trp Asp Gln Ser Ser Gln Pro Val Phe Glu Asn Val	
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Asn Val Lys Ser Phe Asp Arg Cys Thr Gly His Ser Ala Glu His Thr	
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455	460	465	
atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt ggt aac Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val Gly Asn 470 475 480			1615
aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca tcc agt Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser Ser Ser 485 490 495 500			1663
aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc aca aag Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro Thr Lys 505 510 515			1711
att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa gat aca Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu Asp Thr 520 525 530			1759
gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac agt ggg Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp Ser Gly 535 540 545			1807
aca gct gcc cag act tct cta gac att gac aag aat gag aag tgt tac Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys Cys Tyr 550 555 560			1855
ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat gtg gac Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His Val Asp 565 570 575 580			1903
tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct gaa ggg Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro Glu Gly 585 590 595			1951
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gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag gca ggc Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu Ala Gly 645 650 655 660			2143
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Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg	
695 700 705	
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Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe *	
710 715 720	
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atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc	646
Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro	
1 5 10 15	
agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc	694
Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser	
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tca caa agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg Ser Gln Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met 50 55 60	790
cca gag agt tct gca gaa gaa atc act gtt tgt cct gag acc cag cta Pro Glu Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu 65 70 75 80	838
agt tcc tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc Ser Ser Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser 85 90 95	886
aga gat atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt Arg Asp Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val 100 105 110	934
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Ser	Ser	Glu	Thr	Gly	Ala	Phe	Arg	Val	Pro	Ser	Pro	Gly	Met	Glu	Glu	
		275					280					285				
gca	ggc	tgc	agc	aga	gag	atg	cag	agt	tct	ttc	aca	cgt	cgt	gac	tta	1510
Ala	Gly	Cys	Ser	Arg	Glu	Met	Gln	Ser	Ser	Phe	Thr	Arg	Arg	Asp	Leu	
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aat	gaa	tct	ccc	gtc	aag	tct	ttt	gtt	tcc	att	tca	gaa	gcc	aca	gat	1558
Asn	Glu	Ser	Pro	Val	Lys	Ser	Phe	Val	Ser	Ile	Ser	Glu	Ala	Thr	Asp	
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tgc	tta	gtg	gac	ttt	aaa	aag	caa	gtt	act	gtc	cag	cca	ggg	agt	cgg	1606
Cys	Leu	Val	Asp	Phe	Lys	Lys	Gln	Val	Thr	Val	Gln	Pro	Gly	Ser	Arg	
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aca	cgg	acc	aaa	gct	ggc	aga	gga	aga	agg	aga	aaa	ttc	tga	atttcta		1655
Thr	Arg	Thr	Lys	Ala	Gly	Arg	Gly	Arg	Arg	Lys	Phe	*				
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atccccggcct	tgccattagc	atgcctc	atg cat cat	cag atg aca	agg aca											231
			Met His His	Gln Met Thr	Arg Thr											

acc ctc atg acg aag caa cat gaa tta ggg ggc ctc ttg gcc ttg gtc 279
 Thr Leu Met Thr Lys Gln His Glu Leu Gly Gly Leu Leu Ala Leu Val
 10 15 20

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 Gln Asn Cys Gln Ser Glu Met Asn Ile Lys Asp Ser Arg Ala Val Gly
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aga aca gag aga cca ttg tac ctg gca caa ggg ctc ttc atg aaa agg 423
 Arg Thr Glu Arg Pro Leu Tyr Leu Ala Gln Gly Leu Phe Met Lys Arg
 60 65 70

gag act tac tgg gag gtg caa gac agt ggc att tct cct ctc ctc ttg 471
 Glu Thr Tyr Trp Glu Val Gln Asp Ser Gly Ile Ser Pro Leu Leu Leu
 75 80 85

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 Ser Pro Gly Gly Arg Lys Met Leu Gln Glu Pro Thr Leu Ser Met Ser
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 125 130 135

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 Thr Phe Leu Arg Ile Arg Thr His Ser Thr Asp Ala Ser Cys Pro *
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                               Met Glu Asn Ser Glu Lys
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act gaa gtg gtt ctc ctt gct tgt ggt tca ttc aat ccc atc acc aac 160

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Met	His	Leu	Arg	Leu	Phe	Glu	Leu	Ala	Lys	Asp	Tyr	Met	Asn	Gly	Thr		
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gga	agg	tac	aca	gtt	gtc	aaa	ggc	atc	atc	tct	cct	gtt	ggg	gat	gcc	256	
Gly	Arg	Tyr	Thr	Val	Val	Lys	Gly	Ile	Ile	Ser	Pro	Val	Gly	Asp	Ala		
	40					45				50							
tac	aag	aag	aaa	gga	ctc	att	cct	gcc	tat	cac	cgg	gtc	atc	atg	gca	304	
Tyr	Lys	Lys	Lys	Gly	Leu	Ile	Pro	Ala	Tyr	His	Arg	Val	Ile	Met	Ala		
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gaa	ctt	gct	acc	aag	aat	tct	aaa	tgg	gtg	gaa	gtt	gat	aca	tgg	gaa	352	
Glu	Leu	Ala	Thr	Lys	Asn	Ser	Lys	Trp	Val	Glu	Val	Asp	Thr	Trp	Glu		
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Ser	Leu	Gln	Lys	Glu	Trp	Lys	Glu	Thr	Leu	Lys	Val	Leu	Arg	His	His		
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Gln	Glu	Lys	Leu	Glu	Ala	Ser	Asp	Cys	Asp	His	Gln	Gln	Asn	Ser	Pro		
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Thr	Leu	Glu	Arg	Pro	Gly	Arg	Lys	Arg	Lys	Trp	Thr	Glu	Thr	Gln	Asp		
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Val	Lys	Leu	Leu	Cys	Gly	Ala	Asp	Leu	Leu	Glu	Ser	Phe	Ala	Val	Pro		
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Leu	Ile	Cys	Val	Thr	Arg	Ala	Gly	Asn	Asp	Ala	Gln	Lys	Phe	Ile	Tyr		
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gaa	tcg	gat	gtg	ctg	tgg	aaa	cac	cgg	agc	aac	att	cac	gtg	gtg	aat	736	
Glu	Ser	Asp	Val	Leu	Trp	Lys	His	Arg	Ser	Asn	Ile	His	Val	Val	Asn		
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gaa	tgg	atc	gct	aat	gac	atc	tca	tcc	aca	aaa	atc	cgg	aga	gcc	ctc	784	
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	215				220					225					230		
aga	agg	ggc	cag	agc	att	cgc	tac	ttg	gta	cca	gat	ctt	gtc	caa	gaa	832	
Arg	Arg	Gly	Gln	Ser	Ile	Arg	Tyr	Leu	Val	Pro	Asp	Leu	Val	Gln	Glu		

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                235                240                245
tac att gaa aag cat aat ttg tac agc tct gag agt gaa gac agg aat      880
Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser Glu Ser Glu Asp Arg Asn
                250                255                260

gct ggg gtc atc ctg gcc cct ttg cag aga aac act gca gaa gct aag      928
Ala Gly Val Ile Leu Ala Pro Leu Gln Arg Asn Thr Ala Glu Ala Lys
                265                270                275

aca tag gaattctaca gcatgatatt tcagacttcc catttgggga tctgaaacaa      984
Thr *
                280

tctgggagtt aataactggg gaaagaagtt gtgatctgtt gcctaaacta aagcttaaaa    1044

gtt                                                                    1047

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<210> 125
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (28)..(399)

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Met Ala Lys Ile Lys Ala Arg Asp
                1                5

ctt cgc ggg aag aag aag gag gag ctg ctg aaa cag ctg gac gac ctg      99
Leu Arg Gly Lys Lys Lys Glu Leu Leu Lys Gln Leu Asp Asp Leu
                10                15                20

aag gtg gag ctg tcc cag ctg cgc gtc gcc aaa gtg aca ggc ggt gcg      147
Lys Val Glu Leu Ser Gln Leu Arg Val Ala Lys Val Thr Gly Gly Ala
                25                30                35                40

gcc tcc aag ctc tct aag atc cga gtc gtc cgg aaa tcc att gcc cgt      195
Ala Ser Lys Leu Ser Lys Ile Arg Val Val Arg Lys Ser Ile Ala Arg
                45                50                55

gtt ctc aca gtt att aac cag act cag aaa gaa aac ctc agg aaa ttc      243
Val Leu Thr Val Ile Asn Gln Thr Gln Lys Glu Asn Leu Arg Lys Phe
                60                65                70

tac aag ggc aag aag tac aag ccc ctg gac ctg cgg cct aag aag aca      291
Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp Leu Arg Pro Lys Lys Thr
                75                80                85

cgt gcc atg cgc cgc cgg ctc aac aag cac gag gag aac ctg aag acc      339
Arg Ala Met Arg Arg Arg Leu Asn Lys His Glu Glu Asn Leu Lys Thr

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90	95	100	
aag aag cag cag cgg aag gag cgg ctg tac ccg ctg cag aag tac aca			387
Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr Pro Leu Gln Lys Tyr Thr			
105	110	115	120
gtg aac gcc tga acg tcacatgggt tcataaaaga gagctggccg aagagaacaa			442
Val Asn Ala *			
aagaaaagtg tgtatttaaat atgcaattct gt			474

<210> 126
 <211> 2594
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (148)..(576)

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ccagaacaca ctgctacaag gtcccag	
atg gcc acg tct ctg gat ttt aaa	171
Met Ala Thr Ser Leu Asp Phe Lys	
1 5	
act tat gta gat cag gca tgt aga gct gct gag gag ttt gtc aat att	219
Thr Tyr Val Asp Gln Ala Cys Arg Ala Ala Glu Glu Phe Val Asn Ile	
10 15 20	
tac tat gag aca atg gat aaa aga aga cgg gca cta acc agg ctg tat	267
Tyr Tyr Glu Thr Met Asp Lys Arg Arg Arg Ala Leu Thr Arg Leu Tyr	
25 30 35 40	
ctg gac aag gcc acc tta ata tgg aat gga aat gct gtt tca ggg ctg	315
Leu Asp Lys Ala Thr Leu Ile Trp Asn Gly Asn Ala Val Ser Gly Leu	
45 50 55	
gat gcc cta aat aat ttt ttt gac aca ttg cct tct agt gag ttc cag	363
Asp Ala Leu Asn Asn Phe Phe Asp Thr Leu Pro Ser Ser Glu Phe Gln	
60 65 70	
gtc aat atg tta gat tgc caa cca gtt cat gag caa gca act cag tcc	411
Val Asn Met Leu Asp Cys Gln Pro Val His Glu Gln Ala Thr Gln Ser	
75 80 85	
caa act aca gtt ctt gtt gtg acc agt gga act gtg aag ttt gat gga	459
Gln Thr Thr Val Leu Val Val Thr Ser Gly Thr Val Lys Phe Asp Gly	
90 95 100	

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aac aaa caa cat ttc ttc aac cag aac ttc ctg ctg act gct cag tcc      507
Asn Lys Gln His Phe Phe Asn Gln Asn Phe Leu Leu Thr Ala Gln Ser
105                      110                      115                      120

act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt      555
Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe
                      125                      130                      135

caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt      608
Gln Asp Trp Ser Ser Ser  *
                      140

agttccagca attgaaatTT atgtgaatta ttttgattgt agaagcacta taatatgtgc      668

tgaaactaaa tttctttaat attttctatt cctgtcagca ccttttctag cagctgccag      728

tttggagcat tgccctctaa gagctttaaa actatTTTTT tacatgcctt atatacattc      788

cactaatgac attottataa taatattaaa cacatgatct tggTactaac atactcactg      848

tgaaccCagc ctattgcaaa aataaaatct ttttataata ttatctatgg gatgtcagca      908

caatataaca ctctgggaag aagtggagtt ttttggttat taggttaatt ttctagtaaa      968

acacattgcc tgTTTTcagt taacactggT aatgccattt taatatatgg cTTTTtcaaa    1028

tcagttcagt gaaaatagta cagattttagg ttacataac tactctgaca tactggaatt    1088

gcatatagag atgttcagtg gtcgtTTTTc attttaagta atttttgttt tggcattttt    1148

ttgtgtgaag taaattaatc aactagagag gtgcaaaacg ttctcagttg atatctgagt    1208

attgggtgca tttggTggct taaaagcaaa gcttcctaaa aagatttttc ttggcagctc    1268

caggtctata catttaggta atgaatggta gtagaactaa tagctttaac aggagaatag    1328

ggaatgagaa atagaaatcc aaggctgaag ccaaaagtaa ggaggggtggc caaatggtaa    1388

actattggta ctTgttttct acctcctaaa aatgtagctt attttttagga tttaaatacac    1448

taagtaaata agtatccttg ccaagtgatc atgagtgtca tttttgttct aagactaata    1508

tttttagatc tttttacttc acctcactat tatcaccaat gtatatctcc atttattcaa    1568

taacttactg gggtaaaata acagcaataa acctaacctt ttaacagggT ctaacatgag    1628

agttggagtc aaagccattg ttatcttttg gtgacaccct taaattttaa gtcttcCagt    1688

cttccatgtg aacttttaggc ccaaagtTtc ttatgtatca cacatcccc aaataagtga    1748

ttttttccca gtgctttgta ctgtcaactg cattatcttt aattatttaa aggtagaatt    1808

atttaatttt gtgatttgTt ctcccatatg acattgagca aatagatctg tttcaaaata    1868

tgttcccgct atgtggataa ctcttctttt taaaaagaaa atagagaata gcaaattctc    1928

atgataatcc tcaaaagaac aaaatgctta actttatctc ttaatttcta aaggtaaata    1988

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ggt ttt ttc cag act tat gat aca gaa tat tta aaa gtt ggt ttt att Gly Phe Phe Gln Thr Tyr Asp Thr Glu Tyr Leu Lys Val Gly Phe Ile 55 60 65	429
atc tgt cct gga tca aaa gaa agt tca cca agg cca cag tgt gtc att Ile Cys Pro Gly Ser Lys Glu Ser Ser Pro Arg Pro Gln Cys Val Ile 70 75 80	477
tgt gga gag atc tta tcc agt gaa aac atg aag cca gca aat ctt tct Cys Gly Glu Ile Leu Ser Ser Glu Asn Met Lys Pro Ala Asn Leu Ser 85 90 95	525
cat cat ttg aag aca aaa cat tca gaa tta gaa aac aaa cca gta gat His His Leu Lys Thr Lys His Ser Glu Leu Glu Asn Lys Pro Val Asp 100 105 110 115	573
ttt ttt gaa caa aaa tct tta gaa atg gaa tgt caa aat agt tct tta Phe Phe Glu Gln Lys Ser Leu Glu Met Glu Cys Gln Asn Ser Ser Leu 120 125 130	621
aaa aag tgt tta cta gtt gaa aag tca ctt gtg aaa gct tct tat tta Lys Lys Cys Leu Leu Val Glu Lys Ser Leu Val Lys Ala Ser Tyr Leu 135 140 145	669
att gct ttc caa act gct gca agc aag aag cca ttc tcc att gct gaa Ile Ala Phe Gln Thr Ala Ala Ser Lys Lys Pro Phe Ser Ile Ala Glu 150 155 160	717
gaa tta att aaa cca tat tta gta gaa atg tgt tca gaa gtt ttg ggt Glu Leu Ile Lys Pro Tyr Leu Val Glu Met Cys Ser Glu Val Leu Gly 165 170 175	765
tca agt gct gga gac aaa atg aaa act att cca ctt tct aat gtt aca Ser Ser Ala Gly Asp Lys Met Lys Thr Ile Pro Leu Ser Asn Val Thr 180 185 190 195	813
att caa cac agg att gat gaa cta tct gca gac att gaa gac cag ctg Ile Gln His Arg Ile Asp Glu Leu Ser Ala Asp Ile Glu Asp Gln Leu 200 205 210	861
att caa aag gtc aga gag tca aag tgg ttt gcc ctt cag ata gat gag Ile Gln Lys Val Arg Glu Ser Lys Trp Phe Ala Leu Gln Ile Asp Glu 215 220 225	909
tca tca gaa atc tca aat atc aca ctt ctt ttg tgc tat att cgt ttc Ser Ser Glu Ile Ser Asn Ile Thr Leu Leu Leu Cys Tyr Ile Arg Phe 230 235 240	957
att gat tat gat tgt cgt gat gta aaa gaa gaa tta tta ttt tgc att Ile Asp Tyr Asp Cys Arg Asp Val Lys Glu Glu Leu Leu Phe Cys Ile 245 250 255	1005
gaa atg cct act caa ata act ggc ttt gaa ata ttt gaa cta ata aat Glu Met Pro Thr Gln Ile Thr Gly Phe Glu Ile Phe Glu Leu Ile Asn 260 265 270 275	1053

aaa tat att gat agt aaa tct ctg aat tgg aaa cat tgt gtt ggt ctc	1101
Lys Tyr Ile Asp Ser Lys Ser Leu Asn Trp Lys His Cys Val Gly Leu	
280 285 290	
tgt acc gat ggg gct gca agc atg act ggc agg tat tct ggt tta aaa	1149
Cys Thr Asp Gly Ala Ala Ser Met Thr Gly Arg Tyr Ser Gly Leu Lys	
295 300 305	
gca aaa att caa gaa gtt gcc atg aat aca gcg gca ttt aca cat tgt	1197
Ala Lys Ile Gln Glu Val Ala Met Asn Thr Ala Ala Phe Thr His Cys	
310 315 320	
ttt att cac cgt gaa cgt tta gtg gca gaa aag ttg tct cca tgt tta	1245
Phe Ile His Arg Glu Arg Leu Val Ala Glu Lys Leu Ser Pro Cys Leu	
325 330 335	
cat aaa att ctt ttg cag tca gca caa att tta agt ttt ata aag agc	1293
His Lys Ile Leu Leu Gln Ser Ala Gln Ile Leu Ser Phe Ile Lys Ser	
340 345 350 355	
aat gca tta aat tca cgt atg tta aca att ttg tgt gaa gag atg gga	1341
Asn Ala Leu Asn Ser Arg Met Leu Thr Ile Leu Cys Glu Glu Met Gly	
360 365 370	
tct gag cat gtg agt tta ccg ctt cat gct gaa gta cgt tgg ata tca	1389
Ser Glu His Val Ser Leu Pro Leu His Ala Glu Val Arg Trp Ile Ser	
375 380 385	
aga ggg aga atg tta aaa aga tta ttt gaa tta cga cat gag att gaa	1437
Arg Gly Arg Met Leu Lys Arg Leu Phe Glu Leu Arg His Glu Ile Glu	
390 395 400	
ata ttt tta agt caa aag cat tca gat ttg gcc aag tat ttt cat gat	1485
Ile Phe Leu Ser Gln Lys His Ser Asp Leu Ala Lys Tyr Phe His Asp	
405 410 415	
gag gaa tgg gtt gga aag ctg gcc tac tta tca gat ata ttt tca ctt	1533
Glu Glu Trp Val Gly Lys Leu Ala Tyr Leu Ser Asp Ile Phe Ser Leu	
420 425 430 435	
ata aat gaa tta aat tta agt ctc caa gga act ttg act act ttc ttc	1581
Ile Asn Glu Leu Asn Leu Ser Leu Gln Gly Thr Leu Thr Thr Phe Phe	
440 445 450	
aat ttg tgt aat aaa att gat gta ttt aag aga aag tta aaa atg tgg	1629
Asn Leu Cys Asn Lys Ile Asp Val Phe Lys Arg Lys Leu Lys Met Trp	
455 460 465	
ttg aag cgc aca caa gag aat gat tat gac atg ttc cct tca ttt tct	1677
Leu Lys Arg Thr Gln Glu Asn Asp Tyr Asp Met Phe Pro Ser Phe Ser	
470 475 480	
gaa ttc tca aat tca tca ggc tta aat atg aca gac atc aca agg att	1725
Glu Phe Ser Asn Ser Ser Gly Leu Asn Met Thr Asp Ile Thr Arg Ile	
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<222> (97)..(798)

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Met Pro Cys Arg Arg Glu	
1 5	
gag gaa gag gaa gcc ggc gag gag gcg gag ggg gag gaa gag gag gac	162
Glu Glu Glu Glu Ala Gly Glu Glu Ala Glu Gly Glu Glu Glu Glu Asp	
10 15 20	
gac agc ttc ctc ctg ctg cag cag tcg gtg acg ctg ggc agc tcg ggc	210
Asp Ser Phe Leu Leu Leu Gln Gln Ser Val Thr Leu Gly Ser Ser Gly	
25 30 35	
gag gtg gac cgg ctg gtg gcc cag atc ggc gag acg ctg cag ctg gac	258
Glu Val Asp Arg Leu Val Ala Gln Ile Gly Glu Thr Leu Gln Leu Asp	
40 45 50	
gcg gcg cag gac agc ccg gcc tcg ccg tgc gcg ccc ccg ggg gtg ccg	306
Ala Ala Gln Asp Ser Pro Ala Ser Pro Cys Ala Pro Pro Gly Val Pro	
55 60 65 70	
ctg cgg gcc ccg ggg ccc ctg gct gcg gcg gtg ccg acg gac aag gcc	354
Leu Arg Ala Pro Gly Pro Leu Ala Ala Ala Val Pro Thr Asp Lys Ala	
75 80 85	
cgg ccc ccg gcg gtg ccg ctg ctg ctg ccg ccc gct tcg gct gag acg	402
Arg Pro Pro Ala Val Pro Leu Leu Leu Pro Pro Ala Ser Ala Glu Thr	
90 95 100	
gtg ggc ccg gcg ccc tct ggg gcc ctg cgc tgc gcc cta ggg gac cgc	450
Val Gly Pro Ala Pro Ser Gly Ala Leu Arg Cys Ala Leu Gly Asp Arg	
105 110 115	
ggc cgc gtg cgc gga cgc gct gcg ccc tac tgc gtg gcg gag gtc gcc	498
Gly Arg Val Arg Gly Arg Ala Ala Pro Tyr Cys Val Ala Glu Val Ala	
120 125 130	
gca ggc ccc agc gcg ctg ccg ggg ccg tgc cgg cga gga tgg ctc agg	546
Ala Gly Pro Ser Ala Leu Pro Gly Pro Cys Arg Arg Gly Trp Leu Arg	
135 140 145 150	
gac gcg gtc acc tcc cgc cgc ttg cag cag cgc cga tgg acc caa gcc	594
Asp Ala Val Thr Ser Arg Arg Leu Gln Gln Arg Arg Trp Thr Gln Ala	
155 160 165	
ggg gca cgc gcc ggc gac gac gac ccg cat cgg ctc ctc cag cag ctc	642
Gly Ala Arg Ala Gly Asp Asp Asp Pro His Arg Leu Leu Gln Gln Leu	
170 175 180	
gtg ctc tcg gga aac ctc atc aag gaa gcc gtg cgg aga ctc caa cga	690
Val Leu Ser Gly Asn Leu Ile Lys Glu Ala Val Arg Arg Leu Gln Arg	
185 190 195	

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gcc gtc gcc ggc gtt gca gcc acg ggc ccc gca agc gcc cct ggg ccc      738
Ala Val Ala Ala Val Ala Ala Thr Gly Pro Ala Ser Ala Pro Gly Pro
    200                      205                      210

ggg gga ggc cgc agc gga cct gac cgc att gcc ctg cag ccc tca ggc      786
Gly Gly Gly Arg Ser Gly Pro Asp Arg Ile Ala Leu Gln Pro Ser Gly
    215                      220                      225                      230

tcc ttg ctc tga cgc aggcctcctg gaggaggaag tggaggccgc tgcgtagacc      841
Ser Leu Leu  *

caacagcgtc cagttcctac taactctgag ctgaagccga cgtcgccagc ctgggagcga      901

ccactttggc tgcgggggagg cgcgtgggga gagatctcaa ccagagaagt taccagccgc      961

ggcgaggccg tcggagaaaa cttaagcgtg gagaaatgta tgcgccaggg tgcttccgtg     1021

gggcatgaga atttcccggg ccatccaagc ccaaggacct gggataaact gggagaacta     1081

tggcagctac ttgcatcgac ttgtacctca cttagccctt gggggcgctc tgagcttgga     1141

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ctcctcacc cacaatttta tttctctctc ccgtgccagc ccttcttttg tgtctgaaac     1921

cggttttaaa atgtgactct cccagagaag aagccgctgg ctgtatgaaa cttgacggcg     1981

cttttgtaag gtgccacccc caaactttaa ggtagctaaa ccaattttta aaagattcaa     2041

tggcttggtc atcctccaga tgtagctatt gatgtacact tcgcaacgga gtgtctgaaa     2101

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aaaaa                                              2166

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<210> 129
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      Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu
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ccg ccg cgt ttt ctg gag gcc ttc ggg cgg ctg tgg cag gta cag agc      159
Pro Pro Arg Phe Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser
                15                20                25

cgt ctg ggt agc ggc tcc tcc gcc tgc gtg tat cgg gtt cgc tgc tgc      207
Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys
                30                35                40

ggc aac cct ggc tgc ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca      255
Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro
                45                50                55

gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa      303
Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys
                60                65                70                75

gag agg gcg gcg ctg gaa cag ttg cag ggt cac aga aac atc gtg act      351
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr
                80                85                90

ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc      399
Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg
                95                100                105

tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tgc gaa ttg ctc tta      447
Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu
                110                115                120

tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc      495
Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala
                125                130                135

cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc      543
Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val
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cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa      591

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Cys	Phe	Lys	Leu	Ile	Asp	Phe	Gly	Leu	Ser	Phe	Lys	Glu	Gly	Asn	Gln	
			175					180					185			
gat	gta	aag	tat	att	cag	aca	gac	ggg	tat	cgg	gct	cca	gaa	gca	gaa	687
Asp	Val	Lys	Tyr	Ile	Gln	Thr	Asp	Gly	Tyr	Arg	Ala	Pro	Glu	Ala	Glu	
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ttg	caa	aat	tgc	ttg	gcc	cag	gct	ggc	ctg	cag	agt	gat	aca	gaa	tgt	735
Leu	Gln	Asn	Cys	Leu	Ala	Gln	Ala	Gly	Leu	Gln	Ser	Asp	Thr	Glu	Cys	
	205					210					215					
acc	tca	gct	gtt	gat	ctg	tgg	agc	cta	gga	atc	att	tta	ctg	gaa	atg	783
Thr	Ser	Ala	Val	Asp	Leu	Trp	Ser	Leu	Gly	Ile	Ile	Leu	Leu	Glu	Met	
220					225					230					235	
ttc	tca	gga	atg	aaa	ctg	aaa	cat	aca	gtc	aga	tct	cag	gaa	tgg	aag	831
Phe	Ser	Gly	Met	Lys	Leu	Lys	His	Thr	Val	Arg	Ser	Gln	Glu	Trp	Lys	
				240					245					250		
gca	aac	agt	tct	gct	att	att	gat	cac	ata	ttt	gcc	agt	aaa	gca	gtg	879
Ala	Asn	Ser	Ser	Ala	Ile	Ile	Asp	His	Ile	Phe	Ala	Ser	Lys	Ala	Val	
			255					260					265			
gtg	aat	gcc	gca	att	cca	gcc	tat	cac	cta	aga	gac	ctt	atc	aaa	agc	927
Val	Asn	Ala	Ala	Ile	Pro	Ala	Tyr	His	Leu	Arg	Asp	Leu	Ile	Lys	Ser	
		270					275					280				
atg	ctt	cat	gat	gat	cca	agc	aga	aga	att	cct	gct	gaa	atg	gca	ttg	975
Met	Leu	His	Asp	Asp	Pro	Ser	Arg	Arg	Ile	Pro	Ala	Glu	Met	Ala	Leu	
	285					290					295					
tgc	agc	cca	ttc	ttt	agc	att	cct	ttt	gcc	cct	cat	att	gaa	gat	ctg	1023
Cys	Ser	Pro	Phe	Phe	Ser	Ile	Pro	Phe	Ala	Pro	His	Ile	Glu	Asp	Leu	
300					305					310				315		
gtc	atg	ctt	ccc	act	cca	gtg	cta	aga	ctg	ctg	aat	gtg	ctg	gat	gat	1071
Val	Met	Leu	Pro	Thr	Pro	Val	Leu	Arg	Leu	Leu	Asn	Val	Leu	Asp	Asp	
				320					325					330		
gat	tat	ctt	gag	aat	gaa	gag	gaa	tat	gaa	gat	gtt	gta	gaa	gat	gta	1119
Asp	Tyr	Leu	Glu	Asn	Glu	Glu	Glu	Tyr	Glu	Asp	Val	Val	Glu	Asp	Val	
			335					340					345			
aaa	gag	gag	tgt	caa	aaa	tat	gga	cca	gtg	gta	tct	cta	ctt	gtt	cca	1167
Lys	Glu	Glu	Cys	Gln	Lys	Tyr	Gly	Pro	Val	Val	Ser	Leu	Leu	Val	Pro	
		350					355					360				
aag	gaa	aat	cct	ggc	aga	gga	caa	gtc	ttt	gtt	gag	tat	gca	aat	gct	1215
Lys	Glu	Asn	Pro	Gly	Arg	Gly	Gln	Val	Phe	Val	Glu	Tyr	Ala	Asn	Ala	
	365					370					375					
ggg	gat	tcc	aaa	gct	gcg	cag	aaa	tta	ctg	act	gga	agg	atg	ttt	gat	1263
Gly	Asp	Ser	Lys	Ala	Ala	Gln	Lys	Leu	Leu	Thr	Gly	Arg	Met	Phe	Asp	

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380          385          390          395
ggg aag ttt gtt gtg gct aca ttc tac ccg ctg agt gcc tac aag agg      1311
Gly Lys Phe Val Val Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg
          400          405          410

gga tat ctg tat caa acc ttg ctt taa tcagt aacctaagga ctgtttcctt      1363
Gly Tyr Leu Tyr Gln Thr Leu Leu *
          415          420

tttctcctct tccattttctt ggggttattcc acatatgaat gcaggactac ccccttacca      1423

ttttaagaag gtactttata cattttattta atcctactaa tgtgcagcca ttgcccaagc      1483

agtgactgcg ttgcatacat ttggcactga gtaggacaag acctctcagc tatacattga      1543

gggggttttag agcatccatg tgggcaaccc ttttttgtgc gggagagcag gtgttgctct      1603

tcagtatgta gcctaaaaaa atcttaatta tttcatggat catgaagcaa ggatgaataa      1663

tatcatgtct tggtaaatac taacaaattt gttaggtttg gtgacatcat ttacagatta      1723

tttctttatg ttgtccagtg gttcttcctt attgttgata tccataagct ggcactggat      1783

gctctcagta atgttaagta attgtcaagc agcagttacc tactgtgttc ttaacactga      1843

gttgtgaatt ttttcttaaa gcagtactgt agtactgaat attcctttac aggaactgca      1903

gtgagcctat ctaagtcttt gcctactaag gcttcctatg ggagaaaagt catgcttgac      1963

cttgacacct tttcatcact gctctctacg cccgagggaa ggccc                        2008

<210> 130
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<212> DNA
<213> Homo sapiens

<220>
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catgcctgta aacgtaacat ttggggaggc caaggctggg ggatcactta aggccaggat      120

ttcaagacca gcctgggcaa cacagcaaga ccccatatc tctacaaaaa aaacaaaaca      180

aaacaaaaca aacaaacaaa aaaaacagcc ggttgcggtg gcacatgctt gcagtcctcg      240

ttactcaaga agcagaagca agaggattgc ttgagcccaa cagtgccttg aaaagacaaa      300

gaacgcctgc aagcc atg atg acc cac ctg cat gtg aag tct aca gaa ccc      351
          Met Met Thr His Leu His Val Lys Ser Thr Glu Pro

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	1	5	10	
aaa gcc gcc cct cag ccc ttg aat ctg gta tca agt gtc act ctc tcc				399
Lys Ala Ala Pro Gln Pro Leu Asn Leu Val Ser Ser Val Thr Leu Ser	15	20	25	
aag tcc gca tcg gag gct tct cca cag agc tta cct cat act cca acg				447
Lys Ser Ala Ser Glu Ala Ser Pro Gln Ser Leu Pro His Thr Pro Thr	30	35	40	
acc cca acc gcc ccc ctg act ccc gtc acc caa ggc ccc tct gtc atc				495
Thr Pro Thr Ala Pro Leu Thr Pro Val Thr Gln Gly Pro Ser Val Ile	45	50	55	60
aca acc acc agc atg cac acg gtg gga ccc atc cgc agg cgg tac tca				543
Thr Thr Thr Ser Met His Thr Val Gly Pro Ile Arg Arg Arg Tyr Ser	65	70	75	
gac aaa tac aac gtg ccc att tcg tca gca gat att gcg cag aac caa				591
Asp Lys Tyr Asn Val Pro Ile Ser Ser Ala Asp Ile Ala Gln Asn Gln	80	85	90	
gaa ttt tat aag aac gca gaa gtt aga cca cca ttt aca tat gca tct				639
Glu Phe Tyr Lys Asn Ala Glu Val Arg Pro Pro Phe Thr Tyr Ala Ser	95	100	105	
tta att agg cag gcc att ctc gaa tct cca gaa aag cag cta aca cta				687
Leu Ile Arg Gln Ala Ile Leu Glu Ser Pro Glu Lys Gln Leu Thr Leu	110	115	120	
aat gag atc tat aac tgg ttc aca cga atg ttt gct tac ttc cga cgc				735
Asn Glu Ile Tyr Asn Trp Phe Thr Arg Met Phe Ala Tyr Phe Arg Arg	125	130	135	140
aac gcg gcc acg tgg aag aat gca gtg cgt cat aat ctt agt ctt cac				783
Asn Ala Ala Thr Trp Lys Asn Ala Val Arg His Asn Leu Ser Leu His	145	150	155	
aag tgt ttt gtg cga gta gaa aac gtt aaa ggg gca gta tgg aca gtg				831
Lys Cys Phe Val Arg Val Glu Asn Val Lys Gly Ala Val Trp Thr Val	160	165	170	
gat gaa gta gaa ttc caa aaa cga agg cca caa aag atc agt ggt aac				879
Asp Glu Val Glu Phe Gln Lys Arg Arg Pro Gln Lys Ile Ser Gly Asn	175	180	185	
cct tcc ctt att aaa aac atg cag agc agc cac gcc tac tgc aca cct				927
Pro Ser Leu Ile Lys Asn Met Gln Ser Ser His Ala Tyr Cys Thr Pro	190	195	200	
ctc aat gca gct tta cag gct tca atg gct gag aat agt ata cct cta				975
Leu Asn Ala Ala Leu Gln Ala Ser Met Ala Glu Asn Ser Ile Pro Leu	205	210	215	220
tac act acc gct tcc atg gga aat ccc act ctg ggc aac tta gcc agc				1023
Tyr Thr Thr Ala Ser Met Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser	225	230	235	

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gca ata cgg gaa gag ctg aac ggg gca atg gag cat acc aac agc aac      1071
Ala Ile Arg Glu Glu Leu Asn Gly Ala Met Glu His Thr Asn Ser Asn
                240                      245                      250

gag agt gac agc agt cca ggc aga tct cct atg caa gcc gtg cat cct      1119
Glu Ser Asp Ser Ser Pro Gly Arg Ser Pro Met Gln Ala Val His Pro
                255                      260                      265

gta cac gtc aaa gaa gag ccc ctc gat cca gag gaa gct gaa ggg ccc      1167
Val His Val Lys Glu Glu Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro
                270                      275                      280

ctg tcc tta gtg aca aca gcc aac cac agt cca gat ttt gac cat gac      1215
Leu Ser Leu Val Thr Thr Ala Asn His Ser Pro Asp Phe Asp His Asp
                285                      290                      295                      300

aga gat tac gaa gat gaa cca gta aac gag gac atg gag tga ctatcgg      1264
Arg Asp Tyr Glu Asp Glu Pro Val Asn Glu Asp Met Glu *
                305                      310

ggcggggccaa ccccgagaat gaagattgga aaaaggaaaa aaaaaaaaaa      1313

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<212> DNA
<213> Homo sapiens

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aggccttggc tccttgaact tttggccgcc          atg tgc ttc ccg aag gtc ctc      111
                Met Cys Phe Pro Lys Val Leu
                1                      5

tct gat gac atg aag aag ctg aag gcc cga atg cac cag gcc ata gaa      159
Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu
                10                      15                      20

aga ttt tat gat aaa atg caa aat gca gaa tca gga cgt gga cag gtg      207
Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val
                25                      30                      35

atg tcg agc ctg gca gag ctg gag gac gac ttc aaa gag ggc tac ctg      255
Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu
                40                      45                      50                      55

gag aca gtg gcg gct tat tat gag gag cag cac cca gag ctc act cct      303
Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro
                60                      65                      70

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cta ctt gaa aaa gaa aga gat gga tta cgg tgc cga ggc aac aga tcc 351
Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser
      75                      80                      85

cct gtc ccg gat gtt gag gat ccc gca acc gag gag cct ggg gag agc 399
Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser
      90                      95                      100

ttt tgt gac aag gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg 447
Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu
     105                      110                      115

cag acc tgg tgg cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg 495
Gln Thr Trp Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val
    120                      125                      130                      135

gcc ctg gtc cat gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc 543
Ala Leu Val His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe
      140                      145                      150

tgc tgc tct ctg tca gag ctc ttc atg tcc tct ttc cag tcc tac gga 591
Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly
     155                      160                      165

gcc cca cgg ggg gac aag gag gag ctg aca ccc cag aag tgc tct gaa 639
Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu
     170                      175                      180

ccc caa tcc tca aaa tga agatac tgacaccacc ttgcccctcc ccgtcaccgc 693
Pro Gln Ser Ser Lys *
    185

gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg ccctctccccg cacactcagt 753

ccccctgcct ggcgttctct cgcagctct gacctggtcg tgctgccctg gcatcttaat 813

aaaacctgct tataacttccc tgaaaaaaaa aaaa 847

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<210> 132
 <211> 526
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 <213> Homo sapiens

<220>
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 <222> (33)..(419)

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<400> 132
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Met Pro Lys Ser Lys Glu Leu
      1                      5

gtt tct tca agc tct tct ggc agt gat tct gac agt gag gtt gac aaa 101

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Val Ser Ser Ser Ser Ser Gly Ser Asp Ser Asp Ser Glu Val Asp Lys
      10              15              20

aag tta aag agg aaa aag caa gtt gct cca gaa aaa cct gta aag aaa    149
Lys Leu Lys Arg Lys Lys Gln Val Ala Pro Glu Lys Pro Val Lys Lys
      25              30              35

caa aag aca ggt gag act tcg aga gcc ctg tca tct tct aaa cag agc    197
Gln Lys Thr Gly Glu Thr Ser Arg Ala Leu Ser Ser Ser Lys Gln Ser
      40              45              50              55

agc agc agc aga gat gat aac atg ttt cag att ggg aaa atg agg tac    245
Ser Ser Ser Arg Asp Asp Asn Met Phe Gln Ile Gly Lys Met Arg Tyr
              60              65              70

gtt agt gtt cgc gat ttt aaa ggc aaa gtg cta att gat att aga gaa    293
Val Ser Val Arg Asp Phe Lys Gly Lys Val Leu Ile Asp Ile Arg Glu
              75              80              85

tat tgg atg gat cct gaa ggt gaa atg aaa cca gga aga aaa ggt att    341
Tyr Trp Met Asp Pro Glu Gly Glu Met Lys Pro Gly Arg Lys Gly Ile
              90              95              100

tct tta aat cca gaa caa tgg atc cag tcc agc aga aaa gat atg atg    389
Ser Leu Asn Pro Glu Gln Trp Ile Gln Ser Ser Arg Lys Asp Met Met
      105              110              115

aca ttg atg aag cac gtg agc ggt ctg taa t aatgcgagcc agattaattt    440
Thr Leu Met Lys His Val Ser Gly Leu *
      120              125

atcctgtact gttagatttg gggaatctg tcttatcaca aaggatgttg acttctagat    500

gttctccaga ttatgtatat tgtgat    526

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<210> 133
 <211> 1884
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (157)..(864)

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gtaataaatt agacatctct tcattttaga gagaag  atg gaa aca aca ttg ctt    174
              Met Glu Thr Thr Leu Leu
              1              5

ttc ttt tct caa ata aat atg tgt gaa tca aaa gaa aaa act ttt ttc    222

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Phe	Phe	Ser	Gln	Ile	Asn	Met	Cys	Glu	Ser	Lys	Glu	Lys	Thr	Phe	Phe		
			10					15					20				
aag	tta	ata	cat	ggt	tca	gga	aaa	gaa	gaa	aca	agc	aaa	gaa	gcc	aaa	270	
Lys	Leu	Ile	His	Gly	Ser	Gly	Lys	Glu	Glu	Thr	Ser	Lys	Glu	Ala	Lys		
		25					30					35					
atc	aga	gct	aag	gaa	aaa	aga	aat	aga	cta	agt	ctt	ctt	gtg	cag	aaa	318	
Ile	Arg	Ala	Lys	Glu	Lys	Arg	Asn	Arg	Leu	Ser	Leu	Leu	Val	Gln	Lys		
	40					45					50						
cct	gag	ttt	cat	gaa	gac	acc	cgc	tcc	agt	aga	tct	ggg	cac	ttg	gcc	366	
Pro	Glu	Phe	His	Glu	Asp	Thr	Arg	Ser	Ser	Arg	Ser	Gly	His	Leu	Ala		
	55				60					65					70		
aaa	gaa	aca	aga	gtc	tcc	cct	gaa	gag	gca	gtg	aaa	tgg	ggt	gaa	tca	414	
Lys	Glu	Thr	Arg	Val	Ser	Pro	Glu	Glu	Ala	Val	Lys	Trp	Gly	Glu	Ser		
			75						80					85			
ttt	gac	aaa	ctg	ctt	tcc	cat	aga	gat	gga	cta	gag	gct	ttt	acc	aga	462	
Phe	Asp	Lys	Leu	Leu	Ser	His	Arg	Asp	Gly	Leu	Glu	Ala	Phe	Thr	Arg		
			90					95					100				
ttt	ctt	aaa	act	gaa	ttc	agt	gaa	gaa	aat	att	gaa	ttt	tgg	ata	gcc	510	
Phe	Leu	Lys	Thr	Glu	Phe	Ser	Glu	Glu	Asn	Ile	Glu	Phe	Trp	Ile	Ala		
		105					110					115					
tgt	gaa	gat	ttc	aag	aaa	agc	aag	gga	cct	caa	caa	att	cac	ctt	aaa	558	
Cys	Glu	Asp	Phe	Lys	Lys	Ser	Lys	Gly	Pro	Gln	Gln	Ile	His	Leu	Lys		
	120					125					130						
gca	aaa	gca	ata	tat	gag	aaa	ttt	ata	cag	act	gat	gcc	cca	aaa	gag	606	
Ala	Lys	Ala	Ile	Tyr	Glu	Lys	Phe	Ile	Gln	Thr	Asp	Ala	Pro	Lys	Glu		
	135				140				145						150		
gtt	aac	ctt	gat	ttt	cac	aca	aaa	gaa	gtc	att	aca	aac	agc	atc	act	654	
Val	Asn	Leu	Asp	Phe	His	Thr	Lys	Glu	Val	Ile	Thr	Asn	Ser	Ile	Thr		
			155					160						165			
caa	cct	acc	ctc	cac	agt	ttt	gat	gct	gca	caa	agc	aga	gtg	tat	cag	702	
Gln	Pro	Thr	Leu	His	Ser	Phe	Asp	Ala	Ala	Gln	Ser	Arg	Val	Tyr	Gln		
			170					175					180				
ctc	atg	gaa	caa	gac	agt	tat	aca	cgt	ttt	ctg	aaa	tct	gac	atc	tat	750	
Leu	Met	Glu	Gln	Asp	Ser	Tyr	Thr	Arg	Phe	Leu	Lys	Ser	Asp	Ile	Tyr		
		185					190					195					
tta	gac	ttg	atg	gaa	gga	aga	cct	cag	aga	cca	aca	aat	ctt	agg	aga	798	
Leu	Asp	Leu	Met	Glu	Gly	Arg	Pro	Gln	Arg	Pro	Thr	Asn	Leu	Arg	Arg		
		200				205					210						
cga	tca	cgc	tca	ttt	acc	tgc	aat	gaa	ttc	caa	gat	gta	caa	tca	gat	846	
Arg	Ser	Arg	Ser	Phe	Thr	Cys	Asn	Glu	Phe	Gln	Asp	Val	Gln	Ser	Asp		
	215				220					225					230		
gtt	gcc	att	tgg	tta	taa	agaaaa	ttgattttgc	tcattttttat	gacaaactta							900	
Val	Ala	Ile	Trp	Leu	*												

tacatctgct tctaacatat cgcatgttta tgtaagatt tggccccatc ctttaaactg 960
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 catacagtat ctgccagtat attctgtaaa accttctatt tgatgtcatt ccattttataa 1080
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 gtctagttgg gattttttac caaagcagca taatatgtgt tatataaaca taataatact 1260
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 actaaccctg tccaagaat agtaatatca cctctagtta taagccagca acaggaactt 1440
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 gcttgaataa aaaccagaga aggtttttcc caggacgtct catgtttggc cctttagaat 1740
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<211> 1601

<212> DNA

<213> Homo sapiens

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<222> (868)..(1098)

<400> 134

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 agctatggaa acagatgata tggaagacat ccaacaagga ggaaaagcac acgcacgcct 180
 cacccttgcc tcattctctgc ccagggtgt cctgacagca cagacgcttc agggagacag 240

gcctggggac agtcatgtca tcacccttgc aacaaccacc caaaggaaaa gagagcgctg 300
aacagtttag gaaagggctc gcgctctaaga catcaagcga catacagaga tgtgcaaaac 360
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gacttgccga ggcagctgca actagacttg ggctaagccg tctgggtcta ctcaagaatt 780
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cgactgtccc cagggaaggg ctgtgag atg gat ggg cgt gag tca gct ttt 891
Met Asp Gly Arg Glu Ser Ala Phe
1 5
cca aaa ctc aag tac ctg gga cag gac aac tcg cta gca gct cag tca 939
Pro Lys Leu Lys Tyr Leu Gly Gln Asp Asn Ser Leu Ala Ala Gln Ser
10 15 20
cct ccg tgg cgg aca cag ata agg atg tta aga cca gaa aac cag aga 987
Pro Pro Trp Arg Thr Gln Ile Arg Met Leu Arg Pro Glu Asn Gln Arg
25 30 35 40
cta ggg ccc cgt cct cag ccc tca cag cat gac aca gat gcc tcc ctc 1035
Leu Gly Pro Arg Pro Gln Pro Ser Gln His Asp Thr Asp Ala Ser Leu
45 50 55
gga gag cag ggt ctc tcg gca tcc agc ggc gtg gtc tgc att ctg ctc 1083
Gly Glu Gln Gly Leu Ser Ala Ser Ser Gly Val Val Cys Ile Leu Leu
60 65 70
tac ctc atg ctc tag gccccatgcc atcgtctcgg ccctagaccg tgaaaactgc 1138
Tyr Leu Met Leu *
75
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gccccactg aggaccagcg ccaggcccta cctccccaa cctgtgcgca tctcaatcac 1558

tgc cac cgg ccc tcc tgc acc acc gag ggc acc acc agc ccc tgg aca	661
Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr Ser Pro Trp Thr	
145 150 155	
gcc atc gac ctc cag ggc tcc tgc tgt gag ggg tac ctc tgc aac agg	709
Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly Tyr Leu Cys Asn Arg	
160 165 170	
aaa tcc atg acc cag ccc ttc acc agt gct tca gcc acc acc cct ccc	757
Lys Ser Met Thr Gln Pro Phe Thr Ser Ala Ser Ala Thr Thr Pro Pro	
175 180 185	
cga gca cta cag gtc ctg gcc ctg ctc ctc cca gtc ctc ctg ctg gtg	805
Arg Ala Leu Gln Val Leu Ala Leu Leu Leu Pro Val Leu Leu Leu Val	
190 195 200	
ggg ctc tca gca tag accgccccctc caggatgctg gggacagggc tcacacacct	860
Gly Leu Ser Ala *	
205	
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 <213> Homo sapiens

 <220>
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atg gtc aac gtc ttg aaa gga gtg ctt ata gaa tgt gat cct gcc atg	167
Met Val Asn Val Leu Lys Gly Val Leu Ile Glu Cys Asp Pro Ala Met	
1 5 10 15	
aag cag ttt ctg ctg tac ttg gat gag tcc aat gcc ctg ggg aag aag	215
Lys Gln Phe Leu Leu Tyr Leu Asp Glu Ser Asn Ala Leu Gly Lys Lys	
20 25 30	
ttc atc att caa gac att gat gac act cac gtc ttt gta ata gca gaa	263
Phe Ile Ile Gln Asp Ile Asp Asp Thr His Val Phe Val Ile Ala Glu	
35 40 45	
ttg gtt aat gtc ctc cag gag cga gtg ggt gaa tta atg gac caa aat	311
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50 55 60	

<210> 138
 <211> 691
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (197)..(691)

<400> 138

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Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
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Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
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atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc      421
Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
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Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
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Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
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Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
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Gly	His	Val	Val	Asp	Ile	Val	Ala	Leu	Lys	Thr	Met	Lys	Met	Arg	Gly	
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Gln	Ala	Phe	Val	Ile	Phe	Lys	Glu	Leu	Gly	Ser	Ser	Thr	Asn	Ala	Leu	
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Arg	Gln	Leu	Gln	Gly	Phe	Pro	Phe	Tyr	Gly	Lys	Pro	Met	Arg	Ile	Gln	
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Tyr	Ala	Lys	Thr	Asp	Ser	Asp	Ile	Ile	Ser	Lys	Met	Arg	Gly	Thr	Phe	
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Ala	Asp	Lys	Glu	Lys	Lys	Lys	Glu	Lys	Lys	Lys	Ala	Lys	Thr	Val	Glu	
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 Met Glu Leu Asp Ser Ala Leu Glu Ala Pro
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Lys Tyr Ala Ala Pro Ser Lys Glu Glu Glu Gly Gly Gly Asp Gly His	
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Ser Glu Ala Ala Glu Lys Ala Ala Gln Val Gly Leu Leu Phe Leu Lys	
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Trp Gln Thr Gly Leu His His Leu Ala Gly Pro Val Tyr Ile Phe Ala	
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Val Ala Arg Glu Val Leu Thr Ser Leu Leu Gln Val Thr Glu Cys Gly	
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Ser Val Ala Gly Phe Leu His Gly Glu Asn Glu Asp Glu Lys Gly Arg	
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Trp Lys Asn Asn Pro Ala Ile Lys His Val Phe Ser Trp Thr Leu Gln	
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Lys Leu Leu Met Gln His Thr Trp Pro Arg Val Ser Cys Arg Leu Val	
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Thr Asp Cys Leu Ile Leu Leu Asp Arg Cys Ser Gln Gly Arg Val Lys	
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25 30 35

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Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr
40 45 50

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Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly
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90 95 100

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2323

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Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser	
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Ile Ala Ser Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser	
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Phe Cys Ser Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe	
65 70 75	
act gtc cac gtg tct gct gaa gaa cac ttt cat ttt gta agc cag tgc	350
Thr Val His Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys	
80 85 90	
tgc caa gga aag gaa tgc agc aac acc agc gat gcc ctg gac cct ccc	398
Cys Gln Gly Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro	
95 100 105	
ctg aag aac gtg tcc agc aac gca gag tgc cct gct tgt tat gaa tct	446
Leu Lys Asn Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser	
110 115 120 125	
aat gga act tcc tgt cgt ggg aag ccc tgg aaa tgc tat gaa gaa gaa	494
Asn Gly Thr Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu	
130 135 140	
cag tgt gtc ttt cta gtt gca gaa ctt aag aat gac att gag tct aag	542
Gln Cys Val Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys	
145 150 155	

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agt ctc gtg ctg aaa ggc tgt tcc aac gtc agt aac gcc acc tgt cag      590
Ser Leu Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln
      160                      165                      170

ttc ctg tct ggt gaa aac aag act ctt gga gga gtc atc ttt cga aag      638
Phe Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
      175                      180                      185

ttt gag tgt gca aat gta aac agc tta acc ccc acg tct gca cca acc      686
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr
      190                      195                      200                      205

act tcc cac aac gtg ggc tcc aaa gct tcc ctc tac ctc ttg gcc ctt      734
Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu
      210                      215                      220

gcc agc ctc ctt ctt cgg gga ctg ctg ccc tga ggtcctgg ggctgcactt      785
Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro *
      225                      230

tgcccagcac cccatttctg cttctctgag gtccagagca cccctgcgg tgctgacacc      845

ctctttccct gctctgcccc gtttaactgc ccagtaagtg ggagtcacag gtctccaggc      905

aatgcccaca gctgccttgt tcttcattat taaagcactg gttcattcac tgccccaaaa      965
aaaaaa                                                                971

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<210> 144
<211> 1689
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (354)..(1370)

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<220>
<221> misc_feature
<222> (1)...(1689)
<223> n = a,t,c or g

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<400> 144
cctgaatgct ttacgtaccg gcccggaatt cccgggtcga cccacgcgtc cgctcggcca      60

ccgaagccac cctgccctgg tgaaagggct cccgcaccgc ccggtgctcc ccatctgcct      120

ggcgtttgtgc gcagagctgg aaagcatggc tgttataaat gaattctgat tttggggagc      180

agatgccaac ttagagcctc gtaccaatct ctctgtcttt aaaagatgag gtgacttggt      240

gatttttctg gaaaattata ggtgcccagc taagacctga atgccatcac cctccccagg      300

gctctgcagt tttctcgtgg tgaacccttg atggatttgt tggttgcttga gaa atg      356

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[illegible][illegible]

210	215	220	225	
gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg				1076
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr	230	235	240	
tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat				1124
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp	245	250	255	
gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc				1172
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile	260	265	270	
cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag				1220
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys	275	280	285	
ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac				1268
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His	290	295	300	305
agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc				1316
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val	310	315	320	
cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg gta				1364
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Val	325	330	335	
ccg tga aagtttattt ttgtctgaaa gctttcataa gtatttaaata caacacagta				1420
Pro *				
atcaactatt taattgctgc aatcgggtcaa aatttataaaa agccacacac aaatttctct				1480
ccttctacac gtagctccat aactgcccc ttgccaaaca cccttcgggg aaccaatcag				1540
catgacattc ctgggcagtt aatgtgagaa gcgagggcag ggcaccgtcc nagtggactt				1600
tatccttcag ggaggggCGT atcctctctc ttacactctg tgtgtgggta aatttctaaa				1660
gaacaccatt taatccatag ctatatcag				1689

<210> 145
 <211> 480
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (104)..(298)

 <400> 145

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atttcactgt atgtaatgca tttttgttgt tgttgttgtt gtttttagaa acctagctac      60
ttaaagtttt ttttccttat tactgatctt atgcaatttg att  atg ttc ctt ggt      115
                                     Met Phe Leu Gly
                                     1

gta gct ttt cag tgt ttc ttc tgc ttt tgg ttt gtt gag ctt ttt gga      163
Val Ala Phe Gln Cys Phe Phe Cys Phe Trp Phe Val Glu Leu Phe Gly
   5              10              15              20

ttt gtg ggt tta cag tta tta tca aat ttg gaa aaa ttt cag ccc tta      211
Phe Val Gly Leu Gln Leu Leu Ser Asn Leu Glu Lys Phe Gln Pro Leu
          25              30              35

tgt ctt caa ata ttt ttt ctg tct ccc tgc ccc atc cgt agt ctt tat      259
Cys Leu Gln Ile Phe Phe Leu Ser Pro Cys Pro Ile Arg Ser Leu Tyr
          40              45              50

ata ttt gat cat cta aag ttg tct cac agc tca cag tga cactgcttgt      308
Ile Phe Asp His Leu Lys Leu Ser His Ser Ser Gln  *
          55              60              65

ttttccagtc tttttttccc tctaggtgtt tcattttgaa caattgctat tgctatgtct      368
tcaagatcct taatcttttc ttctgtagtg ccacatctta cccagtgaac ttttcacctc      428
agacatggta ttttttattt ctagaaatta ggactttttt tacatttccc ac      480

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<210> 146
 <211> 557
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (158)..(520)

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<400> 146
agagcagaag tgtgaagagt ggaggagcca gtatgaggct ctgaaggagg actggaggac      60
ccttgggacc cagcacaggg agctggagag ccaactccac gtgcttcagt ccaaactgca      120
ggtaccaggc actgggggtg gggaggggaag acagggt atg ggg agg agg gat ggt      175
                                     Met Gly Arg Arg Asp Gly
                                     1              5

gat gaa aga agc tgt tct gga tta ggg act cca aag gca gct gac agc      223
Asp Glu Arg Ser Cys Ser Gly Leu Gly Thr Pro Lys Ala Ala Asp Ser
          10              15              20

atc tgg ctt tca gtt cct cag tca cca cta ctt tgt acc aaa ttc act      271
Ile Trp Leu Ser Val Pro Gln Ser Pro Leu Leu Cys Thr Lys Phe Thr
          25              30              35

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gct gag cca ggc tct gtg atc agc cgg ggg aac tct gtg acc atc cgg Ala Glu Pro Gly Ser Val Ile Ser Arg Gly Asn Ser Val Thr Ile Arg 55 60 65	369
tgt cag ggg acc ctg gag gcc cag gaa tac cgt ctg gtt aaa gag gga Cys Gln Gly Thr Leu Glu Ala Gln Glu Tyr Arg Leu Val Lys Glu Gly 70 75 80	417
agc cca gaa ccc tgg gac aca cag aac cca ctg gag ccc aag aac aag Ser Pro Glu Pro Trp Asp Thr Gln Asn Pro Leu Glu Pro Lys Asn Lys 85 90 95	465
gcc aga ttc tcc atc cca tcc atg aca gag cac cat gca ggg aga tac Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr 100 105 110	513
cgc tgt tac tac tac agc cct gca ggc tgg tca gag ccc agc gac ccc Arg Cys Tyr Tyr Tyr Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro 115 120 125 130	561
ctg gag ctg gtg gtg aca gga ttc tac aac aaa ccc acc ctc tca gcc Leu Glu Leu Val Val Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala 135 140 145	609
ctg ccc agt cct gtg gtg acc tca gga gag aac gtg acc ctc cag tgt Leu Pro Ser Pro Val Val Thr Ser Gly Glu Asn Val Thr Leu Gln Cys 150 155 160	657
ggc tca cgg ctg aga ttc gac agg ttc att ctg act gag gaa gga gac Gly Ser Arg Leu Arg Phe Asp Arg Phe Ile Leu Thr Glu Glu Gly Asp 165 170 175	705
cac aag ctc tcc tgg acc ttg gac tca cag ctg acc ccc agt ggg cag His Lys Leu Ser Trp Thr Leu Asp Ser Gln Leu Thr Pro Ser Gly Gln 180 185 190	753
ttc cag gcc ctg ttc cct gtg ggc cct gtg acc ccc agc cac agg tgg Phe Gln Ala Leu Phe Pro Val Gly Pro Val Thr Pro Ser His Arg Trp 195 200 205 210	801
atg ctc aga tgc tat ggc tct cgc agg cat atc ctg cag gta tgg tca Met Leu Arg Cys Tyr Gly Ser Arg Arg His Ile Leu Gln Val Trp Ser 215 220 225	849
gaa ccc agt gac ctc ctg gag att ccg gtc tca gga gca gct gat aac Glu Pro Ser Asp Leu Leu Glu Ile Pro Val Ser Gly Ala Ala Asp Asn 230 235 240	897
ctc agt ccg tca caa aac aag tct gac tct ggg act gcc tca cac ctt Leu Ser Pro Ser Gln Asn Lys Ser Asp Ser Gly Thr Ala Ser His Leu 245 250 255	945
cag gat tac gca gta gag aat ctc atc cgc atg ggc atg gcc ggc ttg Gln Asp Tyr Ala Val Glu Asn Leu Ile Arg Met Gly Met Ala Gly Leu 260 265 270	993

atc ctg gtg gtc ctt ggg att ctg ata ttt cag gat tgg cac agc cag 1041
 Ile Leu Val Val Leu Gly Ile Leu Ile Phe Gln Asp Trp His Ser Gln
 275 280 285 290

aga agc ccc caa gct gca gct gga agg tga a cagaagagag aacaatgcac 1092
 Arg Ser Pro Gln Ala Ala Ala Gly Arg *
 295 300

cattgaatgc tggagccttg gaagcgaatc tgatggctct aggaggttcg ggaagaccat 1152

ctgaggccta tgccatctgg actgtctgct ggcaattt 1190

<210> 148
 <211> 1260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (156)..(626)

<400> 148
 ctggctagcg tttaaactta agcttgggtac cgagctcgga tccactagtc cagtgtggtg 60
 gaattccagc accccggagg tactccagca gcttgtctcc aatccaagct cccaatcacc 120
 caccgccgca gccccctacg caggccacgc cactg atg cac acc aaa ccc aat 173
 Met His Thr Lys Pro Asn
 1 5

agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga ctt 221
 Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu
 10 15 20

gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt act 269
 Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr
 25 30 35

ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc ctg 317
 Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu
 40 45 50

gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta ccg 365
 Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro
 55 60 65 70

aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc cca 413
 Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro
 75 80 85

ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc etc acc 461
 Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr
 90 95 100

gtggactatg aggagaaata cggccgc	atg ttt cca cgt gag tgg tgc atg	231
	Met Phe Pro Arg Glu Trp Cys Met	
	1 5	
gct gag agg att gcg gtg gaa ttt tgc cat gtg aca agg gca gaa ctt	279	
Ala Glu Arg Ile Ala Val Glu Phe Cys His Val Thr Arg Ala Glu Leu		
10 15 20		
gcc aag att atg cgt acc aga gcg aag gaa att gaa gtg aaa ttg ctt	327	
Ala Lys Ile Met Arg Thr Arg Ala Lys Glu Ile Glu Val Lys Leu Leu		
25 30 35 40		
ctt ttt gct att caa aga aca act aac ttt gag ggg ttt ctt gca aaa	375	
Leu Phe Ala Ile Gln Arg Thr Thr Asn Phe Glu Gly Phe Leu Ala Lys		
45 50 55		
cgc ttc tcc ggc tgc acc ctg acc gat ggg acc ctg aaa aag ctt gag	423	
Arg Phe Ser Gly Cys Thr Leu Thr Asp Gly Thr Leu Lys Lys Leu Glu		
60 65 70		
tct cca ccc cca tct acc aat ccc ttc ctg gaa gat gag cca aca cca	471	
Ser Pro Pro Pro Ser Thr Asn Pro Phe Leu Glu Asp Glu Pro Thr Pro		
75 80 85		
gag atg gag gaa ctg gca acg gag aaa gga gat tta gat caa cca aag	519	
Glu Met Glu Glu Leu Ala Thr Glu Lys Gly Asp Leu Asp Gln Pro Lys		
90 95 100		
aag cct aaa gcc cca gac aat cca ttt cat ggc att gtt tcc aag tgt	567	
Lys Pro Lys Ala Pro Asp Asn Pro Phe His Gly Ile Val Ser Lys Cys		
105 110 115 120		
ttt gag cct cat ctc tac gtg tat atc gaa tcc caa gac aag aac ctc	615	
Phe Glu Pro His Leu Tyr Val Tyr Ile Glu Ser Gln Asp Lys Asn Leu		
125 130 135		
gga gag ctg ata gat cgg ttt gtg gct gat ttc aaa gcc cag ggg cca	663	
Gly Glu Leu Ile Asp Arg Phe Val Ala Asp Phe Lys Ala Gln Gly Pro		
140 145 150		
cct aag ccc aac act gat gaa ggg ggt gcc gtg ctc ccc agc tgc gcc	711	
Pro Lys Pro Asn Thr Asp Glu Gly Gly Ala Val Leu Pro Ser Cys Ala		
155 160 165		
gac ctc ttt gtc tac tac aag aag tgc atg gtg caa tgc tct cag ctc	759	
Asp Leu Phe Val Tyr Tyr Lys Lys Cys Met Val Gln Cys Ser Gln Leu		
170 175 180		
agt act ggg gag ccc atg atc gcc ctg acc acc att ttc cag aag tac	807	
Ser Thr Gly Glu Pro Met Ile Ala Leu Thr Thr Ile Phe Gln Lys Tyr		
185 190 195 200		
ctc cga gaa tac gcc tgg aaa atc ctc tct ggc aac ctg ccc aaa acc	855	
Leu Arg Glu Tyr Ala Trp Lys Ile Leu Ser Gly Asn Leu Pro Lys Thr		
205 210 215		
aca acc agc agt gga gga ctg act atc agc agc ctc ctc aag gaa aag	903	

Thr Thr Ser Ser Gly Gly Leu Thr Ile Ser Ser Leu Leu Lys Glu Lys	
220 225 230	
gag ggc tca gaa gta gcc aag ttc act ctg gag gag ctc tgc ctc atc	951
Glu Gly Ser Glu Val Ala Lys Phe Thr Leu Glu Glu Leu Cys Leu Ile	
235 240 245	
tgt aac atc ctg agc acg gca gag tac tgt ctg gcc acc acc cag cag	999
Cys Asn Ile Leu Ser Thr Ala Glu Tyr Cys Leu Ala Thr Thr Gln Gln	
250 255 260	
cta gaa gaa aaa ctc aaa gaa aaa gtg gat gta agt ctg att gaa cga	1047
Leu Glu Glu Lys Leu Lys Glu Lys Val Asp Val Ser Leu Ile Glu Arg	
265 270 275 280	
atc aat ctg act gga gag atg gac acg ttc agc acc gtc atc tcc agc	1095
Ile Asn Leu Thr Gly Glu Met Asp Thr Phe Ser Thr Val Ile Ser Ser	
285 290 295	
agt att cag ctg ctg gtt cag gat ctg gat gct gcc tgt gat cct gcc	1143
Ser Ile Gln Leu Leu Val Gln Asp Leu Asp Ala Ala Cys Asp Pro Ala	
300 305 310	
ctg act gcc atg agc aag atg cag tgg cag aac gtg gag cac gtt ggt	1191
Leu Thr Ala Met Ser Lys Met Gln Trp Gln Asn Val Glu His Val Gly	
315 320 325	
gac cag agc ccc tac gtc acc tct gtc att ctg cac atc aag cag aac	1239
Asp Gln Ser Pro Tyr Val Thr Ser Val Ile Leu His Ile Lys Gln Asn	
330 335 340	
gtc ccc atc atc cgt gac aac ctg gct tcc aca cgc aag tac ttc act	1287
Val Pro Ile Ile Arg Asp Asn Leu Ala Ser Thr Arg Lys Tyr Phe Thr	
345 350 355 360	
cag ttc tgc gtt aaa ttt gca aac tcc ttc att ccc aaa ttc atc acc	1335
Gln Phe Cys Val Lys Phe Ala Asn Ser Phe Ile Pro Lys Phe Ile Thr	
365 370 375	
cac ctc ttc aag tgc aag cca att agc atg gtg gga gca gaa cag gtg	1383
His Leu Phe Lys Cys Lys Pro Ile Ser Met Val Gly Ala Glu Gln Val	
380 385 390	
aga tgg acg tag tat caggcatttg cctgggcagct tttgtttag atcaagcaca	1438
Arg Trp Thr *	
395	
tattcttcta gtccagatct acttggcagg aataaaattg atgatgtccc ctgtttgggg	1498
acagtataat gactcaccgc gaaggtttct taattcggtc ttccatttat ttttaaaaat	1558
tttgtttgaa cgcctactaa gttctgggtg caggggtataa cacagcaagc accatggaaa	1618
ggtccttgct cctagtgtc acactccaat aagaagaagt ggctgggccc ggcacagcgg	1678
ctcacgtgt aaccccagca tttcggggagg cctgggcagg cagatcacct ggggtaagga	1738

atttgagagc agcctggcca acatggtgaa atcccatctc tactaaaaat acaaaaatta 1798
gctgggcatg ggggcaggct accggggagg ctgaggcagg agaatcactt gaacccggga 1858
ggtggagggtt gcagtgagcc gatatcacac cactgcactc cagcctgggt gacaaagtga 1918
gactccatct c 1929

<210> 150
<211> 1230
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (70)..(555)

<400> 150
aaaaaagttg gtgtatcatc ctccatcctc caaggtctct ggatctctta tagcacagaa 60
ggtcttttcc atg gca ctg gcg tct tta cga aat ctc tac act cca aat 108
Met Ala Leu Ala Ser Leu Arg Asn Leu Tyr Thr Pro Asn
1 5 10
ata aag gtc agc cga ctg ctg att ttg gga ggt gcc aat att aat tac 156
Ile Lys Val Ser Arg Leu Leu Ile Leu Gly Gly Ala Asn Ile Asn Tyr
15 20 25
cgg aca gag gtt tta aat aat gct cca att cta tgt gtt cag tcc cat 204
Arg Thr Glu Val Leu Asn Asn Ala Pro Ile Leu Cys Val Gln Ser His
30 35 40 45
ctt ggt tac aca gaa atg gta gcc ctg ctg ctg gag ttc ggg gcc aac 252
Leu Gly Tyr Thr Glu Met Val Ala Leu Leu Leu Glu Phe Gly Ala Asn
50 55 60
gtg gat gcc tct tct gaa agt ggc ctg act ccc ctg gga tat gct gca 300
Val Asp Ala Ser Ser Glu Ser Gly Leu Thr Pro Leu Gly Tyr Ala Ala
65 70 75
gca gca ggg tac ctg agc att gtg gtg ctg ctg tgc aag aaa cgg gcc 348
Ala Ala Gly Tyr Leu Ser Ile Val Val Leu Leu Cys Lys Lys Arg Ala
80 85 90
aag gtg gat cat ttg gat aag aac ggg cag tgt gct ttg gtt cat gct 396
Lys Val Asp His Leu Asp Lys Asn Gly Gln Cys Ala Leu Val His Ala
95 100 105
gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac 444
Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp
110 115 120 125
tgg acg atg gcc ggc cag cag caa gga gta ttt aag aag agc cat gcc 492
Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala

130	135	140	
atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta			540
Ile Gln Gln Ala Leu Ile Ala Ala Ser Met Gly Tyr Thr Glu Val			
145	150	155	
aga agt agg caa tag gattgttttt tcaagctctg tattgaagga cccaggaaac			595
Arg Ser Arg Gln *			
160			
caggagaaaa gattgcacga agacaaaatt gccaaccaaa ttaatgtgaa ttcgtgatcg			655
ctgctctgaa taataaggag attaaactcc atgaagcact ttactcaaat gccaaagtcc			715
ctcaaattat aggtatagaa aggtgctgagt tggaaaggac cgtggaaatg atataattat			775
tctccatggt ttcctccctg tttaacagac agtggcacca aggctcaaag agatgaatta			835
ttgaggtgta gtcacatggt tagataatgt ggcacaggaa cagcataaca tttagaatct			895
cagaaggacc agatttgagt cccagcctcg ctattcatta actctagccc ttgaacaatt			955
tacctatctc ttagaagttt agtttcccat cagcaaagtg aagctaataa actcctttat			1015
acaaggctgt tgtaagggat gcttggtaaa ctgttaaaca ttatacagtt tatttattaa			1075
tgataataac aataatagtg gcaaagttag ggaattggta gtgtgctagg aaatgtttaa			1135
caaccaactg tgaagagggg tgtgggggtg aacaggggtg tgtgtttgtg tgtgcatacg			1195
tttattataa attttactga tagaatgtgt tgccg			1230

<210> 151
 <211> 1335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(1257)

<400> 151			
gcgactgcgg acaggttaga gttgtggttg gggcggacgc ggaagcagcc caagggcaga			60
gagggagccc gagccaggcc atctccaacc	atg ttc gac gag gcc tcg gcc		111
	Met Phe Asp Glu Ala Ser Ala		
	1 5		
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc			159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu			
10 15 20			
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc			207
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly			

25	30	35	
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc			255
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg			
40	45	50	55
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct			303
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser			
	60	65	70
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca			351
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser			
	75	80	85
tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta gat gat			399
Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu Asp Asp			
	90	95	100
cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc tgc agt			447
Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val Cys Ser			
	105	110	115
gat gtc tct tct tct att agc act tac tgg gat tgg tca gat agc gag			495
Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp Ser Glu			
	120	125	130
ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt gat gta			543
Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser Asp Val			
	140	145	150
ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg ctt cct			591
Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu Leu Pro			
	155	160	165
aaa aag aaa aac aag cac cgg aat tta gat gaa ctc cct tgg agt gca			639
Lys Lys Lys Asn Lys His Arg Asn Leu Asp Glu Leu Pro Trp Ser Ala			
	170	175	180
atg aca aat gat gag cag gtg gaa tat att gag tat ctg agt cgg aaa			687
Met Thr Asn Asp Glu Gln Val Glu Tyr Ile Glu Tyr Leu Ser Arg Lys			
	185	190	195
gtg agt act gag atg ggt ctt cgg gag caa ctt gat att att aag atc			735
Val Ser Thr Glu Met Gly Leu Arg Glu Gln Leu Asp Ile Ile Lys Ile			
	200	205	210
att gat cct tct gct cag atc tcc cct aca gac agg gag ttt att att			783
Ile Asp Pro Ser Ala Gln Ile Ser Pro Thr Asp Arg Glu Phe Ile Ile			
	220	225	230
gaa ctt aac tgt ctc aca gat gaa aaa ctg aag cag gtc aga aac tat			831
Glu Leu Asn Cys Leu Thr Asp Glu Lys Leu Lys Gln Val Arg Asn Tyr			
	235	240	245
atc aag gaa cat agc cct cgc caa cgg cct gca aga gag gcc tgg aag			879
Ile Lys Glu His Ser Pro Arg Gln Arg Pro Ala Arg Glu Ala Trp Lys			
	250	255	260

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aga agc aac ttt agt tgt gca agc acc agt gga gtg agc ggt gcc agt      927
Arg Ser Asn Phe Ser Cys Ala Ser Thr Ser Gly Val Ser Gly Ala Ser
    265                      270                      275

gcc agc gcc agc agc agc agt gcc agc atg gtc agt tct gca agc agc      975
Ala Ser Ala Ser Ser Ser Ser Ala Ser Met Val Ser Ser Ala Ser Ser
    280                      285                      290                      295

agt ggg tcc agt gtt gga aac tct gct tca aac tcc agt gcc aac atg      1023
Ser Gly Ser Ser Val Gly Asn Ser Ala Ser Asn Ser Ser Ala Asn Met
    300                      305                      310

agt cga gca cac agt gac agc aac ctg tct gca agt gca gca gag cgg      1071
Ser Arg Ala His Ser Asp Ser Asn Leu Ser Ala Ser Ala Ala Glu Arg
    315                      320                      325

att cgg gat tca aaa aag cga tcc aag cag cgg aag tta cag cag aag      1119
Ile Arg Asp Ser Lys Lys Arg Ser Lys Gln Arg Lys Leu Gln Gln Lys
    330                      335                      340

gcc ttc cgc aag agg cag ctg aag gag cag agg cag gcc cgg aag gag      1167
Ala Phe Arg Lys Arg Gln Leu Lys Glu Gln Arg Gln Ala Arg Lys Glu
    345                      350                      355

agg ctc agt ggg ctc ttc ctt aac gaa gag gtg ctg tcc ttg aaa gtg      1215
Arg Leu Ser Gly Leu Phe Leu Asn Glu Glu Val Leu Ser Leu Lys Val
    360                      365                      370                      375

act gag gaa gac cat gaa gca gat gtt gat gtt ttg atg taa taagggt      1264
Thr Glu Glu Asp His Glu Ala Asp Val Asp Val Leu Met *
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gatgcaggaa ttcatctaatt ttacttgcc gggcgaggtg tgagagccct agcatctgaa      180

agtggtagcag ttgcgagttg tt atg gag aaa act tgt ata gat gca ctt cct      232

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Met	Glu	Lys	Thr	Cys	Ile	Asp	Ala	Leu	Pro	
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Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe Gly										
15 20 25										
act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt ggt	328									
Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys Gly										
30 35 40										
tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta ctg	376									
Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu										
45 50 55										
ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag tct	424									
Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser										
60 65 70										
ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc aca	472									
Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu Thr										
75 80 85 90										
gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc aac	520									
Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser Asn										
95 100 105										
aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt gct	568									
Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala										
110 115 120										
cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc tca	616									
His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile Ser										
125 130 135										
gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg ttt	664									
Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val Phe										
140 145 150										
gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att gtt	712									
Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile Val										
155 160 165 170										
cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca gcc	760									
Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala Ala										
175 180 185										
aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg ttc	808									
Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg Phe										
190 195 200										
ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat tgt	856									
Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr Cys										
205 210 215										
gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat aat	904									
Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn										

220	225	230	
aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata aca			952
Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr			
235	240	245	250
gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct gcc			1000
Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala Ala			
	255	260	265
att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac tgg			1048
Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp			
	270	275	280
ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct ctg			1096
Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala Leu			
	285	290	295
gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att cga			1144
Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile Arg			
	300	305	310
tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca ata			1192
Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala Ile			
	315	320	325
ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt gat			1240
Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp			
	335	340	345
tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc ttg			1288
Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu Leu			
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gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga gag			1336
Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg Glu			
	365	370	375
ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg tgt			1384
Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys			
	380	385	390
aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct tca			1432
Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser			
	395	400	405
aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc att			1480
Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile			
	415	420	425
cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt gta			1528
Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys Val			
	430	435	440
gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca aaa			1576
Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys			
	445	450	455

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cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct      1632
His *
    460

ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag ttaggaaagt      1692
ttttttctta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt gactgacata      1752
ctggaagaga acaccatttt atctcagggt agtgaagaat cagtgcaggt ccctgactct      1812
tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc aactaaaga      1872
gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaatccaa tagaagtatt      1932
gcagcttcct tctctggctc aagggtgag ttaagtgaaa ggaaaaacag cacaatgggtg      1992
accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga aatgtaaaaa      2052
gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt accatgatga      2112
attctagtga aatgaccctt tgactttgct tttcttaata cagatattta ctgagaggaa      2172
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cttctcccca ggaccccagg gccaactccc cctgccggcc ctctgccatc aaattggcag      180
tggtccagg ggagtccctt ggggatgggg gaccactgtt ggggaccct ctgcgtgcac      240
ccctgtagtt ggggaagcag gacagggggc tggggagacg gaagggcgcc aggggttgag      300
agagg      atg gtg gac gtt gtt gga ctt gaa agg gaa aca ggc cct cgg      347
            Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg
            1             5             10

gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg      395
Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala
15             20             25             30
    
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ccc ctg ctc act tgt ctc tgc cca cag tgc ctg tct gtg gag gac gcc	443
Pro Leu Leu Thr Cys Leu Cys Pro Gln Cys Leu Ser Val Glu Asp Ala	
35 40 45	
ctg ggc ctg ggc gag cct gag ggg tca ggg ctg ccc ccg ggc ccg gtc	491
Leu Gly Leu Gly Glu Pro Glu Gly Ser Gly Leu Pro Pro Gly Pro Val	
50 55 60	
ctg gag gcc agg tac gtc gcc cgc ctc agt gcc gcc gcc gtc ctg tac	539
Leu Glu Ala Arg Tyr Val Ala Arg Leu Ser Ala Ala Ala Val Leu Tyr	
65 70 75	
ctc agc aac ccc gag ggc acc tgt gag gac gct cgg gct ggc ctc tgg	587
Leu Ser Asn Pro Glu Gly Thr Cys Glu Asp Ala Arg Ala Gly Leu Trp	
80 85 90	
gcc tct cat gca gac cac ctc ctg gcc ctg ctc gag agc ccc aag gcc	635
Ala Ser His Ala Asp His Leu Leu Ala Leu Leu Glu Ser Pro Lys Ala	
95 100 105 110	
ctg acc ccg ggc ctg agc tgg ctg ctg cag agg atg cag gcc ccg gct	683
Leu Thr Pro Gly Leu Ser Trp Leu Leu Gln Arg Met Gln Ala Arg Ala	
115 120 125	
gcc ggc cag acc ccc aag acg gcc tgc gta gat atc cct cag ctg ctg	731
Ala Gly Gln Thr Pro Lys Thr Ala Cys Val Asp Ile Pro Gln Leu Leu	
130 135 140	
gag gag gcg gtg ggg gcg ggg gct ccg ggc agt gct ggc ggc gtc ctg	779
Glu Glu Ala Val Gly Ala Gly Ala Pro Gly Ser Ala Gly Gly Val Leu	
145 150 155	
gct gcc ctg ctg gac cat gtc agg agc ggg tct tgc ttc cac gcc ttg	827
Ala Ala Leu Leu Asp His Val Arg Ser Gly Ser Cys Phe His Ala Leu	
160 165 170	
ccg agc cct cag tac ttc gtg gac ttt gtg ttc cag cag cac agc agc	875
Pro Ser Pro Gln Tyr Phe Val Asp Phe Val Phe Gln Gln His Ser Ser	
175 180 185 190	
gag gtc cct atg acg ctg gcc gag ctg tca gcc ttg atg cag cgc ctg	923
Glu Val Pro Met Thr Leu Ala Glu Leu Ser Ala Leu Met Gln Arg Leu	
195 200 205	
ggg gtg ggc agg gag gcc cac agt gac cac agt cat cgg cac agg gga	971
Gly Val Gly Arg Glu Ala His Ser Asp His Ser His Arg His Arg Gly	
210 215 220	
gcc agc agc ccg gac cct gtg ccc ctc atc agc tcc agc aac agc tcc	1019
Ala Ser Ser Arg Asp Pro Val Pro Leu Ile Ser Ser Ser Asn Ser Ser	
225 230 235	
agt gtg tgg gac acg gta tgc ctg agt gcc agg gac gtg atg gct gca	1067
Ser Val Trp Asp Thr Val Cys Leu Ser Ala Arg Asp Val Met Ala Ala	
240 245 250	

tat gga ctg tcg gaa cag gct ggg gtg acc ccg gag gcc tgg gcc caa	1115
Tyr Gly Leu Ser Glu Gln Ala Gly Val Thr Pro Glu Ala Trp Ala Gln	
255 260 265 270	
ctg agc cct gcc ctg ctc caa cag cag ctg agt gga gcc tgc acc tcc	1163
Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu Ser Gly Ala Cys Thr Ser	
275 280 285	
cag tcc agg ccc ccc gtc cag gac cag ctc agc cag tca gag agg tat	1211
Gln Ser Arg Pro Pro Val Gln Asp Gln Leu Ser Gln Ser Glu Arg Tyr	
290 295 300	
ctg tac ggc tcc ctg gcc acg ctg ctc atc tgc ctc tgc gcg gtc ttt	1259
Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile Cys Leu Cys Ala Val Phe	
305 310 315	
ggc ctc ctg ctg ctg acc tgc act ggc tgc agg ggg gtc gcc cac tac	1307
Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys Arg Gly Val Ala His Tyr	
320 325 330	
atc ctg cag acc ttc ctg agc ctg gca gtg ggt gca ctc act ggg gac	1355
Ile Leu Gln Thr Phe Leu Ser Leu Ala Val Gly Ala Leu Thr Gly Asp	
335 340 345 350	
gct gtc ctg cat ctg acg ccc aag gtg ctg ggg ctg cat aca cac agc	1403
Ala Val Leu His Leu Thr Pro Lys Val Leu Gly Leu His Thr His Ser	
355 360 365	
gaa gag ggc ctc agc cca cag ccc acc tgg cgc ctc ctg gct atg ctg	1451
Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp Arg Leu Leu Ala Met Leu	
370 375 380	
gcc ggg ctc tac gcc ttc ttc ctg ttt gag aac ctc ttc aat ctc ctg	1499
Ala Gly Leu Tyr Ala Phe Phe Leu Phe Glu Asn Leu Phe Asn Leu Leu	
385 390 395	
ctg ccc agg gac ccg gag gac ctg gag gac ggg ccc tgc ggc cac agc	1547
Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp Gly Pro Cys Gly His Ser	
400 405 410	
agc cat agc cac ggg ggc cac agc cac ggt gtg tcc ctg cag ctg gca	1595
Ser His Ser His Gly Gly His Ser His Gly Val Ser Leu Gln Leu Ala	
415 420 425 430	
ccc agc gag ctc cgg cag ccc aag ccc ccc cac gag ggc tcc cgc gca	1643
Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro His Glu Gly Ser Arg Ala	
435 440 445	
gac ctg gtg gcg gag gag agc ccg gag ctg ctg aac cct gag ccc agg	1691
Asp Leu Val Ala Glu Glu Ser Pro Glu Leu Leu Asn Pro Glu Pro Arg	
450 455 460	
aga ctg agc cca gag ttg agg cta ctg ccc tat atg atc act ctg ggc	1739
Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro Tyr Met Ile Thr Leu Gly	
465 470 475	
gac gcc gtg cac aac ttc gcc gac ggg ctg gcc gtg ggc gcc gcc ttc	1787

Asp	Ala	Val	His	Asn	Phe	Ala	Asp	Gly	Leu	Ala	Val	Gly	Ala	Ala	Phe		
480						485					490						
gcg	tcc	tcc	tgg	aag	acc	ggg	ctg	gcc	acc	tcg	ctg	gcc	gtg	ttc	tgc	1835	
Ala	Ser	Ser	Trp	Lys	Thr	Gly	Leu	Ala	Thr	Ser	Leu	Ala	Val	Phe	Cys		
495						500				505					510		
cac	gag	ttg	cca	cac	gag	ctg	ggg	gac	ttc	gcc	gcc	ttg	ctg	cac	gcg	1883	
His	Glu	Leu	Pro	His	Glu	Leu	Gly	Asp	Phe	Ala	Ala	Leu	Leu	His	Ala		
				515					520					525			
ggg	ctg	tcc	gtg	cgc	caa	gca	ctg	ctg	ctg	aac	ctg	gcc	tcc	gcg	ctc	1931	
Gly	Leu	Ser	Val	Arg	Gln	Ala	Leu	Leu	Leu	Asn	Leu	Ala	Ser	Ala	Leu		
			530						535					540			
acg	gcc	ttc	gct	ggg	ctc	tac	gtg	gca	ctc	gcg	gtt	gga	gtc	agc	gag	1979	
Thr	Ala	Phe	Ala	Gly	Leu	Tyr	Val	Ala	Leu	Ala	Val	Gly	Val	Ser	Glu		
			545				550					555					
gag	agc	gag	gcc	tgg	atc	ctg	gca	gtg	gcc	acc	ggc	ctg	ttc	ctc	tac	2027	
Glu	Ser	Glu	Ala	Trp	Ile	Leu	Ala	Val	Ala	Thr	Gly	Leu	Phe	Leu	Tyr		
			560			565					570						
gta	gca	ctc	tgc	gac	atg	ctc	ccg	gcg	atg	ttg	aaa	gta	cgg	gac	ccg	2075	
Val	Ala	Leu	Cys	Asp	Met	Leu	Pro	Ala	Met	Leu	Lys	Val	Arg	Asp	Pro		
575					580					585					590		
cgg	ccc	tgg	ctc	ctc	ttc	ctg	ctg	cac	aac	gtg	ggc	ctg	ctg	ggc	ggc	2123	
Arg	Pro	Trp	Leu	Leu	Phe	Leu	Leu	His	Asn	Val	Gly	Leu	Leu	Gly	Gly		
				595					600					605			
ttg	acc	gtc	ctg	ctg	ctg	ctg	tcc	ctg	tac	gag	gat	gac	atc	acc	ttc	2171	
Trp	Thr	Val	Leu	Leu	Leu	Leu	Ser	Leu	Tyr	Glu	Asp	Asp	Ile	Thr	Phe		
			610					615					620				
tga	tacc	ctgccctagt	ccccacctt	tgacttaaga	tcccacacct	cacaaaccta										2228	
*																	
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ccgcgggctg ggacc atg ggc tgc ttc ttc tcc aag aga cgg aag gct gac	171
Met Gly Cys Phe Phe Ser Lys Arg Arg Lys Ala Asp	
1 5 10	
aag gag tgc cgg ccc gag aac gag gag gag cgg cca aag cag tac agc	219
Lys Glu Ser Arg Pro Glu Asn Glu Glu Glu Arg Pro Lys Gln Tyr Ser	
15 20 25	
tgg gat cag cgc gag aag gtt gat cca aaa gac tac atg ttc agt gga	267
Trp Asp Gln Arg Glu Lys Val Asp Pro Lys Asp Tyr Met Phe Ser Gly	
30 35 40	
ctg aag gat gaa aca gta ggt cgc tta cct ggg acg gta gca gga caa	315
Leu Lys Asp Glu Thr Val Gly Arg Leu Pro Gly Thr Val Ala Gly Gln	
45 50 55 60	
cag ttt ctc att caa gac tgt gag aac tgt aac atc tat att ttt gat	363
Gln Phe Leu Ile Gln Asp Cys Glu Asn Cys Asn Ile Tyr Ile Phe Asp	
65 70 75	
cac tct gct aca gtt acc att gat gac tgt act aac tgc ata att ttt	411
His Ser Ala Thr Val Thr Ile Asp Asp Cys Thr Asn Cys Ile Ile Phe	
80 85 90	
ctg gga ccc gtg aaa ggc agc gtg ttt ttc cgg aat tgc aga gat tgc	459
Leu Gly Pro Val Lys Gly Ser Val Phe Phe Arg Asn Cys Arg Asp Cys	
95 100 105	
aag tgc aca tta gcc tgc caa caa ttt cgt gtg cga gat tgt aga aag	507
Lys Cys Thr Leu Ala Cys Gln Gln Phe Arg Val Arg Asp Cys Arg Lys	
110 115 120	
ctg gaa gtc ttt ttg tgt tgt gcc act caa ccc atc att gag tct tcc	555
Leu Glu Val Phe Leu Cys Cys Ala Thr Gln Pro Ile Ile Glu Ser Ser	
125 130 135 140	
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Ser Asn Ile Lys Phe Gly Cys Phe Gln Trp Tyr Tyr Pro Glu Leu Ala	
145 150 155	
ttc cag ttc aaa gat gca ggg cta agt atc ttc gac aat aca tgg agt	651
Phe Gln Phe Lys Asp Ala Gly Leu Ser Ile Phe Asp Asn Thr Trp Ser	
160 165 170	
aac att cat gac ttt aca cct gtg tca gga gaa ctc aac tgg agc ctt	699
Asn Ile His Asp Phe Thr Pro Val Ser Gly Glu Leu Asn Trp Ser Leu	
175 180 185	
ctt cca gaa gat gct gtg gtt cag gac tat gtt cct ata cct act acc	747
Leu Pro Glu Asp Ala Val Val Gln Asp Tyr Val Pro Ile Pro Thr Thr	
190 195 200	
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Glu Glu Leu Lys Ala Val Arg Val Ser Thr Glu Ala Asn Arg Ser Ile	

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Val Pro Ile Ser Arg Gly Gln Arg Gln Lys Ser Ser Asp Glu Ser Cys	225	230	235	
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Leu Val Val Leu Phe Ala Gly Asp Tyr Thr Ile Ala Asn Ala Arg Lys	240	245	250	
cta att gat gag atg gtt ggt aaa ggc ttt ttc cta gtt cag aca aag				939
Leu Ile Asp Glu Met Val Gly Lys Gly Phe Phe Leu Val Gln Thr Lys	255	260	265	
gaa gtg tcc atg aaa gct gag gat gct caa agg gtt ttt cgg gaa aaa				987
Glu Val Ser Met Lys Ala Glu Asp Ala Gln Arg Val Phe Arg Glu Lys	270	275	280	
gca cct gac ttc ctt cct ctt ctg aac aaa ggt cct gtt att gcc ttg				1035
Ala Pro Asp Phe Leu Pro Leu Leu Asn Lys Gly Pro Val Ile Ala Leu	285	290	295	300
gag ttt aat ggg gat ggt gct gta gaa gta tgt caa ctt att gta aac				1083
Glu Phe Asn Gly Asp Gly Ala Val Glu Val Cys Gln Leu Ile Val Asn	305	310	315	
gag ata ttc aat ggg acc aag atg ttt gta tct gaa agc aag gag aca				1131
Glu Ile Phe Asn Gly Thr Lys Met Phe Val Ser Glu Ser Lys Glu Thr	320	325	330	
ggt ttc tgg aga tgt aga cac gct cta aca ctt ggc tga tatacagatg				1180
Gly Phe Trp Arg Cys Arg His Ala Leu Thr Leu Gly *	335	340	345	
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 <221> CDS
 <222> (256)..(873)

gcacgagcta aactctggga ctggcgggcg gtcaggcggc acagggggaa tcccgggggc	60
ctaaggaggt tgtctcagtt tttgtcagca tctccacccc gaggtggttt gaactttgag	120
cctttttag tctgatgaa taatttcatt ttctcaagt ttatgacact cggaacgtca	180
agaactggag gtttgtgcaa tttgagaccg gtcggcactg tgcagagatc agagtactaa	240

aaataataaa ttacatctaa aaattaaaaa aaaaaaaa

1021

<210> 156
 <211> 1581
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(819)

<400> 156

atg gag gca gag gaa tcg gag aag gcc gca acg gag caa gag ccg ctg	48
Met Glu Ala Glu Glu Ser Glu Lys Ala Ala Thr Glu Gln Glu Pro Leu	
1 5 10 15	
 gaa ggg aca gaa cag aca cta gat gcg gag gag gag cag gag gaa tcc	96
Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser	
20 25 30	
 gaa gaa gcg gcc tgt ggc agc aag aag cgg gta gtg cca ggt att gtg	144
Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val	
35 40 45	
 tac ctg ggc cat atc ccg ccg cgc ttc cgg ccc ctg cac gtc cgc aac	192
Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn	
50 55 60	
 ctt ctc agc gcc tat ggc gag gtc gga cgc gtc ttc ttt cag gct gag	240
Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu	
65 70 75 80	
 gac cgg ttc gtg aga cgc aag aag aag gca gca gca gct gcc gga gga	288
Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly	
85 90 95	
 aaa aag cgg tcc tac acc aag gac tac acc gag gga tgg gtg gag ttc	336
Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe	
100 105 110	
 cgt gac aag cgc ata gcc aag cgc gtg gcg gcc agt cta cac aac acg	384
Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr	
115 120 125	
 cct atg ggt gcc cgc agg cgc agc ccc ttc cgt tat gat ctt tgg aac	432
Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn	
130 135 140	
 ctc aag tac ttg cac cgt ttc acc tgg tcc cac ctc agc gag cac ctc	480
Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu	
145 150 155 160	
 gcc ttt gag cgc cag gtg cgc agg cag cgc ttg aga gcg gag gtt gct	528

Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala	
165 170 175	
caa gcc aag cgt gag acc gac ttc tat ctt caa agt gtg gaa cgg gga	576
Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly	
180 185 190	
caa cgc ttt ctt gcg gcc gat ggg gac cct gct cgc cca gat ggc tcc	624
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser	
195 200 205	
tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa	672
Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys	
210 215 220	
gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag	720
Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln	
225 230 235 240	
gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc	768
Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala	
245 250 255	
ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc	816
Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser	
260 265 270	
tga gggc ctgggtggcc ccttccattt cctggccctg ctctgcttcc tgtctacctc	873
*	
atactagaat gatcgtgact acccgggcag acattttact gtgttttctca gaccaagtgt	933
ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg	993
tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc	1053
atatgcttgt tttgtttgac tcttggctgc ctacgtctgt aggggtcccct gaaaatccca	1113
cttctgccc ccagaaaggg cctttatttc caactaggag gataatgcct agtccaggca	1173
atctttctct gtttagcagt cacagggtgag ggtggtatta gcatcttttt tatgtagaaa	1233
aaattgagtt aatgggggtgg actggggttg gaagaaatac atttcctaata gtatttatag	1293
aaaataaaaa tatttttatg tgccttttta tttttgttgg tggggagggtc attggacaag	1353
ttccaacttt catcttgtgt tcccttcacc ttcataacct gatcttagag cccccctccc	1413
cctggcaccc accttactgt ttaacctgga tttttttttc tatttaattt ttgtctaata	1473
tattagccca gtttatcaat cagttatctt aagtcagcat tttctaagcc attgtttgag	1533
ggaacagtga caatagggaa taacaccact tagtattaag ggtttttc	1581

<210> 157
 <211> 1642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (228)..(911)

<400> 157

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aaggatcctt aattaaatta atcccccccc cccccccgag tagcggcagc ggcgacgacg      60
gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag      120
cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca      180
ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag  atg gga ggc      236
                                     Met Gly Gly
                                     1

aag ctc agc aag aag aag aag ggc tac aat gtg aac gac gag aaa gcc      284
Lys Leu Ser Lys Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala
      5                                10                                15

aag gag aaa gac aag aag gcc gag ggc gcg gcg acg gaa gag gag ggg      332
Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Glu Gly
      20                                25                                30                                35

acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc      380
Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Ala Glu Pro Ala Glu Ala
                                40                                45                                50

aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag      428
Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu
                                55                                60                                65

gag aag gag ggc gag aag gac gcg gcg gct gcc aag gag gag gcc ccg      476
Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Ala Lys Glu Glu Ala Pro
      70                                75                                80

aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag      524
Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu
      85                                90                                95

ccc ccg aag gcg ccc gag cag gag cag gcg gcc ccc ggc ccc gct gcg      572
Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala
      100                                105                                110                                115

ggc ggc gag gcc ccc aaa gct gct gag gcc gcc gcg gcc ccg gcc gag      620
Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu
                                120                                125                                130

agc gcg gcc cct gcc gcc ggg gag gag ccc agc aag gag gaa ggg gaa      668
Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu
      135                                140                                145

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ccc aaa aag act gag gcg ccc gca gct cct gcc gcc cag gag acc aaa      716
Pro Lys Lys Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Glu Thr Lys
      150                      155                      160

agt gac ggg gcc cca gct tca gac tca aaa ccc gcc agc tcg gag gct      764
Ser Asp Gly Ala Pro Ala Ser Asp Ser Lys Pro Gly Ser Ser Glu Ala
      165                      170                      175

gcc ccc tct tcc aag gag acc ccc gca gcc acg gaa gcg cct agt tcc      812
Ala Pro Ser Ser Lys Glu Thr Pro Ala Ala Thr Glu Ala Pro Ser Ser
      180                      185                      190                      195

aca ccc aag gcc cag gcc ccc gca gcc tct gca gaa gag ccc aag ccg      860
Thr Pro Lys Ala Gln Gly Pro Ala Ala Ser Ala Glu Glu Pro Lys Pro
      200                      205                      210

gtg gag gcc ccg gca gct aat tcc gac caa acc gta acc gtg aaa gag      908
Val Glu Ala Pro Ala Ala Asn Ser Asp Gln Thr Val Thr Val Lys Glu
      215                      220                      225

tga caag gacagcctat aggaaaaaca ataccactta aaacaatctc ctctctctct      965
*

ctctctctct ctctatctct ctctctatct cctctctctc tctcctctcc tatctctcct      1025

ctctctctct cctatactaa cttgtttcaa attggaagta atgatatgta ttgcccaagg      1085

aaaaatacag gatgttgtcc catcaaggga gggagggggt gggagaatcc aaatagtatt      1145

tttgtgggga aatatctaata ataccttcag tcaactttac caagaagtcc tggatttcca      1205

agatccgcgt ctgaaagtgc agtacatcgt ttgtacctga aactgccgcc acatgcactc      1265

ctccaccgct gagagttgaa tagcttttct tctgcaatgg gagttgggag tgatgcgttt      1325

gattctgccc acagggcctg tgccaaggca atcagatctt tatgagagca gtattttctg      1385

tgttttcttt ttaatttaca gcctttctta ttttgatatt tttttaatgt tgtggatgaa      1445

tgccagcttt cagacagagc ccacttagct tgtccacatg gatctcaatg ccaatcctcc      1505

attcttctct tccagatatt tttgggagtg acaaacattc tctcatccta cttagcctac      1565

ctagatttct catgacgagt taatgcatgt ccgtggttgg gtgcacctgt agttctgttt      1625

attggtcagt ggaaatg                                                    1642

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<210> 158
 <211> 1521
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
 <222> (417)..(1403)

<400> 158

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cgaggagtcg cgccgaggac ggaggccacg atacctgcgt ggctggggct gcgggctccg      120
gggtcaccac cctggggcgac cgggaggtgg cgctccgcc ggccgcagct ggagaggagc      180
gtgtcccca gccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctcccgag cctggcggtgg ggttcttctg cggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
          20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
          35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
          50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
          65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
          85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
          100            105            110

gaa agg tta ttt gtc aat gaa gaa aat gtt aat gag ttt ctt gaa gag      800
Glu Arg Leu Phe Val Asn Glu Glu Asn Val Asn Glu Phe Leu Glu Glu
          115            120            125

gtc ctg agc tct cca ttc aaa cag tct atg tcc ttg acc cca cca tta      848
Val Leu Ser Ser Pro Phe Lys Gln Ser Met Ser Leu Thr Pro Pro Leu
          130            135            140

att gaa gtt ctt caa gtt act gat aat aag att caa att aat gca aag      896
Ile Glu Val Leu Gln Val Thr Asp Asn Lys Ile Gln Ile Asn Ala Lys
          145            150            155            160

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ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga	944
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg	
165 170 175	
gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt	992
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys	
180 185 190	
aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta	1040
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu	
195 200 205	
caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt	1088
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu	
210 215 220	
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa	1136
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys	
225 230 235 240	
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag	1184
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu	
245 250 255	
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca	1232
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr	
260 265 270	
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat	1280
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn	
275 280 285	
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt	1328
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser	
290 295 300	
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag	1376
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln	
305 310 315 320	
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gactttttaa	1428
Asn Ser Leu Leu Tyr Asp Leu Asp *	
325	
tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact	1488
aaagggtatta aagtataaaa ttaaaatttg caa	1521

<210> 159
 <211> 1377
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (417)..(1259)

<400> 159

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gggtcaccac cctggggcgac ccggaggtgg cgctcccgcc ggccgcagct ggagaggagc      180
gtgtcccca gcccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cgagaggtcc ccttgtttgt      300
cctccccgag cctggcggtgg ggttcttctg cggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
             20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
             35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
             50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
             65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
             85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
             100             105             110

ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga      800
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg
             115             120             125

gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt      848
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys
             130             135             140

aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta      896
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu
             145             150             155             160

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caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt 944
 Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu
 165 170 175

gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa 992
 Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys
 180 185 190

atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag 1040
 Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu
 195 200 205

gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca 1088
 Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr
 210 215 220

gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat 1136
 Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn
 225 230 235 240

ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt 1184
 Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser
 245 250 255

gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag 1232
 Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln
 260 265 270

aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gacttttaaa 1284
 Asn Ser Leu Leu Tyr Asp Leu Asp *
 275 280

tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact 1344

aaagggtatta aagtataaaa ttaaaatttg caa 1377

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 ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg 180
 gctgctgcag caccgcgctg gacatgagcg ctccgccc aa cccgacggcg tcagctggcg 240

cgcgcgccccg cgaccgacgt ggcgaggcgc ccacggggccg cgcagccgcc attgctctcc	300
tgccacgggag gggagcgctt ggtggcagtc cgcggggcccg gacggaaggc tgaggcgacg	360
cctcgacgac agcggaccgg agctgcaggg gcaacacatt cagggcgggg tgccccattt	420
aggcctggct gaccggagta agaaactaca acccccgaag tgccttgcg ctaagggtta	480
cggaggcagt gaccacccac cctggagcc atg gtc cac gcc ttc ctc att cac	533
Met Val His Ala Phe Leu Ile His	
1 5	
acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg	581
Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu	
10 15 20	
tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg	629
Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro	
25 30 35 40	
cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct	677
His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala	
45 50 55	
gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct	725
Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser	
60 65 70	
ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg	773
Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val	
75 80 85	
ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac	821
Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn	
90 95 100	
cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta	869
Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu	
105 110 115 120	
ggc ttt gcc ctg gtg ctg gat gcc cat gag aac ctg cta ctg gct gag	917
Gly Phe Ala Leu Val Leu Asp Ala His Glu Asn Leu Leu Leu Ala Glu	
125 130 135	
ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg	965
Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu	
140 145 150	
ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc	1013
Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly	
155 160 165	
atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac	1061
Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Phe Leu Asn Asp	
170 175 180	
cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc	1109

Gln	Phe	Val	Gln	Gly	Leu	Glu	Lys	Glu	Phe	Ser	Ala	Ala	Trp	Pro	Arg
185					190					195					200

tga ttcc tcgttgggat ggtgcttctg agggcaggca gagggtagac acacagccag 1166
*

atgaagcttg gcatctccct cctaccacgc agctctgatg tgctgctata ccaggacaag 1226
tgggtgacac aagcctgcag aaagggggct gggcagaggg tggaggaggt cctgcctgtc 1286
ctcagggttag tggaaccaca gaacttctctg agcctagagc tgctgtgtta cttagaccgc 1346
tgccgtgcgg cagccacgct tgtccttgaa cccaccttcc tccatccctg ccagccgata 1406
gtgctagggt gaggagctgc ctggagctca ccccgctctt cttccaaacc cacagccacc 1466
atgcctggcc tcaatctttt cttttaaaca attattccta tattttattg taatgcagtt 1526
aaccgtgttt gtcagattca atactctgtg acccgtaac caagtctctg tatgtttatt 1586
actgcaattc aagtggccct gtatt 1611

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<213> Homo sapiens

<220>
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<222> (193)..(555)

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accgccgccg agtcgcgcgg aggcggaggc ttgggtgctg tcaagattca gcttcacccg 180
taaccacccg cc atg gcc gag gaa ggc att gct gct gga ggt gta atg 228
Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met
1 5 10
gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac 276
Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His
15 20 25
gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag 324
Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys
30 35 40
cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg 372
Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met
45 50 55 60

tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta	420
Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu	
65 70 75	
att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt	468
Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys	
80 85 90	
aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc	516
Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser	
95 100 105	
tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa	565
Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu *	
110 115 120	
att	568

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aggaaacttc tggttaccaa ttccatctgc ctctttctca gtgactcctg acgagctgct	180
catttacaca cacctgctcc cccccacc ccacagtctg gattgcgaaa cctaccgcac	240
cccccccca gtgcaggaag aaggtgacct tggctctgggg tggggacaga gagtctggga	300
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agaggtgtgg gtgagatccc aggtctgggc cgcaatttct agccacgctg cccaaccttc	480
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ggcgtcaggg cgatctctgg atgccagcc cataagcctg gcctgtctgt gaggaggctg	660
cgtctggctc ccgctctcac agccattgca gtacattgag ctccatagag acagcgccgg	720
ggcaagtgag agccggacgg gcactgggag actctgtgcc tcgctgagga aaaataacta	780

aac atg ggc aaa gga gat cct aag aag ccg aga ggc aaa atg tca tca	828
Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser	
1 5 10 15	
tat gca ttt ttt gtg caa act tgt cgg gag gag cat aag aag aag cac	876
Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His	
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cca gat gct tca gtc aac ttc tca gag ttt tct aag aag tgc tca gag	924
Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu	
35 40 45	
agg tgg aag acc atg tct gct aaa gag aaa gga aaa ttt gaa gat atg	972
Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met	
50 55 60	
gca aag gcg gac aag gcc cgt tat gaa aga gaa atg aaa acc tat atc	1020
Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile	
65 70 75	
cct ccc aaa ggg gag aca aaa aag aag ttc aag gat ccc aat gca ccc	1068
Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro	
80 85 90 95	
aag agg cct cct tgc gcc ttc ttc ctc ttc tgc tct gag tat cgc cca	1116
Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro	
100 105 110	
aaa atc aaa gga gaa cat cct ggc ctg tcc att ggt gat gtt gcg aag	1164
Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys	
115 120 125	
aaa ctg gga gag atg tgg aat aac act gct gca gat gac aag cag cct	1212
Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro	
130 135 140	
tat gaa aag aag gct gcg aag ctg aag gaa aaa tac gaa aag gat att	1260
Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile	
145 150 155	
gct gca tat cga gct aaa gga aag cct gat gca gca aaa aag gga gtt	1308
Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val	
160 165 170 175	
gtc aag gct gaa aaa agc aaa aaa aag aag gaa gag gag gaa gat gag	1356
Val Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu	
180 185 190	
gaa gat gaa gag gat gag gag gag gag gaa gat gaa gaa gat gaa gat	1404
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp	
195 200 205	
gaa gaa gaa gaa gat gat gat atg atg aat aag ttg gtt cta gcg cag	1452
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210 215 220	

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Cys Gly Cys Lys Gly Ile Arg Thr Cys Leu Ile Cys Glu Arg Gln Arg
15 20 25 30

ggc agt gac ccg ccc tgg gag ctg ccc cca gcg aaa aca tac cgt ttc 146
Gly Ser Asp Pro Pro Trp Glu Leu Pro Pro Ala Lys Thr Tyr Arg Phe
35 40 45

att tac tgc tcc gac acc ggc tgg gcc gtg ggc aca gag gag tct gac 194
Ile Tyr Cys Ser Asp Thr Gly Trp Ala Val Gly Thr Glu Glu Ser Asp
50 55 60

ttt gag ggc tgg gcc ttc ccc ttc cca gga gtg atg ctg atc gag gac 242
Phe Glu Gly Trp Ala Phe Pro Phe Pro Gly Val Met Leu Ile Glu Asp
65 70 75

ttt gtg acc cgg gag gaa gaa gcc gag ttg gtg cgg ctc atg gac cgt 290
Phe Val Thr Arg Glu Glu Glu Ala Glu Leu Val Arg Leu Met Asp Arg
80 85 90

gac ccc tgg aag ctc tcc cag tct gga cgg agg aag cag gac tat ggc 338
Asp Pro Trp Lys Leu Ser Gln Ser Gly Arg Arg Lys Gln Asp Tyr Gly
95 100 105 110

ccc aaa gtc aac ttt cgg aaa cag aag cta aag acc gag ggc ttc tgc 386
Pro Lys Val Asn Phe Arg Lys Gln Lys Leu Lys Thr Glu Gly Phe Cys
115 120 125

ggc ctc ccc agc ttc agc cgg gag gtg gtg cgg agg atg ggc ctc tac 434
Gly Leu Pro Ser Phe Ser Arg Glu Val Val Arg Arg Met Gly Leu Tyr
130 135 140

ccg ggg ctg gag ggc ttc cgg ccc gtc gag cag tgc aac ctg gac tac 482
Pro Gly Leu Glu Gly Phe Arg Pro Val Glu Gln Cys Asn Leu Asp Tyr
145 150 155

tgc ccc gag cgg ggc tct gcc att gac ccc cac ctg gac gac gcc tgg 530
Cys Pro Glu Arg Gly Ser Ala Ile Asp Pro His Leu Asp Asp Ala Trp
160 165 170

ctg tgg ggg gag cgg ctg gtc agc ctc aac ctc ctg tcc ccc acc gtg 578
Leu Trp Gly Glu Arg Leu Val Ser Leu Asn Leu Leu Ser Pro Thr Val
175 180 185 190

ctg tcc atg tgt cgg gag gcg ccc ggg agc ctg ctc ctc tgc tgc gcc 626
Leu Ser Met Cys Arg Glu Ala Pro Gly Ser Leu Leu Leu Cys Ser Ala
195 200 205

ccg tgc gct gcc ccg gag gcc ttg gtg gac agc gtg ata gca ccc agc 674
Pro Ser Ala Ala Pro Glu Ala Leu Val Asp Ser Val Ile Ala Pro Ser
210 215 220

cgg tcg gtg cta tgc cag gag gtg gag gtg gcc atc ccc tta ccc gcc Arg Ser Val Leu Cys Gln Glu Val Glu Val Ala Ile Pro Leu Pro Ala 225 230 235	722
cgc tcc ctg ctg gtc ctc acc ggg gcg gca cgg cac cag tgg aag cat Arg Ser Leu Leu Val Leu Thr Gly Ala Ala Arg His Gln Trp Lys His 240 245 250	770
gcc atc cac cgc aga cac atc gag gcc cgc cgc gtc tgc gtc act ttc Ala Ile His Arg Arg His Ile Glu Ala Arg Arg Val Cys Val Thr Phe 255 260 265 270	818
cgg gag ctg tcg gct gag ttt ggc cct gga ggg agg cag caa gag ctg Arg Glu Leu Ser Ala Glu Phe Gly Pro Gly Gly Arg Gln Gln Glu Leu 275 280 285	866
ggc cag gaa ctg ctg cgg atc gcc ctc tcc ttc cag gga aga ccc gtg Gly Gln Glu Leu Leu Arg Ile Ala Leu Ser Phe Gln Gly Arg Pro Val 290 295 300	914
tga accg cctccttggc tccagacttg actgatcccg ggattgaaat gaggagcaca *	971
gaacaggggcc tcctgcaact cacgggggttt caagagaaga tggctgaccc ctgatgctgt	1031
gagcagtgtg agccctgccc aggagcaggt tttgatggga acgtacctcc aggcagcccc	1091
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<222> (40)..(747)

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cac ttc ata gct tcg ggg atg gtc aat cag gag atg tta aac atg tct His Phe Ile Ala Ser Gly Met Val Asn Gln Glu Met Leu Asn Met Ser 25 30 35	150	

aag aaa aca gtt tct tgt ttt gtg aac ttc acc aga cta cag cag atc	198
Lys Lys Thr Val Ser Cys Phe Val Asn Phe Thr Arg Leu Gln Gln Ile	
40 45 50	
aca aat att caa gct gaa atc tac cag aaa aac ctg gaa att gaa ctc	246
Thr Asn Ile Gln Ala Glu Ile Tyr Gln Lys Asn Leu Glu Ile Glu Leu	
55 60 65	
ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt ttg	294
Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe Leu	
70 75 80 85	
gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa gca	342
Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu Ala	
90 95 100	
gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc atg	390
Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro Met	
105 110 115	
tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg gta	438
Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met Val	
120 125 130	
cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc cac	486
His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr His	
135 140 145	
ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag aaa	534
Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys Lys	
150 155 160 165	
atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca gaa	582
Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr Glu	
170 175 180	
gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa gtt	630
Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu Val	
185 190 195	
tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat aaa	678
Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr Lys	
200 205 210	
cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat gtc	726
His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His Val	
215 220 225	
caa act att aat gcc aag tag tc atcaacttta tttttgctta attatgtgta	779
Gln Thr Ile Asn Ala Lys *	
230 235	
gtcatatgaa gtctatttct agttgactgt aacatgggta ttaatagtct ttgctgctgg	839
taatactgaa agaacctgct ttatatggga gtatcaagat ctcagggttca ttaagaccaa	899

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 Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
 10 15 20

cac ttc ata gct tcg ggg atg gtc aat cag aaa aac ctg gaa att gaa 150
 His Phe Ile Ala Ser Gly Met Val Asn Gln Lys Asn Leu Glu Ile Glu
 25 30 35

ctc ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt 198
 Leu Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe
 40 45 50

ttg gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa 246
 Leu Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu
 55 60 65

gca gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc 294
 Ala Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro
 70 75 80 85

atg tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg 342
 Met Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met
 90 95 100

gta cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc 390
 Val His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr
 105 110 115

cac ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag 438
 His Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys
 120 125 130

aaa atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca 486
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 135 140 145

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<213> Homo sapiens

<220>
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<222> (99)..(5618)

<400> 168

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                                         Met Lys Pro Val Leu
                                         1      5

cag tcc ctc tac cac cga gtg ctg ctc tac ccc cca ccc cag cac cgg      161
Gln Ser Leu Tyr His Arg Val Leu Leu Tyr Pro Pro Pro Gln His Arg
                        10                        15                        20

gtg gaa gcc atc aaa ata atg aaa gag ata ctt ggg agc cca cag cgt      209
Val Glu Ala Ile Lys Ile Met Lys Glu Ile Leu Gly Ser Pro Gln Arg
                        25                        30                        35

ctc tgt gac ttg gca gga ccc agc tcc act gaa tca gag tcc aga aaa      257
Leu Cys Asp Leu Ala Gly Pro Ser Ser Thr Glu Ser Glu Ser Arg Lys
                        40                        45                        50

aga tca att tca aaa aga aag tct cat ctg gat ctc ctc aaa ctc atc      305
Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp Leu Leu Lys Leu Ile
                        55                        60                        65

atg gat ggc atg acc gaa gca tgc atc aag ggt ggc atc gaa gct tgc      353
Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly Gly Ile Glu Ala Cys
                        70                        75                        80                        85

tat gca gcc gtg tcc tgt gtc tgc acc ttg ctg ggt gcc ctg gat gag      401
Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu Gly Ala Leu Asp Glu
                        90                        95                        100

ctc agc cag ggg aag ggc ttg agc gaa ggt cag gtg caa ctg ctg ctt      449
Leu Ser Gln Gly Lys Gly Leu Ser Glu Gly Gln Val Gln Leu Leu Leu
                        105                        110                        115

ctg cgc ctt gag gag ctg aag gat ggg gct gag tgg agc cga gat tcc      497
Leu Arg Leu Glu Glu Leu Lys Asp Gly Ala Glu Trp Ser Arg Asp Ser
                        120                        125                        130

atg gag atc aat gag gct gac ttc cgc tgg cag cgg cga gtg ctg tcc      545
Met Glu Ile Asn Glu Ala Asp Phe Arg Trp Gln Arg Arg Val Leu Ser
                        135                        140                        145

tca gaa cac acg ccg tgg gag tca ggg aac gag agg agc ctt gac atc      593
Ser Glu His Thr Pro Trp Glu Ser Gly Asn Glu Arg Ser Leu Asp Ile
                        150                        155                        160                        165

agc atc agt gtc acc aca gac aca ggc cag acc act ctc gag gga gag      641
Ser Ile Ser Val Thr Thr Asp Thr Gly Gln Thr Thr Leu Glu Gly Glu
                        170                        175                        180

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Leu Gly Gln Thr Thr Pro Glu Asp His Ser Gly Asn His Lys Asn Ser	
185 190 195	
ctc aag tcg cca gcc atc cca gag ggt aag gag acg ctg agc aaa gta	737
Leu Lys Ser Pro Ala Ile Pro Glu Gly Lys Glu Thr Leu Ser Lys Val	
200 205 210	
ttg gaa aca gag gcg gta gac cag cca gat gtc gtg cag aga agc cac	785
Leu Glu Thr Glu Ala Val Asp Gln Pro Asp Val Val Gln Arg Ser His	
215 220 225	
acg gtc cct tac cct gac ata act aac ttc ctg tca gta gac tgc agg	833
Thr Val Pro Tyr Pro Asp Ile Thr Asn Phe Leu Ser Val Asp Cys Arg	
230 235 240 245	
aca agg tcc tat gga tct agg tat agt gag agc aat ttt agc gtt gat	881
Thr Arg Ser Tyr Gly Ser Arg Tyr Ser Glu Ser Asn Phe Ser Val Asp	
250 255 260	
gac caa gac ctt tct agg aca gag ttt gat tcc tgt gat cag tac tct	929
Asp Gln Asp Leu Ser Arg Thr Glu Phe Asp Ser Cys Asp Gln Tyr Ser	
265 270 275	
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Met Ala Ala Glu Lys Asp Ser Gly Arg Ser Asp Val Ser Asp Ile Gly	
280 285 290	
tcg gac aac tgt tca cta gcc gat gaa gag cag aca ccc cgg gac tgc	1025
Ser Asp Asn Cys Ser Leu Ala Asp Glu Glu Gln Thr Pro Arg Asp Cys	
295 300 305	
cta ggc cac cgg tcc ctg cga act gcc gcc ctg tct cta aaa ctg ctg	1073
Leu Gly His Arg Ser Leu Arg Thr Ala Ala Leu Ser Leu Lys Leu Leu	
310 315 320 325	
aag aac cag gag gcg gat cag cac agc gcc agg ctg ttc ata cag tcc	1121
Lys Asn Gln Glu Ala Asp Gln His Ser Ala Arg Leu Phe Ile Gln Ser	
330 335 340	
ctg gaa ggc ctc ctc cct cgg ctc ctg gct ctc tcc aat gta gag gag	1169
Leu Glu Gly Leu Leu Pro Arg Leu Leu Ala Leu Ser Asn Val Glu Glu	
345 350 355	
gtg gac acc gct ctg cag aac ttt gcc tct act ttc tgc tca ggc atg	1217
Val Asp Thr Ala Leu Gln Asn Phe Ala Ser Thr Phe Cys Ser Gly Met	
360 365 370	
atg cac tct cct ggc ttt gac ggg aat agc agc ctc agc ttc cag atg	1265
Met His Ser Pro Gly Phe Asp Gly Asn Ser Ser Leu Ser Phe Gln Met	
375 380 385	
ctg atg aac gca gac agc ctc tac aca gct gca cac tgc gcc ctg ctc	1313
Leu Met Asn Ala Asp Ser Leu Tyr Thr Ala Ala His Cys Ala Leu Leu	
390 395 400 405	

ctc aac ctg aag ctc tcc cac ggt gac tac tac agg aag cgg ccg acc	1361
Leu Asn Leu Lys Leu Ser His Gly Asp Tyr Tyr Arg Lys Arg Pro Thr	
410 415 420	
ctg gcg cca ggc gtg atg aag gac ttc atg aag cag gtg cag acc agc	1409
Leu Ala Pro Gly Val Met Lys Asp Phe Met Lys Gln Val Gln Thr Ser	
425 430 435	
ggc gtg ctg atg gtc ttc tct cag gcc tgg att gag gag ctc tac cat	1457
Gly Val Leu Met Val Phe Ser Gln Ala Trp Ile Glu Glu Leu Tyr His	
440 445 450	
cag gtg ctc gac agg aac atg ctt gga gag gct ggc tat tgg ggc agc	1505
Gln Val Leu Asp Arg Asn Met Leu Gly Glu Ala Gly Tyr Trp Gly Ser	
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Pro Glu Asp Asn Ser Leu Pro Leu Ile Thr Met Leu Thr Asp Ile Asp	
470 475 480 485	
ggc tta gag agc agt gcc att ggt ggc cag ctg atg gcc tcg gct gct	1601
Gly Leu Glu Ser Ser Ala Ile Gly Gly Gln Leu Met Ala Ser Ala Ala	
490 495 500	
aca gag tct cct ttc gcc cag agc agg aga att gat gac tcc aca gtg	1649
Thr Glu Ser Pro Phe Ala Gln Ser Arg Arg Ile Asp Asp Ser Thr Val	
505 510 515	
gca ggc gtg gca ttt gct cgc tat att ctg gtg ggc tgc tgg aag aac	1697
Ala Gly Val Ala Phe Ala Arg Tyr Ile Leu Val Gly Cys Trp Lys Asn	
520 525 530	
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Leu Ile Asp Thr Leu Ser Thr Pro Leu Thr Gly Arg Met Ala Gly Ser	
535 540 545	
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Ser Lys Gly Leu Ala Phe Ile Leu Gly Ala Glu Gly Ile Lys Glu Gln	
550 555 560 565	
aac cag aag gag cgg gac gcc atc tgc atg agc ctc gac ggg ctg cgg	1841
Asn Gln Lys Glu Arg Asp Ala Ile Cys Met Ser Leu Asp Gly Leu Arg	
570 575 580	
aaa gcc gca cgg ctg agc tgc gct cta ggc gtt gct gct aac tgc gcc	1889
Lys Ala Ala Arg Leu Ser Cys Ala Leu Gly Val Ala Ala Asn Cys Ala	
585 590 595	
tca gcc ctt gcc cag atg gca gct gcc tcc tgt gtc caa aaa aaa aaa	1937
Ser Ala Leu Ala Gln Met Ala Ala Ser Cys Val Gln Lys Lys Lys	
600 605 610	
gaa gag agg gag gcc caa gaa ccc agt gat gcc atc aca caa gtg aaa	1985
Glu Glu Arg Glu Ala Gln Glu Pro Ser Asp Ala Ile Thr Gln Val Lys	
615 620 625	
cta aaa gtg gag cag aaa ctg gag cag att ggg aag gtg cag ggg gtg	2033

agc agt gag gat gga att gaa tca gtc ctg tct gat ttt gat gat gac	3425
Ser Ser Glu Asp Gly Ile Glu Ser Val Leu Ser Asp Phe Asp Asp Asp	
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Thr Gly Leu Ile Glu Val Trp Ile Ile Leu Leu Glu Gln Leu Thr Ala	
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Ala Val Ser Asn Cys Pro Arg Gln His Gln Pro Pro Thr Leu Asp Leu	
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ctc ttt gag ctg ttg aga gat gtg acg aaa aca cca gga cca ggg ttt	3569
Leu Phe Glu Leu Leu Arg Asp Val Thr Lys Thr Pro Gly Pro Gly Phe	
1145 1150 1155	
ggt atc tat gca gtg gtt cac ctc ctc ctt cct gtg atg tcc gtt tgg	3617
Gly Ile Tyr Ala Val Val His Leu Leu Leu Pro Val Met Ser Val Trp	
1160 1165 1170	
ctc cgc cgg agc cat aaa gac cat tcc tac tgg gat atg gcc tct gcc	3665
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Ile Gln Ser Phe Leu His Ser Asp Ile Arg Tyr Glu Ser Met Ile Asn	
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Thr Met Leu Lys Asp Leu Phe Glu Leu Leu Val Ala Cys Val Ala Lys	
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Cys Cys Ala Leu Gln Asp Ala Phe Ser Ala Thr Leu Lys Pro Val Lys	
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Val Leu Thr Val Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe			
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Thr Ala Leu Gln Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys			
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Arg Val Gly Arg Val Tyr Asp Ile Ile Val *			
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Met Glu Ile Asp Gln Gly Glu
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Lys Asn Glu Asp Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu
10 15 20
aat gtt att gaa gat aac aaa agt gag aat atc tta gaa aat aca gac 567
Asn Val Ile Glu Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp
25 30 35
tct atg gag aca gat gaa atc att cct att ttg gaa aag ctt gca cct 615
Ser Met Glu Thr Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro
40 45 50 55
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Ser Glu Asp Glu Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile
60 65 70
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Asp Glu Thr Asn Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly
75 80 85
tca cca tct aaa caa gaa agt agt gag agt ttg cca aaa gaa gcc ttt 759
Ser Pro Ser Lys Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe
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Leu Val Leu Ser Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser
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Glu Val Ile Ser Gln Asn Glu Thr Cys Ser Pro Gly *
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ttgcacgtat tcgtcatagg atg ctg tgg ccc ggc gca gga ttg gag gga 170
Met Leu Trp Pro Gly Ala Gly Leu Glu Gly
1 5 10
cat aga cct ggt gga agg cgt ggg gct gcc ctg acc cag gga ttt ggc 218
His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly
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Ser Cys Ser Ala Ala Gly Gln Arg Ser Ala Gly Ala Ala Gly Thr Ser
30 35 40
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Trp Pro Thr Leu Ala Ala Ala Ser Cys Thr Ala Ser Gly Gly Val Arg	
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Thr His Ser Ser Asp Val Gly Ala Ser Gly His Gly Gly Ala Glu Ile	
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Gln Val Gly Phe Ser Pro Gln Leu Pro Ala Gly Trp *	
75 80 85	
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Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp	
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Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr	
30 35 40	
ctg aag ccc aag gaa cca cgg gcc ctg gca gag ccg agg gcg ggg gag	194
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu	
45 50 55 60	

gcc ccc agg aag gtc tca ggc agc ttt gct ggg agt gtc cac atc acc	242
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr	
65 70 75	
ctg acc ccc gtg agg cct gac agg acc cca cgc cca gcc agc cca gga	290
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly	
80 85 90	
ccc agc ctc cca gcc agg tcc ccc tcc cca ccc cgc cgc agg aga ctg	338
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Arg Leu	
95 100 105	
gcc gtc cct gcc agc ctc gac gtt tgt gac aac tgg ctt cgg ccg gag	386
Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu	
110 115 120	
ccc cct ggc cag gaa gcc cga gtg cag agc tgg aag gag gag gag aag	434
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys	
125 130 135 140	
aaa cct cac ctt cag ggc aaa cca ggg aga ccc ttg tcc ccg gcc aat	482
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn	
145 150 155	
gtc cct gct ctg cct ggc gag acg gtg acc tcc cca gtc agg ctg cac	530
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His	
160 165 170	
ccc gac tac ctc tcc ccg gag gag ata cag agg cag ctg cag gac atc	578
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile	
175 180 185	
gag agg cgg ctg gac gcc ctg gag ctc cgc ggc gtg gag ctg gag aag	626
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys	
190 195 200	
cga ctg cgg gcg gcc gag gga gat gac gct gag gat agc ctc atg gtg	674
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val	
205 210 215 220	
gac tgg ttc tgg ctc att cac gag aag cag ctt ctg ctg aga cag gag	722
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu	
225 230 235	
tca gag ctg atg tac aag tcc aag gcc cag cgt ctg gag gag cag cag	770
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln	
240 245 250	
ctg gac atc gag ggc gag ctg cgc cgg ctc atg gcc aag ccc gag gct	818
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala	
255 260 265	
ctg aag tca ctg cag gag cgg cgg cgg gag cag gag ctg ctg gag cag	866
Leu Lys Ser Leu Gln Glu Arg Arg Arg Glu Gln Glu Leu Leu Glu Gln	
270 275 280	

tac gtg agc acc gtg aac gac cgc agt gac atc gtg gac tcg ctg gac	914
Tyr Val Ser Thr Val Asn Asp Arg Ser Asp Ile Val Asp Ser Leu Asp	
285 290 295 300	
gag gac cgg ctc cgg gaa caa gag gag gat cag atg ctg cgg gac atg	962
Glu Asp Arg Leu Arg Glu Gln Glu Glu Asp Gln Met Leu Arg Asp Met	
305 310 315	
att gag aag ctg ggc ctc cag agg aag aag tcc aag ttc cgc ttg tcc	1010
Ile Glu Lys Leu Gly Leu Gln Arg Lys Lys Ser Lys Phe Arg Leu Ser	
320 325 330	
aag atc tgg tca cca aaa agc aaa agc agc ccc tcc cag tag tagccag	1059
Lys Ile Trp Ser Pro Lys Ser Lys Ser Ser Pro Ser Gln *	
335 340 345	
tagggccgtg ggctcggccc ggacctggca tccggacttg gactcggggc catgggcttg	1119
gccccggaccc ggaaccggga cttgtactcg gggccgtggg ctcggccccg acccggcatt	1179
cggacttgga ctcgggaagg gcctcctgtc cctacaaggg gcatgtggac agcagggacc	1239
tgcgctaccg tctgtgtgtct caataaagaa accgaccaca tggaaaaaaaa aaaaaaaaa	1297
<210> 173	
<211> 546	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (131)..(502)	
<400> 173	
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tcccagtcct cagggcctca agacagctct gcaatccgcc gcacagaatt caagttcgga	120
ttcggctttg atg acc tta atc cag gca aat cct aaa tcc tat cca gtc	169
Met Thr Leu Ile Gln Ala Asn Pro Lys Ser Tyr Pro Val	
1 5 10	
ggc agc atc cag atg aac cac aac tcc ttc ctc agc gca acc agg cca	217
Gly Ser Ile Gln Met Asn His Asn Ser Phe Leu Ser Ala Thr Arg Pro	
15 20 25	
agg gag tgc tcc atc ccc tgc ctc gca gtt act gat tct cca agc cgg	265
Arg Glu Cys Ser Ile Pro Cys Leu Ala Val Thr Asp Ser Pro Ser Arg	
30 35 40 45	
gcg ccg ccc agt cct ggc ggg gct tcc ccc acc cct ctc cgc gcc ggg	313
Ala Pro Pro Ser Pro Gly Gly Ala Ser Pro Thr Pro Leu Arg Ala Gly	
50 55 60	

caa tcg cgc gtt ctt tct tta ctt gtg ctc cac tgg tgg gca gca tgt	361
Gln Ser Arg Val Leu Ser Leu Leu Val Leu His Trp Trp Ala Ala Cys	
65 70 75	
gct ccc gcg tcc aca gct ctg ttt cgc ctt ccg gtc ccc gta gct ctg	409
Ala Pro Ala Ser Thr Ala Leu Phe Arg Leu Pro Val Pro Val Ala Leu	
80 85 90	
cag ggg aac ggg atc tct gcc gcc tcc tcg gcc gct aag cga ccc ggg	457
Gln Gly Asn Gly Ile Ser Ala Ala Ser Ser Ala Ala Lys Arg Pro Gly	
95 100 105	
gct gcc cga cct agc gag tgc gca cga ccg ccc agc gag ggg tag ccg	505
Ala Ala Arg Pro Ser Glu Cys Ala Arg Pro Pro Ser Glu Gly *	
110 115 120	
agtcgaggca gcacggttcc caaggcagcc aaggctgcgc c	546

<210> 174
 <211> 1009
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(793)

<400> 174

gcacgagggc acgagctgta tgagtggtag cttttccct caaccagca	atg gag	55
	Met Glu	
	1	
gag cag ccc cag atg caa gac gcc gac gag ccc gcg gac tcc gga ggg	103	
Glu Gln Pro Gln Met Gln Asp Ala Asp Glu Pro Ala Asp Ser Gly Gly		
5 10 15		
gaa ggc cgg gca ggc ggg cca ccg cag gtc gcc ggc gcc cag gcg gcg	151	
Glu Gly Arg Ala Gly Gly Pro Pro Gln Val Ala Gly Ala Gln Ala Ala		
20 25 30		
tgc agc gag gac cgc atg acc ctg ctc ctc agg ctg aga gca cag aca	199	
Cys Ser Glu Asp Arg Met Thr Leu Leu Leu Arg Leu Arg Ala Gln Thr		
35 40 45 50		
aaa caa caa ctc tta gaa tat aaa tca atg gtt gat gca agt gaa gaa	247	
Lys Gln Gln Leu Leu Glu Tyr Lys Ser Met Val Asp Ala Ser Glu Glu		
55 60 65		
aaa act cca gaa caa att atg caa gaa aag caa atc gaa gct aaa att	295	
Lys Thr Pro Glu Gln Ile Met Gln Glu Lys Gln Ile Glu Ala Lys Ile		
70 75 80		
gaa gac ctg gaa aat gaa att gaa gag gta aaa gtt gct ttt gag ata	343	
Glu Asp Leu Glu Asn Glu Ile Glu Glu Val Lys Val Ala Phe Glu Ile		

85	90	95	
aaa aag ctt gca tta gac agg atg aga ctt tca act gca ctt aaa aaa			391
Lys Lys Leu Ala Leu Asp Arg Met Arg Leu Ser Thr Ala Leu Lys Lys			
100	105	110	
aac ctg gag aaa att agc aga cag tct agt gtg ctc atg gat aac atg			439
Asn Leu Glu Lys Ile Ser Arg Gln Ser Ser Val Leu Met Asp Asn Met			
115	120	125	130
aaa cac cta tta gag cta aat aaa tta ata atg aaa tca cag cag gaa			487
Lys His Leu Leu Glu Leu Asn Lys Leu Ile Met Lys Ser Gln Gln Glu			
135	140	145	
tct tgg gat tta gag gaa aaa ctg ctt gat att aga aag aag aga ttg			535
Ser Trp Asp Leu Glu Glu Lys Leu Leu Asp Ile Arg Lys Lys Arg Leu			
150	155	160	
caa tta aaa caa gct tca gaa agt aag ctt tta gaa ata cag act gaa			583
Gln Leu Lys Gln Ala Ser Glu Ser Lys Leu Leu Glu Ile Gln Thr Glu			
165	170	175	
aag aac aaa cag aag att gat ttg gac agt atg gaa aac tca gag agg			631
Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg			
180	185	190	
ata aag atc ata cga caa aac cta cag atg gag ata aaa att act act			679
Ile Lys Ile Ile Arg Gln Asn Leu Gln Met Glu Ile Lys Ile Thr Thr			
195	200	205	210
gtt att caa cat gtg ttc cag aac ctt att ttg ggg agt aaa gtc aat			727
Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn			
215	220	225	
tgg gca gag gat cct gcc ctt aag gaa att gtt ctg cag ctt gag aag			775
Trp Ala Glu Asp Pro Ala Leu Lys Glu Ile Val Leu Gln Leu Glu Lys			
230	235	240	
aat gtt gac atg atg taa taagaa ttcatttctg acatatttta catttctggc			829
Asn Val Asp Met Met *			
245			
aatctcaact cttatttgga atacttctgt gcatttgtct gtccaccgta attttagaaa			889
agcatatcca taacgttttac agttgtagta cagttgtggt tagttatttg tagtgggatt			949
gaaagtaatt tttttctttt tatatttcta tattcagggtt gggttttttg tgccgttcgc			1009

<210> 175
 <211> 834
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
 <222> (12)..(833)

<400> 175

tttcgtcaag g atg aca tcc att cga gct gta ttt ata ttc ctg tgg ctg	50
Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu	
1 5 10	
cag ctg gac ttg gtg aat gga gag aat gtg gag cag cat cct tca acc	98
Gln Leu Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr	
15 20 25	
ctg agt gtc cag gag gga gac agc gct gtt atc aag tgt act tat tca	146
Leu Ser Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser	
30 35 40 45	
gac agt gcc tca aac tac ttc cct tgg tat aag caa gaa ctt gga aaa	194
Asp Ser Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys	
50 55 60	
aga cct cag ctt att ata gac att cgt tca aat gtg ggc gaa aag aaa	242
Arg Pro Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys	
65 70 75	
gac caa cga att gct gtt aca ttg aac aag aca gcc aaa cat ttc tcc	290
Asp Gln Arg Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser	
80 85 90	
ctg cac atc aca gag acc caa cct gaa gac tcg gct gtc tac ttc tgt	338
Leu His Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys	
95 100 105	
gca gca agt aac ggc cag gca gga act gct ctg atc ttt ggg aag gga	386
Ala Ala Ser Asn Gly Gln Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly	
110 115 120 125	
acc acc tta tca gtg agt tcc aat atc cag aac cct gac cct gcc gtg	434
Thr Thr Leu Ser Val Ser Ser Asn Ile Gln Asn Pro Asp Pro Ala Val	
130 135 140	
tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc cta ttc	482
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe	
145 150 155	
acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat tct gat	530
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp	
160 165 170	
gtg tat atc aca gac aaa act gtg cta gac atg agg tct atg gac ttc	578
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe	
175 180 185	
aag agc aac agt gct gtg gcc tgg agc aac aaa tct gac ttt gca tgt	626
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys	
190 195 200 205	
gca aac gcc ttc aac aac agc att att cca gaa gac acc ttc ttc ccc	674

Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro		
				210					215					220			
agc	cca	gaa	agt	tcc	tgt	gat	gtc	aag	ctg	gtc	gag	aaa	agc	ttt	gaa	722	
Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu		
			225					230					235				
aca	gat	acg	aac	cta	aac	ttt	caa	aac	ctg	tca	gtg	att	ggg	ttc	cga	770	
Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg		
			240				245					250					
atc	ctc	ctc	ctg	aaa	gtg	gcc	ggg	ttt	aat	ctg	ctc	atg	acg	ctg	cgg	818	
Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg		
	255					260					265						
ctg	tgg	tcc	agc	tga	g											834	
Leu	Trp	Ser	Ser	*													
270																	

<210> 176
 <211> 778
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (34)..(576)

 <220>
 <221> misc_feature
 <222> (1)...(778)
 <223> n = a,t,c or g

<400> 176																
tttcgtagac	ctctctgtct	tgtagcatct	gcc	atg	aga	atc	agg	ctc	ctg	tgc						54
				Met	Arg	Ile	Arg	Leu	Leu	Cys						
				1				5								
tgt	gtg	gcc	ttt	tct	ctc	ctg	tgg	gca	ggc	cca	gtg	att	gct	ggg	atc	102
Cys	Val	Ala	Phe	Ser	Leu	Leu	Trp	Ala	Gly	Pro	Val	Ile	Ala	Gly	Ile	
		10					15					20				
acc	cag	gca	cca	aca	tct	cag	atc	ctg	gca	gca	gga	cgg	cgc	atg	aca	150
Thr	Gln	Ala	Pro	Thr	Ser	Gln	Ile	Leu	Ala	Ala	Gly	Arg	Arg	Met	Thr	
		25				30					35					
ctg	aga	tgt	acc	cag	gat	atg	aga	cat	aat	gcc	atg	tac	tgg	tat	aga	198
Leu	Arg	Cys	Thr	Gln	Asp	Met	Arg	His	Asn	Ala	Met	Tyr	Trp	Tyr	Arg	
	40				45				50					55		
caa	gat	cta	gga	ctg	ggg	cta	agg	ctc	atc	cat	tat	tca	aat	act	gca	246
Gln	Asp	Leu	Gly	Leu	Gly	Leu	Arg	Leu	Ile	His	Tyr	Ser	Asn	Thr	Ala	
			60					65					70			

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ggt acc act ggc aaa gga gaa gtc cct gat ggt tat agt gtc tcc aga      294
Gly Thr Thr Gly Lys Gly Glu Val Pro Asp Gly Tyr Ser Val Ser Arg
      75                      80                      85

gca aac aca gat gat ttc ccc ctc acg ttg gcg tct gct gta ccc tct      342
Ala Asn Thr Asp Asp Phe Pro Leu Thr Leu Ala Ser Ala Val Pro Ser
      90                      95                      100

cag aca tct gtg tac ttc tgt gcc agc agt gac ggg gct agc ggg agt      390
Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly Ala Ser Gly Ser
      105                      110                      115

ccc cac acc ggg gag ctg ttt ttt gga gaa ggc tct agg ctg acc gta      438
Pro His Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val
      120                      125                      130                      135

ctg gag gac ctg aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag      486
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
      140                      145                      150

cca tca gaa gca gag atc tcc cac acc caa aag gcc aca ctg gtg tgc      534
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
      155                      160                      165

ctg gcc aca ggc ttc tac ccc gac cac gtg gag ctg agc tga ttttttc      583
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser *
      170                      175                      180

atagactatg agcttctaaa aaatcatccc catattcgtc attacattct tgggatcaaa      643

tatactgcat gaaaaaagat gctcagaaaa gtctatgtta agttaatgta gaatatatga      703

atgagtgaag gaaagtgttt tgaaaccatc ataggaata taataagata anattacact      763

agaataaaat gaaac                                                    778

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<210> 177
 <211> 708
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (176)..(493)

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<400> 177
gagggcgggga gaggcagatg agtaaattgga tccttacact aagtgtgatg agcagaaacc      60

caggcgctct ggggcatgag cagggaatac taaccagcc ctggggggctc aatctctccc      120

cacccttgca ggagaggctt ggggtgagtt ttgggaataa ggaccatcca gccac atg      178
Met
1

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acg aag ggg aag gaa aat ccc cat caa ggc aaa aac aca gtc caa ggc 226
Thr Lys Gly Lys Glu Asn Pro His Gln Gly Lys Asn Thr Val Gln Gly
      5              10              15

tct gag gcc caa att ccg ggg aga ggg gtg aag gtt gtt tgt cgc acc 274
Ser Glu Ala Gln Ile Pro Gly Arg Gly Val Lys Val Val Cys Arg Thr
      20              25              30

tgg gtt aaa ggg tgg ggg tgg aga gta gga gaa gag gct aca cag gtg 322
Trp Val Lys Gly Trp Gly Trp Arg Val Gly Glu Glu Ala Thr Gln Val
      35              40              45

aga agg tgt cag atc aca aag ggc ctt gta tgc caa act aag aag act 370
Arg Arg Cys Gln Ile Thr Lys Gly Leu Val Cys Gln Thr Lys Lys Thr
      50              55              60              65

gaa ctt gac cat gaa gtt agg cag acc ctc tgg aga gtt tta aag caa 418
Glu Leu Asp His Glu Val Arg Gln Thr Leu Trp Arg Val Leu Lys Gln
      70              75              80

gga gtc gtg tgg atg aac aaa cct gtg atg ggc tgg ggt tac caa gga 466
Gly Val Val Trp Met Asn Lys Pro Val Met Gly Trp Gly Tyr Gln Gly
      85              90              95

ggg ctt cct gga gga ggt cag act tga gctga gggaaggata ggatttggag 518
Gly Leu Pro Gly Gly Gly Gln Thr *
      100              105

agctgacatt ctgatgagcg gcttcggtta aagctcacia aaacccttcc ctcccccatg 578

ccctttgaaa tcatttgaat caaagattgc gtgtgttaaa gacatgtttg tctgttatct 638

gaaagctgtg gtttctcttt aacagattca gggcctcatc ctttgactcg gaccaagaag 698

gaattatgag 708

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<210> 178
 <211> 1463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(1175)

<220>
 <221> misc_feature
 <222> (1)...(1463)
 <223> n = a,t,c or g

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<400> 178
tttcgtgcaa agaaaactgt gagagagaga atttttaaaa agcagctggg gcctgaggtt 60

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ccg gcc atc aag gcc ctg atg cgg cca gac ccg cgc ctc aag tgg gcg Pro Ala Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala 35 40 45	205
gtg ctg gtg ctg gtg ctg gtg cag atg ctg gcc tgc tgg ctg gtg cgc Val Leu Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg 50 55 60	253
ggg ctg gcc tgg cgc tgg ctg ctg ttc tgg gcc tac gcc ttt ggt ggc Gly Leu Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly 65 70 75	301
tgc gtg aac cac tcg ctg acg ctg gcc atc cac gac atc tcg cac aac Cys Val Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn 80 85 90	349
gcg gcc ttc ggc acg ggc cgt gcg gca cgc aac cgc tgg ctg gcc gtg Ala Ala Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val 95 100 105 110	397
ttc gcc aac ctg ccc gtg ggt gtg ccc tac gcc gcc tcc ttc aag aag Phe Ala Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys 115 120 125	445
tac cac gtg gac cac cac cgc tac ctg ggc ggc gac ggg ctg gac gtg Tyr His Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val 130 135 140	493
gac gtg ccc acg cgt ctg gag ggc tgg ttc ttc tgc acg ccc gcc cgc Asp Val Pro Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg 145 150 155	541
aag ctg ctc tgg ctg gtg ctg cag ccc ttc ttc tac tca cta cgg ccg Lys Leu Leu Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro 160 165 170	589
ctc tgc gtc cac ccc aag gcc gtg acc cgc atg gag gtg ctc aac acg Leu Cys Val His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr 175 180 185 190	637
ctg gtg cag ctg gcg gcc gac ctg gcc atc ttt gcc ctt tgg ggg ctc Leu Val Gln Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu 195 200 205	685
aag ccc gtg gtc tac ctg ctg gcc agc tcc ttc ctg ggc ctg ggc ctg Lys Pro Val Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu 210 215 220	733
cac ccc atc tcg ggc cac ttc gtg gcc gag cac tac atg ttc ctc aag His Pro Ile Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys 225 230 235	781
ggc cac gag acc tac tcc tac tat ggg cct ctc aac tgg atc acc ttc Gly His Glu Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe 240 245 250	829
aat gtg ggc tac cac gtg gag cac cac gac ttc ccc agc atc ccg ggc	877

Asn Val Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly	
255 260 265 270	
tac aac ctg ccg ctg gtg cgg aag atc gcg ccc gag tac tac gac cac	925
Tyr Asn Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His	
275 280 285	
ctg ccg cag cac cac tcc tgg gtg aag gtg ctc tgg gat ttt gtg ttt	973
Leu Pro Gln His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe	
290 295 300	
gag gac tcc ctg ggg ccc tat gcc agg gtg aag cgg gtg tac agg ctg	1021
Glu Asp Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu	
305 310 315	
gca aaa gat ggt ctg tga gcccgg gctgcctcct ggtggtggcc attgtcccc	1075
Ala Lys Asp Gly Leu *	
320	
atcgccccct cagccttgca cccagcact gagaagctac atttccttcc tgtgctctgg	1135
actgctgccc ttgtccccga ggagtgtccc gcgcagccac acctggcaac agcagtgtgg	1195
gctgcagggc tccgtctgca cgtggacttg ccctggacct tgagtgtggc cctccctttc	1255
tgggcoctccc caggtgagggc ctggccctgc cccaccatga cctgggtgct ctgagcccac	1315
ggttcccaag gagctgactt ctccgggggtg cctgtgcctt acattaaacc cggcgtttgt	1375
ttcacagcca aaaaaaaaaa a	1396

<210> 182
 <211> 2728
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22)..(2688)

<400> 182	
ctggatggac tagccggggc c atg gcc ggc gcg gcg gcg gag tca ggg cgg	51
Met Ala Gly Ala Ala Ala Glu Ser Gly Arg	
1 5 10	
gag ctg tgg acc ttc gcg ggt tcc cgg gac ccg agc gca ccg cgg cta	99
Glu Leu Trp Thr Phe Ala Gly Ser Arg Asp Pro Ser Ala Pro Arg Leu	
15 20 25	
gcc tac ggc tac ggc ccg ggc agc ctg cgc gag ctg cgg gcg cgc gag	147
Ala Tyr Gly Tyr Gly Pro Gly Ser Leu Arg Glu Leu Arg Ala Arg Glu	
30 35 40	
ttc agc cgc ctg gca gga act gtc tat ctt gac cat gca ggt gcc acc	195

Phe	Ser	Arg	Leu	Ala	Gly	Thr	Val	Tyr	Leu	Asp	His	Ala	Gly	Ala	Thr	
		45					50					55				
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Leu	Phe	Ser	Gln	Ser	Gln	Leu	Glu	Ser	Phe	Thr	Ser	Asp	Leu	Met	Glu	
	60					65					70					
aac	act	tat	ggg	aat	cct	cac	agc	cag	aac	atc	agc	agc	aag	ctc	acc	291
Asn	Thr	Tyr	Gly	Asn	Pro	His	Ser	Gln	Asn	Ile	Ser	Ser	Lys	Leu	Thr	
	75				80					85					90	
cat	gac	act	gtg	gag	cag	gtg	cgc	tac	aga	atc	ctg	gcg	cac	ttc	cac	339
His	Asp	Thr	Val	Glu	Gln	Val	Arg	Tyr	Arg	Ile	Leu	Ala	His	Phe	His	
			95						100					105		
acc	acc	gca	gaa	gac	tac	act	gtg	atc	ttc	act	gcc	ggg	agc	acg	gct	387
Thr	Thr	Ala	Glu	Asp	Tyr	Thr	Val	Ile	Phe	Thr	Ala	Gly	Ser	Thr	Ala	
		110						115					120			
gct	ctc	aaa	ctg	gtg	gca	gag	gcc	ttt	cca	tgg	gtg	tcc	cag	ggc	cca	435
Ala	Leu	Lys	Leu	Val	Ala	Glu	Ala	Phe	Pro	Trp	Val	Ser	Gln	Gly	Pro	
	125						130					135				
gag	agc	agt	ggg	agt	cgc	ttc	tgt	tac	ctc	acc	gac	agc	cac	acc	tcc	483
Glu	Ser	Ser	Gly	Ser	Arg	Phe	Cys	Tyr	Leu	Thr	Asp	Ser	His	Thr	Ser	
	140					145					150					
gta	gtg	ggg	atg	agg	aac	gtg	acc	atg	gct	ata	aat	gtc	ata	tcc	atc	531
Val	Val	Gly	Met	Arg	Asn	Val	Thr	Met	Ala	Ile	Asn	Val	Ile	Ser	Ile	
	155				160					165					170	
ccg	gtc	agg	cca	gag	gac	ctg	tgg	tct	gca	gag	gaa	cgt	ggg	gct	tca	579
Pro	Val	Arg	Pro	Glu	Asp	Leu	Trp	Ser	Ala	Glu	Glu	Arg	Gly	Ala	Ser	
			175						180					185		
gcc	agc	aac	cca	gac	tgc	cag	ctg	ccg	cat	ctc	ttc	tgc	tac	cca	gct	627
Ala	Ser	Asn	Pro	Asp	Cys	Gln	Leu	Pro	His	Leu	Phe	Cys	Tyr	Pro	Ala	
		190						195					200			
cag	agt	aac	ttt	tct	gga	gtc	aga	tac	ccc	ctg	tcc	tgg	ata	gaa	gag	675
Gln	Ser	Asn	Phe	Ser	Gly	Val	Arg	Tyr	Pro	Leu	Ser	Trp	Ile	Glu	Glu	
	205					210						215				
gtc	aag	tct	ggg	cgg	ttg	cgc	cct	gtg	agc	acg	cct	ggg	aag	tgg	ttt	723
Val	Lys	Ser	Gly	Arg	Leu	Arg	Pro	Val	Ser	Thr	Pro	Gly	Lys	Trp	Phe	
	220					225					230					
gtg	ctg	ctg	gat	gca	gcc	tcc	tac	gtg	agc	acc	tgc	cct	ttg	gac	ctg	771
Val	Leu	Leu	Asp	Ala	Ala	Ser	Tyr	Val	Ser	Thr	Ser	Pro	Leu	Asp	Leu	
	235				240					245					250	
tca	gct	cac	cag	gcc	gac	ttt	gtc	ccc	atc	tcc	ttc	tat	aag	atc	ttc	819
Ser	Ala	His	Gln	Ala	Asp	Phe	Val	Pro	Ile	Ser	Phe	Tyr	Lys	Ile	Phe	
			255					260					265			
ggg	ttt	cct	aca	ggc	ctg	ggc	gct	ctg	ctg	gtc	cat	aat	cgt	gcg	gct	867
Gly	Phe	Pro	Thr	Gly	Leu	Gly	Ala	Leu	Leu	Val	His	Asn	Arg	Ala	Ala	

270	275	280	
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Pro Leu Leu Arg Lys Thr Tyr Phe Gly Gly Gly Thr Ala Ser Ala Tyr			
285	290	295	
cta gca gga gaa gac ttc tac atc ccg agg cag tcg gta gct cag agg			963
Leu Ala Gly Glu Asp Phe Tyr Ile Pro Arg Gln Ser Val Ala Gln Arg			
300	305	310	
ttt gaa gat ggc acc atc tca ttc ctt gat gtt atc gcg cta aaa cat			1011
Phe Glu Asp Gly Thr Ile Ser Phe Leu Asp Val Ile Ala Leu Lys His			
315	320	325	330
gga ttt gac acc cta gag cgc ctc aca ggt gga atg gag aat ata aag			1059
Gly Phe Asp Thr Leu Glu Arg Leu Thr Gly Gly Met Glu Asn Ile Lys			
335	340	345	
cag cac acc ttc acc ttg gct cag tat acc tac atg gcc ctg tcc tct			1107
Gln His Thr Phe Thr Leu Ala Gln Tyr Thr Tyr Met Ala Leu Ser Ser			
350	355	360	
ctc cag tac ccc aat gga gcc cct gtg gtg cgg att tac agc gat tct			1155
Leu Gln Tyr Pro Asn Gly Ala Pro Val Val Arg Ile Tyr Ser Asp Ser			
365	370	375	
gag ttc agc agc cct gag gtt cag ggc ccg atc atc aat ttt aat gtg			1203
Glu Phe Ser Ser Pro Glu Val Gln Gly Pro Ile Ile Asn Phe Asn Val			
380	385	390	
ctg gat gac aaa ggg aac atc att ggt tac tcc cag gtg gac aaa atg			1251
Leu Asp Asp Lys Gly Asn Ile Ile Gly Tyr Ser Gln Val Asp Lys Met			
395	400	405	410
gcc agt ctt tac aac atc cac ctg cga act ggc tgc ttc tgt aac act			1299
Ala Ser Leu Tyr Asn Ile His Leu Arg Thr Gly Cys Phe Cys Asn Thr			
415	420	425	
ggg gcc tgc cag agg cac ctg ggc ata agc aac gag atg gtc agg aag			1347
Gly Ala Cys Gln Arg His Leu Gly Ile Ser Asn Glu Met Val Arg Lys			
430	435	440	
cat ttt cag gct ggt cat gtc tgt ggg gac aat atg gac ctc ata gat			1395
His Phe Gln Ala Gly His Val Cys Gly Asp Asn Met Asp Leu Ile Asp			
445	450	455	
ggg cag ccc aca gga tct gtg agg att tca ttt gga tac atg tcg acg			1443
Gly Gln Pro Thr Gly Ser Val Arg Ile Ser Phe Gly Tyr Met Ser Thr			
460	465	470	
ctg gat gat gtc cag gcc ttt ctt agg ttc atc ata gac act cgc ctg			1491
Leu Asp Asp Val Gln Ala Phe Leu Arg Phe Ile Ile Asp Thr Arg Leu			
475	480	485	490
cac tca tca ggg gac tgg cct gtc cct cag gcc cat gct gac acc ggg			1539
His Ser Ser Gly Asp Trp Pro Val Pro Gln Ala His Ala Asp Thr Gly			
495	500	505	

gag act gga gcc cca tca gca gac agc cag gct gat gtt ata cct gct	1587
Glu Thr Gly Ala Pro Ser Ala Asp Ser Gln Ala Asp Val Ile Pro Ala	
510 515 520	
gtc atg ggc aga cgt agc ctc tcg cct cag gaa gat gcc ctc aca ggc	1635
Val Met Gly Arg Arg Ser Leu Ser Pro Gln Glu Asp Ala Leu Thr Gly	
525 530 535	
tcc agg gtt tgg aac aac tcg tct act gtg aat gct gtg cct gtg gcc	1683
Ser Arg Val Trp Asn Asn Ser Ser Thr Val Asn Ala Val Pro Val Ala	
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Pro Pro Val Cys Asp Val Ala Arg Thr Gln Pro Thr Pro Ser Glu Lys	
555 560 565 570	
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Ala Ala Gly Val Leu Glu Gly Ala Leu Gly Pro His Val Val Thr Asn	
575 580 585	
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Leu Tyr Leu Tyr Pro Ile Lys Ser Cys Ala Ala Phe Glu Val Thr Arg	
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tgg cct gta gga aac caa ggg ctg cta tat gac cgg agc tgg atg gtt	1875
Trp Pro Val Gly Asn Gln Gly Leu Leu Tyr Asp Arg Ser Trp Met Val	
605 610 615	
gtg aat cac aat ggt gtt tgc ctg agt cag aag cag gaa ccc cgg ctc	1923
Val Asn His Asn Gly Val Cys Leu Ser Gln Lys Gln Glu Pro Arg Leu	
620 625 630	
tgc ctg atc cag ccc ttc atc gac ttg cgg caa agg atc atg gtc atc	1971
Cys Leu Ile Gln Pro Phe Ile Asp Leu Arg Gln Arg Ile Met Val Ile	
635 640 645 650	
aaa gcc aaa ggg atg gag cct ata gag gtg cct ctt gag gaa aat agt	2019
Lys Ala Lys Gly Met Glu Pro Ile Glu Val Pro Leu Glu Glu Asn Ser	
655 660 665	
gaa cgg act cag att cgc caa agc agg gtc tgt gct gac aga gta agt	2067
Glu Arg Thr Gln Ile Arg Gln Ser Arg Val Cys Ala Asp Arg Val Ser	
670 675 680	
act tat gat tgt gga gaa aaa att tca agc tgg ttg tca aca ttt ttt	2115
Thr Tyr Asp Cys Gly Glu Lys Ile Ser Ser Trp Leu Ser Thr Phe Phe	
685 690 695	
ggc cgt cct tgt aat ttg atc aaa caa agt tca aac tct caa agg aat	2163
Gly Arg Pro Cys Asn Leu Ile Lys Gln Ser Ser Asn Ser Gln Arg Asn	
700 705 710	
gca aag aag aaa cat gga aaa gat caa ctt cct ggt aca atg gcc acc	2211
Ala Lys Lys Lys His Gly Lys Asp Gln Leu Pro Gly Thr Met Ala Thr	
715 720 725 730	

ctt tct ctg gtg aat gag gca cag tat ctg ctg atc aac aca tcc agt	2259
Leu Ser Leu Val Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser	
735 740 745	
att ttg gaa ctt cac cgg caa cta aac acc agt gat gag aat gga aag	2307
Ile Leu Glu Leu His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys	
750 755 760	
gag gaa tta ttc tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat	2355
Glu Glu Leu Phe Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn	
765 770 775	
att att atc aat gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag	2403
Ile Ile Ile Asn Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu	
780 785 790	
att tca att ggc tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga	2451
Ile Ser Ile Gly Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg	
795 800 805 810	
tgc cag atg att tgc atc gac cag caa act ggg caa cga aac cag cat	2499
Cys Gln Met Ile Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His	
815 820 825	
gtt ttc caa aaa ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc	2547
Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly	
830 835 840	
atg tac ctg atg cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg	2595
Met Tyr Leu Met His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu	
845 850 855	
tct gta gga tct cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt	2643
Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly	
860 865 870	
cat gat tta cct gca tct gag aaa cac cag gat gtt acc tcc taa aaa	2691
His Asp Leu Pro Ala Ser Glu Lys His Gln Asp Val Thr Ser *	
875 880 885	
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ctgtgaggtg tgcgaagccc cagccgagcg ggtgtgcgcg gcctgcacag tcacttatta 180
ctggtctggg ccgaatcggt caggctgaag aatatctatt ccaagcccag tggacagtcc 240
tcaaataaac tgactgtagt aatgccaccc actctttact gcacgcgaat ctgggacttc 300
tctatatagc taagaaaaac tatgaagagg cccgttatca tctggccaat gatatttatt 360
ttgccagttg tgcatttgga acagaggaca ttaggacttc aggaggctac ttccacctgg 420
ctaatatatt ctatgacctt aaaaagttgg acctggcaga cacattgtac accaaggtct 480
ctgagatctg gcacgcatat ttgaacaatc actatcaagt cctctcacag gctcacatcc 540
aaciaa atg gat tta ctg ggc aaa cta ttt gag aat gac act ggc ttg 587
Met Asp Leu Leu Gly Lys Leu Phe Glu Asn Asp Thr Gly Leu
1 5 10
gat gaa gcc caa gaa gca gaa gcc att cgc atc ctg act tca atc ttg 635
Asp Glu Ala Gln Glu Ala Glu Ala Ile Arg Ile Leu Thr Ser Ile Leu
15 20 25 30
aac att cga gaa tct aca tct gac aaa gcc ccc caa aaa acc atc ttt 683
Asn Ile Arg Glu Ser Thr Ser Asp Lys Ala Pro Gln Lys Thr Ile Phe
35 40 45
gtt ctg aag atc ctg gtc atg ctt tac tac ctg atg atg aat tct tca 731
Val Leu Lys Ile Leu Val Met Leu Tyr Tyr Leu Met Met Asn Ser Ser
50 55 60
aag gca cag gaa tat ggc atg agg gcc ctc agt cta gcc aaa gaa caa 779
Lys Ala Gln Glu Tyr Gly Met Arg Ala Leu Ser Leu Ala Lys Glu Gln
65 70 75
cag ctt gat gtc cat gag caa agc acc att caa gag tta tta agt ctc 827
Gln Leu Asp Val His Glu Gln Ser Thr Ile Gln Glu Leu Leu Ser Leu
80 85 90
att tca act gaa gac cat ccc att act tag t gacccatgag ctctgcatca 878
Ile Ser Thr Glu Asp His Pro Ile Thr *
95 100
agggttattc caggggctac tgaagatcta atatattcca gccttgacac actgctttga 938
ggtactgtag actgctgaag tttccaccct cttcccctgg gattgcacac atagctgtta 998
tttttttctt acacagcata ttaaggggaat ataaagcttt aggcatagaa atcactaaaa 1058
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gtagtcagat cactaatatg gtatttgtaa ttaaactaca aatagtttgt catttcccag 1178
aagtcttcca acgatgcatg tttcatacac ttttgctaaa ggaggggtaa aggagggggg 1238
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 <213> Homo sapiens

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cccagtgaga gcggctttcc aggacggtgc gatgtgctgc gcagcgaaga ggcaggaggc      180
cggttctctg gggtagcggg acaggcgggc gcttactctg tgcgcttgct tccccaaccc      240
tgcaccggcc  atg cgc ccg gcc ttg gcg gtg ggc ctg gtg ttc gca ggc      289
              Met Arg Pro Ala Leu Ala Val Gly Leu Val Phe Ala Gly
              1              5              10

tgc tgc agt aac gtg atc ttc cta gag ctc ctg gcc cgg aag cat cca      337
Cys Cys Ser Asn Val Ile Phe Leu Glu Leu Leu Ala Arg Lys His Pro
              15              20              25

gga tgt ggg aac att gtg aca ttt gca caa ttt tta ttt att gct gtg      385
Gly Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val
              30              35              40              45

gaa ggc ttc ctc ttt gaa gct gat ttg gga agg aag cca cca gct atc      433
Glu Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile
              50              55              60

cca ata agg tac tat gcc ata atg gtg acc atg ttc ttc acc gtg agc      481
Pro Ile Arg Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser
              65              70              75

gtg gtg aac aac tat gcc ctg aat ctc aac att gcc atg ccc ctg cat      529
Val Val Asn Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His
              80              85              90

atg ata ttt aga tcc ggt tct cta att gcc aac acg att cta gga att      577
Met Ile Phe Arg Ser Gly Ser Leu Ile Ala Asn Thr Ile Leu Gly Ile
              95              100              105

atc att ttg aag aaa aga tac agt ata ttc aaa tat acc tcc att gcc      625
Ile Ile Leu Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala
              110              115              120              125

ctg gtg tct gtg ggg ata ttt att tgc act ttt atg tca gca aag cag      673
Leu Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln
              130              135              140

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gtg act tcc cag tcc agc ttg agt gag aat gat gga ttc cag gca ttt	721
Val Thr Ser Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe	
145 150 155	
gtg tgg tgg tta cta ggt att ggg gca ttg act ttt gct ctt ctg atg	769
Val Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met	
160 165 170	
tca gca agg atg ggg ata ttc caa gag act ctc tac aaa cga ttt ggg	817
Ser Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly	
175 180 185	
aaa cac tcc aag gag gct ttg ttt tat aat cac gcc ctt cca ctt ccg	865
Lys His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro	
190 195 200 205	
ggg ttc gtc ttc ttg gct tct gat att tat gac cat gca gtt cta ttc	913
Gly Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe	
210 215 220	
aat aag tct gag tta tat gaa att ccc gtc atc gga gtg acc ctg ccc	961
Asn Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro	
225 230 235	
atc atg tgg ttc tac ctc ctc atg aac atc atc act cag tac gtg tgc	1009
Ile Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys	
240 245 250	
atc cgg ggt gtg ttt atc ctc acc aca gaa tgc gcc tcc ctc acc gtc	1057
Ile Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val	
255 260 265	
acg ctc gtc gtg acc cta cgc aaa ttt gtg agc ctc atc ttt tcc atc	1105
Thr Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile	
270 275 280 285	
ttg tac ttc cag aac ccc ttc acc ctg tgg cac tgg ctg ggc acc ttg	1153
Leu Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu	
290 295 300	
ttt gtc ttc att ggg acc tta atg tac aca gag gtg tgg aac aac cta	1201
Phe Val Phe Ile Gly Thr Leu Met Tyr Thr Glu Val Trp Asn Asn Leu	
305 310 315	
ggg acc aca aaa agt gag cct cag aag gac agc aag aag aac tga ggc	1249
Gly Thr Thr Lys Ser Glu Pro Gln Lys Asp Ser Lys Lys Asn *	
320 325 330	
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<222> (837)..(3743)

<400> 185

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aggaagaaga cgcagaagca ggacgaccct gaaagattca gcctcttcat cctcaaacag      180
gtcgcttctc gggagttctt ggtgttgaa tattttacag caaagcagtc gaccaggcct      240
cctcttccca cctgtccagc agcatgaaag cagcatgatt ggccgaccgc aggagaagcc      300
cccagaacca ggcccccaac tcagccatct gcggaggcca aggtgtgagc gacgtctcct      360
caccacagtg ctgtgtggtc tatacctcag ccaggagag gatgtgaaac cccccgcct      420
gcacatgagt ggtacaggcc aacaggaaca cctggctcca gccacgttca cagacatgtc      480
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atgggtgacc agcaactgta caagaccaac catgtggccc atggtagtga gaaccttttc      660
taccaacagc caccacttgg cgtccacagc gggctgagcc cactgatggc taccaatata      720
cctactccca ggccagcgag atccggaccc agaagcttac cagcgggtgtc ttacacaagc      780

tggaactcttt caccaggtg tttgccaaac aaaacctgcy aattcagggtc aacaat      836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct      884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
   1             5             10            15

gac agt gct ctg cgc cag ctg ctg tct cag aag ccc atg gag ccc cca      932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
           20             25             30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac      980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
           35             40             45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag      1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
           50             55             60

cac cct acc caa ggg cac ctg tat tat gac tac cag cag cct ctg gct      1076
His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
           65             70             75             80

cag gtg cca gtg cag gga gga cag cca ctg cag gcc cca cag atg ctg      1124
Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
           85             90             95
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tca cag cac atg caa cag atg cag cag cac cag tat tac cca ccg cag	1172
Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln	
100 105 110	
caa cag cag caa gcc ggg caa cag cgt atc tcc atg caa gaa ata cag	1220
Gln Gln Gln Gln Ala Gly Gln Gln Arg Ile Ser Met Gln Glu Ile Gln	
115 120 125	
acg cag ccg caa caa att cgc cca tca cag cca cag ccg ccg cca cag	1268
Thr Gln Pro Gln Gln Ile Arg Pro Ser Gln Pro Gln Pro Pro Pro Gln	
130 135 140	
cag cag cag ccg cag cag cta cag ctg cag cag cgg cag ggt tca atg	1316
Gln Gln Gln Pro Gln Gln Leu Gln Leu Gln Gln Arg Gln Gly Ser Met	
145 150 155 160	
cag ata cct cag tat tat cag ccc caa ccc atg atg cag cac ttg caa	1364
Gln Ile Pro Gln Tyr Tyr Gln Pro Gln Pro Met Met Gln His Leu Gln	
165 170 175	
gag cag cag cag caa cag atg cac ctg cag cct cct tct tat cac agg	1412
Glu Gln Gln Gln Gln Gln Met His Leu Gln Pro Pro Ser Tyr His Arg	
180 185 190	
gac cct cac cag tat acc cca gag cag gca cac act gtc cag ctg att	1460
Asp Pro His Gln Tyr Thr Pro Glu Gln Ala His Thr Val Gln Leu Ile	
195 200 205	
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Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly

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Gly	Lys	Lys	Ile	Gly	Cys	Gly	Asn	Phe	Gly	Glu	Leu	Arg	Leu	Gly	Glu	
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Met	Val	Leu	Glu	Leu	Leu	Gly	Pro	Ser	Leu	Glu	Asp	Leu	Phe	Asp	Leu	
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Cys	Asp	Arg	Thr	Phe	Thr	Leu	Lys	Thr	Val	Leu	Met	Ile	Ala	Ile	Gln	
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Leu	Leu	Ser	Arg	Met	Glu	Tyr	Val	His	Ser	Lys	Asn	Leu	Ile	Tyr	Arg	
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Asp	Val	Lys	Pro	Glu	Asn	Phe	Leu	Ile	Gly	Arg	Gln	Gly	Asn	Lys	Lys	
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Glu	His	Val	Ile	His	Ile	Ile	Asp	Phe	Gly	Leu	Ala	Lys	Glu	Tyr	Ile	
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gac	ccc	gaa	acc	aaa	aaa	cac	ata	cct	tat	agg	gaa	cac	aaa	agt	tta	888
Asp	Pro	Glu	Thr	Lys	Lys	His	Ile	Pro	Tyr	Arg	Glu	His	Lys	Ser	Leu	
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Thr	Gly	Thr	Ala	Arg	Tyr	Met	Ser	Ile	Asn	Thr	His	Leu	Gly	Lys	Glu	
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caa	agc	cgg	aga	gat	gat	ttg	gaa	gcc	cta	ggc	cat	atg	ttc	atg	tat	984
Gln	Ser	Arg	Arg	Asp	Asp	Leu	Glu	Ala	Leu	Gly	His	Met	Phe	Met	Tyr	
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ttc	ctt	cga	ggc	agc	ctc	ccc	tgg	caa	gga	ctc	aag	gct	gac	aca	tta	1032
Phe	Leu	Arg	Gly	Ser	Leu	Pro	Trp	Gln	Gly	Leu	Lys	Ala	Asp	Thr	Leu	
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Lys	Glu	Arg	Tyr	Gln	Lys	Ile	Gly	Asp	Thr	Lys	Arg	Asn	Thr	Pro	Ile	
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Glu	Ala	Leu	Cys	Glu	Asn	Phe	Pro	Glu	Glu	Met	Ala	Thr	Tyr	Leu	Arg	
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Tyr Val Arg Arg Leu Asp Phe Phe Glu Lys Pro Asp Tyr Glu Tyr Leu	
255 260 265 270	
cgg acc ctc ttc aca gac ctc ttt gaa aag aaa ggc tac acc ttt gac	1224
Arg Thr Leu Phe Thr Asp Leu Phe Glu Lys Lys Gly Tyr Thr Phe Asp	
275 280 285	
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Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro Val Gly Ser	
290 295 300	
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Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr	
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His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn Gln Val Val	
320 325 330	
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Ser Ser Thr Asn Gly Glu Leu Asn Val Asp Asp Pro Thr Gly Ala His	
335 340 345 350	
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Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val Val Glu Glu	
355 360 365	
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Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys Thr Ala Gln	
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Arg His Lys *	
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gatatccaaa ctaaaaagaa gaaaacagat gccccagaa ggggccagtg cgggcagcca	1687
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ctcttctct gtgcctgtgc agcattcatc ccagctggcc ttgggggttca ggttcttct	2107
tccctccctc ctgtgaagtt aactgtagg acacaagctg tgagcaatct gcagtctact	2167

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cctggctgtg gtggcctgtg gcaatcggct ggaggagacg ctggtcatgc tcaaatacgc 180
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cgagtttgat aagcagttac gccatggcct gactcatata caaagaagtt tgagcacaga 300
atctacccca tcacattttc tgttggaac cctcaggagt ggaagaaatt gttcaaacc 360
tgtgctgccc agagactctt tcttccggtg attttaaagg atgtggactc acttctctac 420
gtggacaccg atgtcctctt tctgagacct gttgatgaca tctggaagct tctgaggctg 480
ttaattcca ccagcttgc agcc atg gcc cct gag cac gaa atc ccc aag 531
Met Ala Pro Glu His Glu Ile Pro Lys
1 5
att ggc tgg tac agc cgc ttt gct agg cat cct ttc tat ggc tct gca 579
Ile Gly Trp Tyr Ser Arg Phe Ala Arg His Pro Phe Tyr Gly Ser Ala
10 15 20 25
gga gtt aat tca gga gtc atg tta atg aat tta act cgg ata aga agt 627
Gly Val Asn Ser Gly Val Met Leu Met Asn Leu Thr Arg Ile Arg Ser
30 35 40
acc cag ttc aag aac agc atg att cca aca ggc ctg gct tgg gag gac 675
Thr Gln Phe Lys Asn Ser Met Ile Pro Thr Gly Leu Ala Trp Glu Asp
45 50 55
atg ttg tac cct ctg tac cag aag tac aag aat gcc atc acg tgg gga 723
Met Leu Tyr Pro Leu Tyr Gln Lys Tyr Lys Asn Ala Ile Thr Trp Gly
60 65 70
gac cag gat tta tta aat att att ttt tat ttc aac cca gag tgt ctc 771
Asp Gln Asp Leu Leu Asn Ile Ile Phe Tyr Phe Asn Pro Glu Cys Leu

75	80	85	
tat gta ttc ccc tgc cag tgg aac tac cgt ccc gat cac tgc atg tac			819
Tyr Val Phe Pro Cys Gln Trp Asn Tyr Arg Pro Asp His Cys Met Tyr			
90	95	100	105
gga agc aac tgc aga gag gct gag cat gaa ggt gtg tct gtt ctg cat			867
Gly Ser Asn Cys Arg Glu Ala Glu His Glu Gly Val Ser Val Leu His			
110	115		120
gga aac cga ggc gtc tac cat gac gat aag caa cca acg ttc aga gca			915
Gly Asn Arg Gly Val Tyr His Asp Asp Lys Gln Pro Thr Phe Arg Ala			
125	130		135
ctc tat gaa gca ata cgg gat ttt ccc ttt caa gac aat ctc ttt caa			963
Leu Tyr Glu Ala Ile Arg Asp Phe Pro Phe Gln Asp Asn Leu Phe Gln			
140	145		150
tcc atg tat tac ccc ctt cag ctg aag ttt ttg gag act gtg cac act			1011
Ser Met Tyr Tyr Pro Leu Gln Leu Lys Phe Leu Glu Thr Val His Thr			
155	160		165
tta tgt gga cga atc ccg caa gtt ttt ctg aag caa att gag aaa aca			1059
Leu Cys Gly Arg Ile Pro Gln Val Phe Leu Lys Gln Ile Glu Lys Thr			
170	175		180
atg aaa agg gct tat gag aaa cac gtc atc atc cat gtt ggc ccc aac			1107
Met Lys Arg Ala Tyr Glu Lys His Val Ile Ile His Val Gly Pro Asn			
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Gln Met His *			
205			
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gactgttgag ttttaaaaac ctcgttaaata tttgccaaat cagttgcccc caaaagggaa			1282
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 cactgccttc aggccagaag caaaccaaatt ttaccaggtt tggctggagg agttttgtga 1335
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 ggcgcggggc cactgactgac tggctggacc atg aac gtg ttc cga atc ctc 171
 Met Asn Val Phe Arg Ile Leu
 1 5
 ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ctg ggg aag atc 219
 Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Leu Gly Lys Ile
 10 15 20
 tgg agg tcc aag tgc tgc aag gcc atc tct ggg aag agc cag atc ctg 267
 Trp Arg Ser Lys Cys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
 25 30 35

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ttt gct ctc gtc ttc acc acc agg tac ctg gac ctg ttc acc aac ttc      315
Phe Ala Leu Val Phe Thr Thr Arg Tyr Leu Asp Leu Phe Thr Asn Phe
 40                      45                      50                      55

atc tcc atc tac aac aca gta atg aag atc ctc tgg act ttc tct atc      363
Ile Ser Ile Tyr Asn Thr Val Met Lys Ile Leu Trp Thr Phe Ser Ile
                      60                      65                      70

tat ctg gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag      411
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys
                      75                      80                      85

act gga gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt      459
Thr Gly Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly
                      90                      95                      100

ctg tac cgg gca ctc tac ctg gct aac tgg atc aag cgg tac cag act      507
Leu Tyr Arg Ala Leu Tyr Leu Ala Asn Trp Ile Lys Arg Tyr Gln Thr
                      105                      110                      115

gag aat ttc tat gac caa att gca gtc ggg tct gga gta gta caa acc      555
Glu Asn Phe Tyr Asp Gln Ile Ala Val Gly Ser Gly Val Val Gln Thr
                      120                      125                      130                      135

atc ttc tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag      603
Ile Phe Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys
                      140                      145                      150

gga aag aag tta agt ctt cca atg cca atc tga ggaccttc agagacagtc      654
Gly Lys Lys Leu Ser Leu Pro Met Pro Ile *
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catgttggcc aggctggtct caaactcctg acctcaggcg atccgcccac cttggcctcc      240

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cag ttc atg cgt att cag aat gta ggc caa aag aaa gct gaa gag agt	727
Gln Phe Met Arg Ile Gln Asn Val Gly Gln Lys Lys Ala Glu Glu Ser	
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cca gca gaa att atc atc cag gct att cct cag tat gct att cct tgt	775
Pro Ala Glu Ile Ile Ile Gln Ala Ile Pro Gln Tyr Ala Ile Pro Cys	
230 235 240	
cac tcc agc tcc aat gtg gtg gtg gag ccc agt ggg ctt ctt gag cta	823
His Ser Ser Ser Asn Val Val Val Glu Pro Ser Gly Leu Leu Glu Leu	
245 250 255	
aac aac ttc act agt caa cag ctg gat gat gag gag aca gca atg gag	871
Asn Asn Phe Thr Ser Gln Gln Leu Asp Asp Glu Glu Thr Ala Met Glu	
260 265 270 275	
cag gac ata gac agt agc acg gag gat gga act gaa ccc agc cct tct	919
Gln Asp Ile Asp Ser Ser Thr Glu Asp Gly Thr Glu Pro Ser Pro Ser	
280 285 290	
cag agc tct gct gaa cgg tcc tag tgtttggaca caatagtgca ctttaaaacc	973
Gln Ser Ser Ala Glu Arg Ser *	
295	
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gagctcccat taggagccgc tggctgcggc agcaggggac tagcgtgaga gttggctaaa	180
aaaaagaaaa gaac atg gag gca gat ata atc aca aat ctt cga tgc agg	230
Met Glu Ala Asp Ile Ile Thr Asn Leu Arg Cys Arg	
1 5 10	
ctc aaa gag gct gaa gaa gag cga cta aaa gct gca cag tat ggt tta	278
Leu Lys Glu Ala Glu Glu Glu Arg Leu Lys Ala Ala Gln Tyr Gly Leu	
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cgt aat gaa atg atg acc atg act gag agt tat gaa caa gaa aaa tat Arg Asn Glu Met Met Thr Met Thr Glu Ser Tyr Glu Gln Glu Lys Tyr 45 50 55 60	374
acc ctt caa aga gaa gtt gaa ctc aag agt cga atg tta gaa agt ttg Thr Leu Gln Arg Glu Val Glu Leu Lys Ser Arg Met Leu Glu Ser Leu 65 70 75	422
agc tgc gaa tgt gaa gct att aaa caa caa caa aaa atg cac ctg gag Ser Cys Glu Cys Glu Ala Ile Lys Gln Gln Gln Lys Met His Leu Glu 80 85 90	470
aaa ttg gaa gaa caa cta agc aga agc cat gga cag gaa gtg aat gaa Lys Leu Glu Glu Gln Leu Ser Arg Ser His Gly Gln Glu Val Asn Glu 95 100 105	518
cta aaa act aag ata gaa aaa ctg aaa gtg gaa tta gat gaa gcc agg Leu Lys Thr Lys Ile Glu Lys Leu Lys Val Glu Leu Asp Glu Ala Arg 110 115 120	566
ctt agt gaa aag cag ctg aag cac caa gta gat cat cag aag gaa ctc Leu Ser Glu Lys Gln Leu Lys His Gln Val Asp His Gln Lys Glu Leu 125 130 135 140	614
ctc tct tgt aaa tca gag gaa ctg cgc gta atg tct gaa cgt gtg cag Leu Ser Cys Lys Ser Glu Glu Leu Arg Val Met Ser Glu Arg Val Gln 145 150 155	662
gaa agc atg tct tca gag atg ctg gct ctt caa att gag ctg aca gaa Glu Ser Met Ser Ser Glu Met Leu Ala Leu Gln Ile Glu Leu Thr Glu 160 165 170	710
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Lys Gly Asn Ser Leu Phe Ala Glu Val Glu Asp Arg Arg Ala Ala Met	
255 260 265	
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Glu Arg Gln Leu Ile Ser Met Lys Val Lys Tyr Gln Ser Leu Lys Lys	
270 275 280	
caa aat gta ttt aac aga gaa cag atg cag aga atg aag tta caa att	1094
Gln Asn Val Phe Asn Arg Glu Gln Met Gln Arg Met Lys Leu Gln Ile	
285 290 295 300	
gcc acg ttg cta cag atg aaa ggg tct caa act gaa ttt gag cag cag	1142
Ala Thr Leu Leu Gln Met Lys Gly Ser Gln Thr Glu Phe Glu Gln Gln	
305 310 315	
gaa cgg ttg ctt gcc atg ttg gag cag aag aat ggt gaa ata aaa cat	1190
Glu Arg Leu Leu Ala Met Leu Glu Gln Lys Asn Gly Glu Ile Lys His	
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Leu Leu Gly Glu Ile Arg Asn Leu Glu Lys Phe Lys Asn Leu Tyr Asp	
335 340 345	
agt atg gaa tcc aag cct tca gtc gac tct ggt act ctg gaa gat aac	1286
Ser Met Glu Ser Lys Pro Ser Val Asp Ser Gly Thr Leu Glu Asp Asn	
350 355 360	
acc tat tat aca gat tta ctt cag atg aag ctg gat aac tta aac aaa	1334
Thr Tyr Tyr Thr Asp Leu Leu Gln Met Lys Leu Asp Asn Leu Asn Lys	
365 370 375 380	
gaa att gaa agc act aaa ggt gaa ttg tcc ata cag cga atg aaa gca	1382
Glu Ile Glu Ser Thr Lys Gly Glu Leu Ser Ile Gln Arg Met Lys Ala	
385 390 395	
tta ttt gag agc cag cgg gct cta gat att gag cga aaa ctt ttt tgc	1430
Leu Phe Glu Ser Gln Arg Ala Leu Asp Ile Glu Arg Lys Leu Phe Cys	
400 405 410	
aaa tga aagatgcctc cagctttcag aaagtgaaaa tatgaaactg agagctaaac	1486
Lys *	
tagatgaatt gaaactaaaa tatgaacctg aagagacagt tgaagtgcct gtactgaaaa	1546
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acaccccaaa ctctcccagg ttagctgctg aatcaaagct tcaaacagaa gttaaagaag	1906

gtg cca ggg aga agc aag gag gat ggg ctt tgg act aga aat agc cca	584
Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg Asn Ser Pro	
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ggc tcc tcc cag cat cca gaa agt ccc agg ctg ccc aac cct ctc tgg	632
Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn Pro Leu Trp	
20 25 30 35	
gac aga gga aaa att ggc aag gtt gaa ggt cac cag cac att cag gtt	680
Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His Ile Gln Val	
40 45 50	
agt act tcc tca gcc tgt gtc tgg cag ctg gct tac cct cca gtt tgg	728
Ser Thr Ser Ser Ala Cys Val Trp Gln Leu Ala Tyr Pro Pro Val Trp	
55 60 65	
ccc aac ctc cct gct gtc cct att cag gat ttc tct caa aag tcc cat	776
Pro Asn Leu Pro Ala Val Pro Ile Gln Asp Phe Ser Gln Lys Ser His	
70 75 80	
ctg ccg tct att gtg gtg gaa tcc agt gag gtg aat gaa gag agt ggg	824
Leu Pro Ser Ile Val Val Glu Ser Ser Glu Val Asn Glu Glu Ser Gly	
85 90 95	
gat ctc cat ttg ccc cat gag gag ctg ctg ctg ctc act gat ggt gag	872
Asp Leu His Leu Pro His Glu Glu Leu Leu Leu Leu Thr Asp Gly Glu	
100 105 110 115	
gaa gag gat gct gag gcc ttc ttc caa gac caa agt gaa gag cca ggt	920
Glu Glu Asp Ala Glu Ala Phe Phe Gln Asp Gln Ser Glu Glu Pro Gly	
120 125 130	
gag gga ggt ggc tca ttc agg ggg cca ctg tga gctgaatg ttctgggcag	971
Glu Gly Gly Gly Ser Phe Arg Gly Pro Leu *	
135 140	
agccaagatg gaagtcagtt acggcccctg cattcagcag taaaaggcac acagcaggtg	1031
ctcaataaat g	1042

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	1 5 10

gtt ctg aat cta gtg acg tct gcc agg agc cag aag aca gaa cct cta	97
Val Leu Asn Leu Val Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu	
15 20 25	
agt ggc tct ggg gac cag cca ctc ttc cgt gga gct gat cga tat gac	145
Ser Gly Ser Gly Asp Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp	
30 35 40	
ttt gcc atc atg ata cct cca gga ggc acg gaa tgc ttt tgg caa ttt	193
Phe Ala Ile Met Ile Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe	
45 50 55	
gcc cac cag act gga tac ttc tat ttc agt tac gag gtt cag cgg aca	241
Ala His Gln Thr Gly Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr	
60 65 70 75	
gtg ggg atg tca cat gac cgg cat gtt gct gcc acg gca cat aac cca	289
Val Gly Met Ser His Asp Arg His Val Ala Ala Thr Ala His Asn Pro	
80 85 90	
cag gga ttt ctc ata gac acc tcc cag ggt gtt cgg ggc cag att aac	337
Gln Gly Phe Leu Ile Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn	
95 100 105	
ttc tct acc caa gag aca ggt ttt tat cag ctt tgt cta agt aat cag	385
Phe Ser Thr Gln Glu Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln	
110 115 120	
cat aat cac ttc ggt tct gtg caa gtg tac ctc aac ttt ggg gtc ttc	433
His Asn His Phe Gly Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe	
125 130 135	
tat gag ggg cct gag act gat cac aaa cag aag gaa aga aaa caa ctg	481
Tyr Glu Gly Pro Glu Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu	
140 145 150 155	
aat gat act ctg gat gca att gag gac ggc aca caa aag gtg cag aac	529
Asn Asp Thr Leu Asp Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn	
160 165 170	
aat atc ttt cac atg tgg cga tac tac aac ttt gcc cgg atg agg aaa	577
Asn Ile Phe His Met Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys	
175 180 185	
atg gct gac ttt ttc ctt atc caa tca aac tat aac tac gtg aac tgg	625
Met Ala Asp Phe Phe Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp	
190 195 200	
tgg tgg aca gcc cag agc ctt gtt att att ctt tct ggg atc ctg caa	673
Trp Ser Thr Ala Gln Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln	
205 210 215	
ctg tat ttc ttg aag cgt ctc ttc aat gtt cca aca act aca gat aca	721
Leu Tyr Phe Leu Lys Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr	
220 225 230 235	
aag aag cca aga tgc taa gctaag gtgactatag caccctggct gttttcttct	775

Lys Lys Pro Arg Cys *
240

ggggcttagt cgaatcagct ttgtaatggt atgggacaaa aatcaattat ctcattaatg 835
tttttagtctg ctgcacacat ctaaaaaagc aaaatggcaa taaaatcata acagtgtaaaa 895
aaaaaaaaa 903

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala
1 5 10

cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct ctc 99
Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu
15 20 25

att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg 147
Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala
30 35 40

act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat 195
Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn
45 50 55

gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat 243
Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp
60 65 70 75

tgt gcc gcg agg gct cag gtg acc gat ggc tcc tgg ggt gct ttc tca 291
Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser
80 85 90

gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa 344
Gly Lys Glu Trp Gly Arg *
95

aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt 404

ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac 464

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg 524

aatgggaaaa tcattttgaa aaatgtaaat tgctgctcaa gtagacatta ttgtgtgaaa 584

tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg 644
ctagg 649

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<213> Homo sapiens

<220>
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Met Pro Val Ala Val Gly
1 5

ccc tac gga cag tcc cag cca agc tgc ttc tac cgt gta aaa atg ggc 101
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Tyr Arg Val Lys Met Gly
10 15 20

ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc 149
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly
25 30 35

acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 197
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
40 45 50

ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 245
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
55 60 65 70

atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct 296
Met Ala Ile Gly Met Gly Ile Arg Cys *
75 80

gtcccttccc atcaatccca gcccatgtac taataaaaga aagtctttga gtaaaaaaaaa 356
aaaa 360

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<212> DNA
<213> Homo sapiens

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<222> (206)..(535)

<400> 198
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 ggccatcttt ctggggagga ctctcccagg tagggaaggc cagaggtggc ccagtgcctg 180
 gagggttagg gtctctgcct gggat atg caa gag gaa gta gga aag gga ggt 232
 Met Gln Glu Glu Val Gly Lys Gly Gly
 1 5
 ctc atg gat gat cct agg ctg cta gaa gtc ctt aag gcc cca tct agt 280
 Leu Met Asp Asp Pro Arg Leu Leu Glu Val Leu Lys Ala Pro Ser Ser
 10 15 20 25
 cca ttc cac tcc cta ccc cca ttc cag agc cga gta gta agt tta cag 328
 Pro Phe His Ser Leu Pro Pro Phe Gln Ser Arg Val Val Ser Leu Gln
 30 35 40
 atg ttt ccc cca tta cgt acc ccc acc cat ccc tgc tgc agc gag cct 376
 Met Phe Pro Pro Leu Arg Thr Pro Thr His Pro Cys Cys Ser Glu Pro
 45 50 55
 gag agc cag gca gag cca ggc aca gct cct cag tct tct cac aca gtc 424
 Glu Ser Gln Ala Glu Pro Gly Thr Ala Pro Gln Ser Ser His Thr Val
 60 65 70
 ctg ccg gtg gcc ttc cct cat gac cct tgc ttg gga ggg tgg agc act 472
 Leu Pro Val Ala Phe Pro His Asp Pro Cys Leu Gly Gly Trp Ser Thr
 75 80 85
 ggc tcc ttg acc cta aaa ggt agc tgg cag ggg caa gat ggg ggc cag 520
 Gly Ser Leu Thr Leu Lys Gly Ser Trp Gln Gly Gln Asp Gly Gly Gln
 90 95 100 105
 cta cct aat gga tga aagccacaag tgaatacagt tcttgtcacc aggggtgccc 575
 Leu Pro Asn Gly *
 110
 tgccctcact cggcagggag ttctgacacc ccagggcccg tgagctacct gcttgagccc 635
 ctgtttctgg ggcaccttcg aggaggcgtt gtggagggca tcgccccctg tttattcaca 695
 acaccctcag gggcaaacag gcctgggacc cgctgacacc attttgggta gctggatgca 755
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 caccctgca cacaggtaca gtgcatctgg gcacagcttt tggatccaca cctctgcaca 995
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 aacatgagac ttctgtgac cagtccacc tggctcccag ctgtctgtat cctcctgccc 1115

cgccctggcg agtgcctacc ctggcagaac ccagggagga gtggaggctg cctctgcctg 1175
 ggcctccaca cagcatcctg tacatacgcc acctgggctg ggggtgggga ggcagggcca 1235
 ggagcatcga ttaaagatca catcctgggg cttccaggga gctca 1280

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 <213> Homo sapiens

<220>
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 <222> (284)..(1741)

<400> 199

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 ctgccgggaa cggcagcttc tgacgctggg ccattggacg ctgcggaacc aggcttcttc 180
 actttgagtt tccgcgcga agcgccagtc cgggcccagg agggagcctt tactacttct 240
 ccctggtttc attcatgttc tgaggagggt gtgagaagga acc atg gat ccc aca 295
 Met Asp Pro Thr
 1
 gcc ttg gtg gaa gcc att gtg gaa gaa gtg gcc tgt ccc atc tgt atg 343
 Ala Leu Val Glu Ala Ile Val Glu Glu Val Ala Cys Pro Ile Cys Met
 5 10 15 20
 acc ttc ctg agg gag ccc atg agc att gac tgt ggc cac agc ttc tgc 391
 Thr Phe Leu Arg Glu Pro Met Ser Ile Asp Cys Gly His Ser Phe Cys
 25 30 35
 cac agc tgt ctc tct gga ctc tgg gag atc cca gga gaa tcc cag aac 439
 His Ser Cys Leu Ser Gly Leu Trp Glu Ile Pro Gly Glu Ser Gln Asn
 40 45 50
 tgg ggt tac acc tgt ccc ctc tgt cga gct cct gtc cag cca agg aac 487
 Trp Gly Tyr Thr Cys Pro Leu Cys Arg Ala Pro Val Gln Pro Arg Asn
 55 60 65
 ctg cgg cct aat tgg cag ctg gcc aat gtt gta gaa aaa gtc cgt ctg 535
 Leu Arg Pro Asn Trp Gln Leu Ala Asn Val Val Glu Lys Val Arg Leu
 70 75 80
 cta agg cta cat cca gga atg ggg ctg aag ggt gac ctg tgt gag cgc 583
 Leu Arg Leu His Pro Gly Met Gly Leu Lys Gly Asp Leu Cys Glu Arg
 85 90 95 100
 cat ggg gaa aag ctg aag atg ttc tgc aaa gag gat gtc ttg ata atg 631

His Gly Glu Lys Leu Lys Met Phe Cys Lys Glu Asp Val Leu Ile Met	
105 110 115	
tgt gag gcc tgc agc cag tcc cca gag cat gag gcc cac agt gtt gtg	679
Cys Glu Ala Cys Ser Gln Ser Pro Glu His Glu Ala His Ser Val Val	
120 125 130	
cca atg gag gat gtt gcc tgg gag tac aag tgg gaa ctt cat gag gcc	727
Pro Met Glu Asp Val Ala Trp Glu Tyr Lys Trp Glu Leu His Glu Ala	
135 140 145	
ctc gaa cat ctg aag aaa gag caa gaa gag gcc tgg aag ctt gaa gtt	775
Leu Glu His Leu Lys Lys Glu Gln Glu Glu Ala Trp Lys Leu Glu Val	
150 155 160	
ggt gaa agg aaa cga act gcc acc tgg aag ata cag gtg gaa acc cga	823
Gly Glu Arg Lys Arg Thr Ala Thr Trp Lys Ile Gln Val Glu Thr Arg	
165 170 175 180	
aaa cag agt att gta tgg gag ttt gaa aaa tac cag cga tta cta gag	871
Lys Gln Ser Ile Val Trp Glu Phe Glu Lys Tyr Gln Arg Leu Leu Glu	
185 190 195	
aaa aag cag cca cca cat cgg cag ctg ggg gca gag gta gca gca gct	919
Lys Lys Gln Pro Pro His Arg Gln Leu Gly Ala Glu Val Ala Ala Ala	
200 205 210	
ctg gcc agc cta cag cgg gag gca gcg gag acc atg cag aaa ctg gag	967
Leu Ala Ser Leu Gln Arg Glu Ala Ala Glu Thr Met Gln Lys Leu Glu	
215 220 225	
ttg aac cat agc gag ctc atc cag cag agc cag gtc ctg tgg agg atg	1015
Leu Asn His Ser Glu Leu Ile Gln Gln Ser Gln Val Leu Trp Arg Met	
230 235 240	
att gca gag ttg aaa gag agg tcg cag agg cct gtc cgc tgg atg ttg	1063
Ile Ala Glu Leu Lys Glu Arg Ser Gln Arg Pro Val Arg Trp Met Leu	
245 250 255 260	
cag gat att cag gaa gtg tta aac agg agc aaa tct tgg agc ttg cag	1111
Gln Asp Ile Gln Glu Val Leu Asn Arg Ser Lys Ser Trp Ser Leu Gln	
265 270 275	
cag cca gaa cca atc tcc ctg gag ttg aag aca gat tgc cgt gtg ctg	1159
Gln Pro Glu Pro Ile Ser Leu Glu Leu Lys Thr Asp Cys Arg Val Leu	
280 285 290	
ggg cta aga gag atc ctg aag act tat gca gct gat gtg cgc ttg gat	1207
Gly Leu Arg Glu Ile Leu Lys Thr Tyr Ala Ala Asp Val Arg Leu Asp	
295 300 305	
cca gat act gct tac tcc cgt ctc atc gtg tct gag gac aga aaa cgt	1255
Pro Asp Thr Ala Tyr Ser Arg Leu Ile Val Ser Glu Asp Arg Lys Arg	
310 315 320	
gtg cac tat gga gac acc aac cag aaa ctg cca gac aat cct gag aga	1303
Val His Tyr Gly Asp Thr Asn Gln Lys Leu Pro Asp Asn Pro Glu Arg	

325	330	335	340	
ttt tac cgc tat aat atc gtc ctg gga agc cag tgc atc tcc tca ggc				1351
Phe Tyr Arg Tyr Asn Ile Val Leu Gly Ser Gln Cys Ile Ser Ser Gly	345	350	355	
cgg cac tac tgg gag gtg gag gtg gga gac agg tct gag tgg ggc ctg				1399
Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Ser Glu Trp Gly Leu	360	365	370	
gga gta tgt aag caa aat gta gac cgg aag gag gtg gtc tac tta tcc				1447
Gly Val Cys Lys Gln Asn Val Asp Arg Lys Glu Val Val Tyr Leu Ser	375	380	385	
ccc cac tat gga ttc tgg gtg ata agg ctg agg aag gga aat gag tac				1495
Pro His Tyr Gly Phe Trp Val Ile Arg Leu Arg Lys Gly Asn Glu Tyr	390	395	400	
cga gca ggc acc gat gag tac cca atc ctg tcc ttg ccg gtc cct cct				1543
Arg Ala Gly Thr Asp Glu Tyr Pro Ile Leu Ser Leu Pro Val Pro Pro	405	410	415	420
cgc cgg gtg gga atc ttc gtg gat tat gag gcc cat gac att tct ttc				1591
Arg Arg Val Gly Ile Phe Val Asp Tyr Glu Ala His Asp Ile Ser Phe	425	430	435	
tac aat gtg act gac tgt ggc tcc cac atc ttc act ttc ccc cgc tat				1639
Tyr Asn Val Thr Asp Cys Gly Ser His Ile Phe Thr Phe Pro Arg Tyr	440	445	450	
ccc ttc cct ggg cgc ctc ctg ccc tat ttt agt cct tgc tac agc att				1687
Pro Phe Pro Gly Arg Leu Leu Pro Tyr Phe Ser Pro Cys Tyr Ser Ile	455	460	465	
gga acc aac aac act gct cct ctg gcc atc tgc tcc ctg gat ggg gag				1735
Gly Thr Asn Asn Thr Ala Pro Leu Ala Ile Cys Ser Leu Asp Gly Glu	470	475	480	
gac taa gaaagctacc accctaacca cagaggcttg gaattgggcc tggcccccat				1791
Asp *				
485				
ggggcttggga ggaccgagcc actgacaggt atcccctgaa actgagctga gcccagtatc				1851
caaggattcc tctgtctgat cctttggtct ttgctaccag gctgaagtct gtcatgaaac				1911
cacttatttt aaaaagcaga ggcccagtca aatgagcatt gcatcccatg agggaagcac				1971
gacagggctg atggtgagga tcagagcagt tctaaggtga ctcgttgggg taaggatcag				2031
gactttgtcc atgtagtagc caaccaccct cttccctgat tcccgtccgg tgtcacagtt				2091
cagtcagtga ggatgatgaa gtagatacag tcttcaggac accattagat gggctttccc				2151
aataggccaa aaaaatgctg cgcatacca gagctggttg ttgtgctgag gccagtcaga				2211
ggatgcttcc cctgaggttt gctataacta agcaaccttt atgtgactct caccttctga				2271

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cctcctggca agagaaattc agtgcagcag ggggacacag acctgcccac gccaccccac 2331
tgccgttccc tctctgagca caagctgggc aaatcactgt cccttggact ccagtagacc 2391
agtgtcctag tcttgccttt tttctctaag tggcaggatc agaaaacctg cgagcttttag 2451
tttgtatttt cactttatga atgaggaaac tgaaatggcc ttaagggagc aagttatttc 2511
tttttttttg agactcctca aaaaagaaaa aaaaaaaa 2549

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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (331)..(1047)

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tctcaccagc agagaacagc tgacgggtctt tccataagtg cttctaagag agatgtgtgg 180
taccctgggc taagtagaca gcaactgagc cctccctccc accccagggc tcccagagca 240
acaggggagc gggagcatag gacctggccg cagccaggaa tctacactga ccggtctcagc 300
ccatgaagta tcttgggctg aagtcacagg      atg aga ctg ttt gta tct gta 351
                                   Met Arg Leu Phe Val Ser Val
                                   1             5

act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc 399
Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
      10             15             20

tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca 447
Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
      25             30             35

gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc 495
Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser
      40             45             50             55

tct ctc tca ggc tgt ggg agc tgg cag ccc cgg aag ctg cca gtc ttc 543
Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe
      60             65             70

aag tcc ctc cgg cac atg agg cag gtc ctg ggt gcc cct tct ttc cgc 591
Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
      75             80             85

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atg ctg gcc tgg cac gtt ctc atg ggg aac cag gtg atc tgg aaa agc	639
Met Leu Ala Trp His Val Leu Met Gly Asn Gln Val Ile Trp Lys Ser	
90 95 100	
aga gac gtg gac ctc gtc cag tca gct ttt gaa gta ctt cgg acc atg	687
Arg Asp Val Asp Leu Val Gln Ser Ala Phe Glu Val Leu Arg Thr Met	
105 110 115	
ctt ccc gtg ggc tgc gtc cgc atc atc cca tac agc agc cag tac gag	735
Leu Pro Val Gly Cys Val Arg Ile Ile Pro Tyr Ser Ser Gln Tyr Glu	
120 125 130 135	
gag gcc tat cgg tgc aac ttc ctg ggg ctc agc ccg cac gtg cag atc	783
Glu Ala Tyr Arg Cys Asn Phe Leu Gly Leu Ser Pro His Val Gln Ile	
140 145 150	
ccc ccc cac gtg ctc tcc tca gag ttt gct gtc atc gtg gag gtc cac	831
Pro Pro His Val Leu Ser Ser Glu Phe Ala Val Ile Val Glu Val His	
155 160 165	
gca gcc gca cgt tcc acc ctc cac cct gtg ggg tgt gag gat gac cag	879
Ala Ala Ala Arg Ser Thr Leu His Pro Val Gly Cys Glu Asp Asp Gln	
170 175 180	
tct ctc agc aag tac gag ttt gtg gtg acc agt ggg agc cct gta gct	927
Ser Leu Ser Lys Tyr Glu Phe Val Val Thr Ser Gly Ser Pro Val Ala	
185 190 195	
gca gac cga gtg ggc ccc acc atc ctg aat aag att gaa gcg gct ctg	975
Ala Asp Arg Val Gly Pro Thr Ile Leu Asn Lys Ile Glu Ala Ala Leu	
200 205 210 215	
acc aac cag aac ctg tct gtg gat gtg gtg gac cag tgc ctc gtc tgc	1023
Thr Asn Gln Asn Leu Ser Val Asp Val Val Asp Gln Cys Leu Val Cys	
220 225 230	
ctc aag gag gag tgg atg aag taa gcaacagtgt ggggtgaggcc cctttgcttg	1077
Leu Lys Glu Glu Trp Met Lys *	
235	
cgaccctgga gaaaacctgg agctgtttcc aaaagaggag ctgggccgtg gccactgagg	1137
gaggagctga gagaagaggt tgggggcggg gttccaactc cacgtccgcc actgcaaagc	1197
tcaggtggcc tcgggaggcg gtcattcatgt ctgcctccgg ctccctgcatg gggaggtggg	1257
gggtctatcat gactagtgt gctgtgaaca ttcttgatcc ggtctctgac aaacacgcct	1317
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 <211> 441
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(416)

<400> 201

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accactgaag ctgatcatga gatgactgt atg ctg aca cac ccc ctt cag ggg 113
Met Leu Thr His Pro Leu Gln Gly
1 5

cct ggc ctt gac tta ggg ctg cac tgt atc ctc agc aac ggc ctt gca 161
Pro Gly Leu Asp Leu Gly Leu His Cys Ile Leu Ser Asn Gly Leu Ala
10 15 20

gga gcc cct ttt gga ctg ctt tcc cta ttc agc cca aag ttg ggg tgg 209
Gly Ala Pro Phe Gly Leu Leu Ser Leu Phe Ser Pro Lys Leu Gly Trp
25 30 35 40

tgg gag aag agg ggt tgg agt gaa tcc atc tct att caa att cca gct 257
Trp Glu Lys Arg Gly Trp Ser Glu Ser Ile Ser Ile Gln Ile Pro Ala
45 50 55

ggg att act cta gga gtc ttc ctg gct tgt ttt ggg ctc aaa ctt agc 305
Gly Ile Thr Leu Gly Val Phe Leu Ala Cys Phe Gly Leu Lys Leu Ser
60 65 70

tac att gtt tat tgg ctc cca aag tcg gga ttg aag agt gaa aag atg 353
Tyr Ile Val Tyr Trp Leu Pro Lys Ser Gly Leu Lys Ser Glu Lys Met
75 80 85

cag gca atg aat cct tct gca cac tcc tcc ccc cac att cct gac act 401
Gln Ala Met Asn Pro Ser Ala His Ser Ser Pro His Ile Pro Asp Thr
90 95 100

agt aag aac caa taa acacttggtg acggaaaaaa aaaaa 441
Ser Lys Asn Gln *
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      Met Lys Phe Gln Glu Cys His Ser Glu Val Met Arg His
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gga cag aaa ata tac ccc tca cat cat cgg att gag atg gca gtc gaa 158
Gly Gln Lys Ile Tyr Pro Ser His His Arg Ile Glu Met Ala Val Glu
      15             20             25

ata gct tca ttg aag tgt cag cac tca tcc atc aat caa tca ccc aca 206
Ile Ala Ser Leu Lys Cys Gln His Ser Ser Ile Asn Gln Ser Pro Thr
      30             35             40             45

agg aaa aat agc aac agt aca acg ggg tgg ctt tta tgg gat tta ctc 254
Arg Lys Asn Ser Asn Ser Thr Thr Gly Trp Leu Leu Trp Asp Leu Leu
           50             55             60

atg ggc ata ggg aat agc ggc tca aat gta gtt ctg aca tga aaagcaa 303
Met Gly Ile Gly Asn Ser Gly Ser Asn Val Val Leu Thr *
           65             70             75

ggtgctgata ttatttttta tgatgggagg atcataaagt gaattgagaa cagtgaggtc 363

tgtctttgct taacctattc aaccagaaat gaatggagct cgactggaaa ggaacagtct 423

tcagatgggt taagattgaa ggggtggactg gactctactg agcaccgtcc ttcaacaagg 483

aaattctatt aaaggaaaaat caatgcatta gtattgggggt tctcgtagct gttaaaaatt 543

gtctgtctcca atccaggggtt attaggccaa agttacataa ttcagatctc actgcaacca 603

tccaaaagtg gattctcgag cccttgctcc aatgggggga ggagatcaat acaattccca 663

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                                Met Pro
                                1

gtg ttg ggt tct gta tcc agt gta aca aaa aca gcc ttg aac aag aaa 164
Val Leu Gly Ser Val Ser Ser Val Thr Lys Thr Ala Leu Asn Lys Lys

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Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro			
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Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr			
35	40	45	50
ttt cag cct ccc agt agc att gga tgc agg aaa aaa tac att gac ggt			308
Phe Gln Pro Pro Ser Ser Ile Gly Cys Arg Lys Lys Tyr Ile Asp Gly			
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gaa aaa caa gcc gaa cca gtt gta gtt tta gat cct gtt tct aca cat			356
Glu Lys Gln Ala Glu Pro Val Val Val Leu Asp Pro Val Ser Thr His			
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gaa ccc caa acc aaa gac cag gtt gct gaa aaa gat cca act caa cac			404
Glu Pro Gln Thr Lys Asp Gln Val Ala Glu Lys Asp Pro Thr Gln His			
85	90	95	
aag gag gat gaa ggc gaa att caa cca gaa aac aaa gaa gac agc att			452
Lys Glu Asp Glu Gly Glu Ile Gln Pro Glu Asn Lys Glu Asp Ser Ile			
100	105	110	
gaa aac gtg aga gag aca gac agc tcc aac tgc tga tcca taaaccagaa			502
Glu Asn Val Arg Glu Thr Asp Ser Ser Asn Cys *			
115	120	125	
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cttttgtaag tagcaactat aaacataagt aagctgttta gcaaaacaca cattcctagt			682
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gagttcttat gtacagtatg gtgaagataa gtgacaagca cacatttttc ttgcttcact			1342

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acgcagactg acgtgctttt gggaggggtgt gccgtgaagc ctgcagtacg tgtgccgtga 180
ggctcatagt tg atg agg gac ttt ccc tgc tcc acc gtc act ccc cca 228
Met Arg Asp Phe Pro Cys Ser Thr Val Thr Pro Pro
1 5 10
act ctg ccc gcc tct gtc ccc gcc tca gtc ccc gcc tcc atc ccc gcc 276
Thr Leu Pro Ala Ser Val Pro Ala Ser Val Pro Ala Ser Ile Pro Ala
15 20 25
tct gtc ccc tgg cct tgg cgg cta ttt ttg cca cct gcc ttg ggt gcc 324
Ser Val Pro Trp Pro Trp Arg Leu Phe Leu Pro Pro Ala Leu Gly Ala
30 35 40
cag gag tcc cct act gct gtg ggc tgg ggt tgg ggg cac agc agc ccc 372
Gln Glu Ser Pro Thr Ala Val Gly Trp Gly Trp Gly His Ser Ser Pro
45 50 55 60
aag cct gag agg ctg gag ccc atg gct agt ggc tca tcc cca ctg cat 420
Lys Pro Glu Arg Leu Glu Pro Met Ala Ser Gly Ser Ser Pro Leu His
65 70 75
tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat 468
Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn
80 85 90
gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg 516
Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu
95 100 105
tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga 564
Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys *
110 115 120

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Met Ala Ser Val Ala Ser Cys Asp Ser Arg Pro Ser Ser
1 5 10
gac gag ctc cct gga gac ccc tct tca caa gaa gaa gat gag gac tat 157
Asp Glu Leu Pro Gly Asp Pro Ser Ser Gln Glu Glu Asp Glu Asp Tyr
15 20 25
gat ttt gaa gat cgg gtc agc gac tcg ggt tca tat tcc tca gcg agt 205
Asp Phe Glu Asp Arg Val Ser Asp Ser Gly Ser Tyr Ser Ser Ala Ser
30 35 40 45
agc gat tat gat gat ctt gag cct gaa tgg ctg gac agt gtg cag aaa 253
Ser Asp Tyr Asp Asp Leu Glu Pro Glu Trp Leu Asp Ser Val Gln Lys
50 55 60
aat gga gag ctg ttt tat ttg gaa ttg agt gag gat gaa gaa gaa agc 301
Asn Gly Glu Leu Phe Tyr Leu Glu Leu Ser Glu Asp Glu Glu Glu Ser
65 70 75
ctc ctt cct gag aca cca act gtg aac cat gtc agg ttc agt gaa aat 349
Leu Leu Pro Glu Thr Pro Thr Val Asn His Val Arg Phe Ser Glu Asn
80 85 90
gag att atc att gaa gat gac tac aaa gaa aga aaa aag tat gaa ccc 397
Glu Ile Ile Ile Glu Asp Asp Tyr Lys Glu Arg Lys Lys Tyr Glu Pro
95 100 105
aaa ctc aag cag ttt acc aaa att tta aga agg aaa aga ctt tta ccc 445
Lys Leu Lys Gln Phe Thr Lys Ile Leu Arg Arg Lys Arg Leu Leu Pro
110 115 120 125
aag cgc tgc aat aaa aaa aat agc aat gac aat gga cca gta tcc att 493
Lys Arg Cys Asn Lys Lys Asn Ser Asn Asp Asn Gly Pro Val Ser Ile
130 135 140

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Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg	
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Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile	
160 165 170	
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Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile	
175 180 185	
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His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly	
190 195 200 205	
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Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys	
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Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val	
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Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
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Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
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Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
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Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
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Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
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Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	

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Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt	1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
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Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
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Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	
gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct	1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala	
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Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr	
465 470 475	
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Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu	
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Glu Ala Ala Asp Phe Ala Glu Leu Ser Glu Asp Tyr Tyr Asp Met Arg	
495 500 505	
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Arg Leu Tyr Thr Ile Leu Gly Ser Ser Leu Phe Tyr Lys Gly Tyr Leu	
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Ile Cys Ser His Leu Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr	
530 535 540	
tgt cgc cac tat tgc ctg ctg cct tta gca gca aaa caa aga att ggt	1741
Cys Arg His Tyr Cys Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly	
545 550 555	
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560 565 570	
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Leu Ala Asp Ser Ser Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr	
575 580 585	
ttt ttg cta gtt gtt ggc ttg aaa cat tat atg cta tgt gta cta tta	1885

Phe	Leu	Leu	Val	Val	Gly	Leu	Lys	His	Tyr	Met	Leu	Cys	Val	Leu	Leu	
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Glu	Ala	Gly	Gly	Cys	Ala	Ser	Lys	Ala	Ile	Gly	Ser	Pro	Gly	Pro	Asp	
				610					615					620		
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Cys	Val	Tyr	Val	Asp	Gln	Val	Lys	Thr	Thr	Leu	His	Gln	Leu	Asp	Gly	
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Val	Asp	Ser	Arg	Ile	Asp	Glu	Arg	Leu	Ala	Ser	Ser	Pro	Val	Pro	Cys	
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Ser	Leu	Thr	Thr	Ser	Pro	Ile	Leu	Ser	Arg	Leu	Gln	Gly	Thr	Ser	Lys	
670					675					680					685	
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Val	Ala	Thr	Ser	Pro	Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser	
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Leu	Lys	Thr	Arg	Lys	Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp	
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aat	ggg	tgt	gaa	ggg	gga	gaa	gat	gat	ggc	ttt	agc	ccc	cat	act	aca	2269
Asn	Gly	Cys	Glu	Gly	Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr	
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Pro	Asp	Ala	Val	Arg	Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu	
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Pro	Asn	Pro	Phe	His	Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys	
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Glu	Leu	Glu	Ile	Tyr	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn	
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Thr	Leu	Phe	His	Tyr	Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile	
		800					805					810				
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Thr	Pro	Thr	Leu	Glu	Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro	

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Phe Gln Gln Thr Leu Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly			
	850	855	860
gac cat tca gat tct gca aag tca gtg tct tct ctt aac cct gtt aaa			2701
Asp His Ser Asp Ser Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys			
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Glu His Gly Val Leu Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln			
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Leu His Pro Lys Pro Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val			
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aca gaa att gcc att gaa ata gct ttt aaa ttg ttc ttt ggg tta acc			2893
Thr Glu Ile Ala Ile Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr			
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Leu *			
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 <222> (71)..(2836)

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Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
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335 340 345	
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Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
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tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa	1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt	1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
400 405 410	
atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct	1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct	1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	

gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct	1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala	
450 455 460	
tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca	1501
Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr	
465 470 475	
ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg	1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu	
480 485 490	
gag gct gca gat ttt gca gaa ctg ggt tat ttg ata tgc agt cat ttg	1597
Glu Ala Ala Asp Phe Ala Glu Leu Gly Tyr Leu Ile Cys Ser His Leu	
495 500 505	
ccc aag gat gat ctt att gat att gcc gta tac tgt cgc cac tat tgc	1645
Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr Cys Arg His Tyr Cys	
510 515 520 525	
ctg ctg cct tta gca gca aaa caa aga att ggt cag ttg atc ata ttg	1693
Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly Gln Leu Ile Ile Trp	
530 535 540	
aga gaa gtg ttt cct cag cat cac ctc cga cct ttg gca gac tca agc	1741
Arg Glu Val Phe Pro Gln His His Leu Arg Pro Leu Ala Asp Ser Ser	
545 550 555	
act gaa gtc ttt ccg gaa cct gaa gga aga tat ttt ttg cta gtt gtt	1789
Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr Phe Leu Leu Val Val	
560 565 570	
ggc ttg aaa cat tat atg cta tgt gta cta tta gaa gct gga ggt tgc	1837
Gly Leu Lys His Tyr Met Leu Cys Val Leu Leu Glu Ala Gly Gly Cys	
575 580 585	
gca tcc aaa gct att ggg agt cct gga cca gac tgt gta tat gtg gat	1885
Ala Ser Lys Ala Ile Gly Ser Pro Gly Pro Asp Cys Val Tyr Val Asp	
590 595 600 605	
caa gtc aaa aca act ctt cac cag ctg gat gga gta gat tct cgc ata	1933
Gln Val Lys Thr Thr Leu His Gln Leu Asp Gly Val Asp Ser Arg Ile	
610 615 620	
gat gaa cgg cta gca tct tct cca gtc ccc tgt ttg tct tgt gct gac	1981
Asp Glu Arg Leu Ala Ser Ser Pro Val Pro Cys Leu Ser Cys Ala Asp	
625 630 635	
tgg ttc ctt act gga tca cgt gaa aaa aca gat agc ttg acc act tcg	2029
Trp Phe Leu Thr Gly Ser Arg Glu Lys Thr Asp Ser Leu Thr Thr Ser	
640 645 650	
cct att ctc agt agg cta caa ggt act tcc aaa gta gca act tct cca	2077
Pro Ile Leu Ser Arg Leu Gln Gly Thr Ser Lys Val Ala Thr Ser Pro	
655 660 665	
aca tgc aga aga acg ctt ttt ggt gac tat tcc tta aag aca cgc aag	2125

Thr Cys Arg Arg Thr Leu Phe Gly Asp Tyr Ser Leu Lys Thr Arg Lys	
670 675 680 685	
cct agt cct tcc tgt agt agt gga gga tct gac aat ggt tgt gaa ggt	2173
Pro Ser Pro Ser Cys Ser Ser Gly Gly Ser Asp Asn Gly Cys Glu Gly	
690 695 700	
gga gaa gat gat ggc ttt agc ccc cat act aca ccg gat gca gta cgg	2221
Gly Glu Asp Asp Gly Phe Ser Pro His Thr Thr Pro Asp Ala Val Arg	
705 710 715	
aag caa aga gaa tct cag ggc tct gat ggt tta gaa gaa agt ggg acc	2269
Lys Gln Arg Glu Ser Gln Gly Ser Asp Gly Leu Glu Glu Ser Gly Thr	
720 725 730	
ttg ctt aag gtc act aaa aag aag tct act ctt cca aat cca ttt cat	2317
Leu Leu Lys Val Thr Lys Lys Lys Ser Thr Leu Pro Asn Pro Phe His	
735 740 745	
ttg gga aac ttg aaa aag gac ctt cca gaa aaa gaa tta gaa ata tat	2365
Leu Gly Asn Leu Lys Lys Asp Leu Pro Glu Lys Glu Leu Glu Ile Tyr	
750 755 760 765	
aac aca gtg aaa ctg aca tct ggt cct gag aac aca ctt ttc cac tac	2413
Asn Thr Val Lys Leu Thr Ser Gly Pro Glu Asn Thr Leu Phe His Tyr	
770 775 780	
gtt gcc tta gaa aca gtg caa gga atc ttt att act cct acc ctt gaa	2461
Val Ala Leu Glu Thr Val Gln Gly Ile Phe Ile Thr Pro Thr Leu Glu	
785 790 795	
gag gtg gca cag cta agt ggc tct atc cac cct cag cta ata aag aat	2509
Glu Val Ala Gln Leu Ser Gly Ser Ile His Pro Gln Leu Ile Lys Asn	
800 805 810	
ttc cat cag tgt tgt ctt tcc att cgt gca gtt ttc caa cag aca ttg	2557
Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val Phe Gln Gln Thr Leu	
815 820 825	
gtg gaa gag aaa aag aaa gga cta aat agt gga gac cat tca gat tct	2605
Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly Asp His Ser Asp Ser	
830 835 840 845	
gca aag tca gtg tct tct ctt aac cct gtt aaa gaa cat ggt gtg ttg	2653
Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys Glu His Gly Val Leu	
850 855 860	
ttt gaa tgt tca cct gga aac tgg act gat cag aaa aaa gca cca cca	2701
Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln Lys Lys Ala Pro Pro	
865 870 875	
gtt atg gct tac tgg gta gta ggg aga ctt ttt ctt cat cca aaa cct	2749
Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe Leu His Pro Lys Pro	
880 885 890	
caa gaa ctt tat gtc tgt ttt cat gac tca gtc aca gaa att gcc att	2797
Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val Thr Glu Ile Ala Ile	

895	900	905	
gaa ata gct ttt aaa ttg ttc ttt ggg tta acc ttg tag ctgtgctttc			2846
Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr Leu *			
910	915	920	
ttgatgcgta gaaacacgtg catggaggat caaacactgt cagaattgct gaaatcaata			2906
cacaaagaga taaagtttag cttcttttta ctattcaata ttgaacataa tattgttaaa			2966
tattgagatg aaatgctggt ggatttgata cattaaatct taatgtaata ttgtaagact			3026
tttgagaata tacttgatta aaatgtgaaa gaagggttg ttaacttatt gctatttttg			3086
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 <222> (1)...(1595)
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gtggaaacat gtcttgcgac acccaccagc gactgctaca acccagcggc ggcgntgntg			120
gtcacggagc tggggccggg ggcagcccg gagctggctg gggccctgc aaggaccgtc			180
tcgggcctgc ccagccaaga gtgtgtgcaa cacatcgggtg ctgagcagca gcctgcagtc			240
actggagtat ctcatcaacg acatccggcc gccctgcatc aaggagcaga tgctgggcaa			300
gggct	atg aga cgg tgg ccg tgc ccc ggc tac tcg acc acc agc atg		347
	Met Arg Arg Trp Pro Cys Pro Gly Tyr Ser Thr Thr Ser Met		
	1 5 10		
ccc aca tcc gcc tac ccg tct aca gat aag gcc tgc ctg cgg aca tac			395
Pro Thr Ser Ala Tyr Pro Ser Thr Asp Lys Ala Cys Leu Arg Thr Tyr			
15	20	25 30	
gga cat gcg gac agg gcg cag agc cgg gag gca ggc cgc aga aca ggg			443
Gly His Ala Asp Arg Ala Gln Ser Arg Glu Ala Gly Arg Arg Thr Gly			
	35	40 45	

tgg gcg gct cgc agg ggc gct cag ccc cac cct gtg cct gct gat gcc	491
Trp Ala Ala Arg Gly Ala Gln Pro His Pro Val Pro Ala Asp Ala	
50 55 60	
cac agg gga gcc agg ctg gct gcc gcc tcg ctg tgg ccg gat gga ggg	539
His Arg Gly Ala Arg Leu Ala Ala Ala Ser Leu Trp Pro Asp Gly Gly	
65 70 75	
tgg cag ggc aac ctc aca tac caa ggc ccc tcc cca cca tcg gtt gcc	587
Trp Gln Gly Asn Leu Thr Tyr Gln Gly Pro Ser Pro Pro Ser Val Ala	
80 85 90	
cca gga cac agt gag ggc ctg ggg gca gcc act gac gcc cat gcc ttc	635
Pro Gly His Ser Glu Gly Leu Gly Ala Ala Thr Asp Ala His Ala Phe	
95 100 105 110	
ctt tat cta agc tgg cag agg cag gga gag aga aac cac tca aaa aca	683
Leu Tyr Leu Ser Trp Gln Arg Gln Gly Glu Arg Asn His Ser Lys Thr	
115 120 125	
gga atg gtt ctt tct ggg cct cct ggg aca ggg gcc cag gcc aag gtg	731
Gly Met Val Leu Ser Gly Pro Pro Gly Thr Gly Ala Gln Ala Lys Val	
130 135 140	
ggg tgc agg agg aaa cag gcg cac cag agt cag ggt ggg ggc agg gca	779
Gly Cys Arg Arg Lys Gln Ala His Gln Ser Gln Gly Gly Gly Arg Ala	
145 150 155	
gcc ccc cca ggg gtc agg cag ctg tgt ctc ccc aca ctg gct ccc cag	827
Ala Pro Pro Gly Val Arg Gln Leu Cys Leu Pro Thr Leu Ala Pro Gln	
160 165 170	
tat tct gga aaa ggg gta cag gag gcc gat agg aag tca ctg ggc cca	875
Tyr Ser Gly Lys Gly Val Gln Glu Ala Asp Arg Lys Ser Leu Gly Pro	
175 180 185 190	
aag tgt ctc ccc acc agc cag gtg aag acc act ctg aca gag gct cca	923
Lys Cys Leu Pro Thr Ser Gln Val Lys Thr Thr Leu Thr Glu Ala Pro	
195 200 205	
ggg act ata cca gtc ccc ctg ttc ctc ctt ccc cta ccc cca cca ttc	971
Gly Thr Ile Pro Val Pro Leu Phe Leu Leu Pro Leu Pro Pro Pro Phe	
210 215 220	
ctt cct aac aca gag ttg cac ccc cat ccc cat tct cca aac cct gga	1019
Leu Pro Asn Thr Glu Leu His Pro His Pro His Ser Pro Asn Pro Gly	
225 230 235	
cta cca tat tcc ccc ttc cct cca ata cat ctt ata ggg ctg ctg ggt	1067
Leu Pro Tyr Ser Pro Phe Pro Pro Ile His Leu Ile Gly Leu Leu Gly	
240 245 250	
aca gtt gtt cag gct gtg cac tgc aca agg gca cct tgt cca agg aga	1115
Thr Val Val Gln Ala Val His Cys Thr Arg Ala Pro Cys Pro Arg Arg	
255 260 265 270	

cac cac ttt cac cca aac ttg tat att tat tac aat ttt ctg cat ctt His His Phe His Pro Asn Leu Tyr Ile Tyr Tyr Asn Phe Leu His Leu 275 280 285	1163
gag gaa ggg gcg tca ttt tcc tgt tgc cac aaa ggc acc aca ggg gct Glu Glu Gly Ala Ser Phe Ser Cys Ser His Lys Gly Thr Thr Gly Ala 290 295 300	1211
aac agt ggg cct gca atc tta gat ccc atc ctt gcc ttc ttc gag gga Asn Ser Gly Pro Ala Ile Leu Asp Pro Ile Leu Ala Phe Phe Glu Gly 305 310 315	1259
tct ctt ggg acc ctc ctg gtt tta act ggg agg ccc aga cca act cct Ser Leu Gly Thr Leu Leu Val Leu Thr Gly Arg Pro Arg Pro Thr Pro 320 325 330	1307
ttc ctg caa acc acc ctc caa ggc ctg tcc cac acg atc aag gca ggg Phe Leu Gln Thr Thr Leu Gln Gly Leu Ser His Thr Ile Lys Ala Gly 335 340 345 350	1355
aaa gat agg cag gag tcc cct cac gaa gtc ctc aag tcc tgg ccc ctc Lys Asp Arg Gln Glu Ser Pro His Glu Val Leu Lys Ser Trp Pro Leu 355 360 365	1403
tgg cgc tct gga agc ggt act gta tct ctc tcc aag gcc tgg tca agc Trp Arg Ser Gly Ser Gly Thr Val Ser Leu Ser Lys Ala Trp Ser Ser 370 375 380	1451
act aag tgc att tac aaa tct ctg aga atg ttt ttt tta tac taa aat Thr Lys Cys Ile Tyr Lys Ser Leu Arg Met Phe Phe Leu Tyr * 385 390 395	1499
tgaccattat attctactgt gagaagtgc gctctgcacta tattgtttta aaaacgaaga	1559
gaaagaagaa aaaggaaaac acagaaaaaa aaaaaa	1595

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<212> DNA
<213> Homo sapiens

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<222> (288)..(1235)

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gccgcttctc tgcccagatt aggtttcgcc cagcgcaatt tctttctcta tgtactttgc	180
gaataagttt cggagcatcg gttaacagcc tatgggtgaa atttggtttt cattcatgaa	240

tgagaaatta ttcttgacag aagtatttta aaagaaaaat ctttacg	atg gcc tca	296
	Met Ala Ser	
	1	
gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt gcc ctg tta		344
Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe Ala Leu Leu		
5 10 15		
caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga aaa ggt aaa		392
Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly Lys Gly Lys		
20 25 30 35		
ggt cga aat act gga aag tct caa act tta gga agc aag tca act aca		440
Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys Ser Thr Thr		
40 45 50		
aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa cag caa cag		488
Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu Gln Gln Gln		
55 60 65		
agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa att ccc cag		536
Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys Ile Pro Gln		
70 75 80		
aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt cca ttg tca		584
Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu Pro Leu Ser		
85 90 95		
aac cca gta cag aag gat tca cga gaa gaa aat tgg caa gag tgg aga		632
Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln Glu Trp Arg		
100 105 110 115		
caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca gat ctt gag		680
Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala Asp Leu Glu		
120 125 130		
aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac aaa aag gag		728
Lys Ala Leu Leu Ser Lys Leu Glu Tyr Glu Glu His Lys Lys Glu		
135 140 145		
tat gaa gat gct gaa aat act tca act cag tcc aaa gtt atg aat aaa		776
Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val Met Asn Lys		
150 155 160		
aaa gat aaa aga aag aat cat cag gga aaa gac aga cct ctc aca gta		824
Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro Leu Thr Val		
165 170 175		
tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa aag act gag		872
Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys Lys Thr Glu		
180 185 190 195		
gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag tta gag ctt		920
Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys Leu Glu Leu		
200 205 210		
gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta atc act caa		968

Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val Ile Thr Gln	
215 220 225	
tgg gag gca aag tat aag gaa gta aag gca aga aat gca caa tta ttg	1016
Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala Gln Leu Leu	
230 235 240	
aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa ata ctt ctg	1064
Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu Ile Leu Leu	
245 250 255	
caa gtt gat gaa tca caa agt atc aag aat gag ctc act att cag gtg	1112
Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr Ile Gln Val	
260 265 270 275	
act tca ctt cat gct gca tta gaa caa gaa aga tct aaa gtg aaa gta	1160
Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys Val Lys Val	
280 285 290	
tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa ggg aaa aga	1208
Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys Gly Lys Arg	
295 300 305	
aac tct gaa tcc gac cag tgt agg tga ttaca ttagcctttg aagtcaacac	1260
Asn Ser Glu Ser Asp Gln Cys Arg *	
310 315	
aaagtttaaa acttcagga ttttgcaaag ttgtatatat ttaatgctgt gcaactgcta	1320
aactatgcag tttttgttga aggaactaaa agcaactagc tccctaattgg tctataat	1380
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tctacagtta tgccccaata gtagccaaag gaaaaagggg gaagatgata gtttgactaa	120
acaaatacca gttcatacat tcttgttcca ataggagtt atg gga gga aaa att	174
Met Gly Gly Lys Ile	
1 5	
att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt	222

cctaacaagc acgcagttcc tgatgattgg cctcaggtcc cagagagctc cagcaggtgt 480

aggagtccat gggcctgaca cctttgctgg tctctgctgg atcccgacga agtcaggtcc 540

tttctggaaa ggggttcgaa gtccacatac tctccgact acccccagga agtacgtcct 600

tgggtgtgtg tttgggggag tgagaggaat gaagaaccac tccccctata gcctggccat 660

actccccaaag atgaggggcag taagggtgtg aggaccctgg aagtaacttg cttttctcaa 720

cttctcagga gaaggccatc agcatttggg agtcaaagaa tttctttttt gaacttgagc 780

ctctgccagg ggcctgggaa gctgtcaagg ag atg gcc agc cta caa aac act 833
Met Ala Ser Leu Gln Asn Thr
1 5

gac gtc ttc atc tgc aca agc ccc atc aag atg ttc aag tac tgt ccc 881
Asp Val Phe Ile Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro
10 15 20

tat gag aag tat gcc tgg gtg gag aag tac ttt ggc cct gac ttt ctg 929
Tyr Glu Lys Tyr Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu
25 30 35

gag cag att gtg ctg acc aga gac aag acc gtg gtc tct gct gac ctt 977
Glu Gln Ile Val Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu
40 45 50 55

ctc ata gac gac cgg ccg gac atc aca ggg gcc gag cca acc ccc agc 1025
Leu Ile Asp Asp Arg Pro Asp Ile Thr Gly Ala Glu Pro Thr Pro Ser
60 65 70

tgg gag cat gtc ctc ttc acc gcc tgc cac aac cag cac ctg cag ctg 1073
Trp Glu His Val Leu Phe Thr Ala Cys His Asn Gln His Leu Gln Leu
75 80 85

cag ccc ccc cgc cgc agg ctg cac tgc tgg gcg gac gac tgg aag gcc 1121
Gln Pro Pro Arg Arg Arg Leu His Ser Trp Ala Asp Asp Trp Lys Ala
90 95 100

att ctg gac agc aag cgg ccc tgc tga gctgg actgtgcttc gggctcctct 1173
Ile Leu Asp Ser Lys Arg Pro Cys *
105 110

gtggggctct gacctcaggg ctcccagctc ggggcctgtg gggccagtat gctggctctgg 1233

gagtccctcc tagactcctg ggccccatga cctcctgctg catgtccctt cccttcccca 1293

gccccctgcca ggccttaacc tgatcacggg gcagggctgg gccctctggg cgcttgagca 1353

taacaacgtg gtcccaggcc gttcagcctg acctcaggca gcaggcacca agctgccaga 1413

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 gctggggggac gatactggcc ctggcctcga ccagcttaaa ggtttttcac acctttgttc 1773
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 aaccaggggt gctaaaaata accaggccca aatggaccag aagcaactcc catggacttt 180
 ggcttgcagt catggtcaga agagatacag gcacagatcc cactattacg aaggagccaa 240
 aatatctgcc aagataaaaa tggaagtaac tcctctggat ttatgtgtcc aggggtggat 300
 atggaaagac ttgtgaagta ttaatcaaaa atcaccgag gctttttcag actattattc 360
 aaatgacaca gaatgaagac ctccgagaaa acatgtacgg caagttctgg agcatttgtc 420
 tcagcacagt gaaagccagt acctaaagat tctaacaagc cttgctgaag ttgctacaac 480
 aaatggtcac aaactgctta gcctctctag caattatgat gctcaa atg aag agc 535
 Met Lys Ser
 1
 ctt tta agg att gtg aga atg ttt tgt cac gtc ttt cga att ggt cca 583
 Leu Leu Arg Ile Val Arg Met Phe Cys His Val Phe Arg Ile Gly Pro
 5 10 15
 tcc tcc ccc agt aat gga att gat atg ggc tac aat ggg aat aaa act 631
 Ser Ser Pro Ser Asn Gly Ile Asp Met Gly Tyr Asn Gly Asn Lys Thr
 20 25 30 35
 cca aaa agc cag gtg ttc aag cct ctg gaa ttg ctt tgg cac tcg tta 679
 Pro Lys Ser Gln Val Phe Lys Pro Leu Glu Leu Leu Trp His Ser Leu
 40 45 50

gat gaa tgg cta gtt tta ata gcc cca gaa ttg atg aaa aac aaa aga Asp Glu Trp Leu Val Leu Ile Ala Pro Glu Leu Met Lys Asn Lys Arg	727
55 60 65	
gac tca aca gag atc act tct att tta ctg aaa caa aaa ggc caa gat Asp Ser Thr Glu Ile Thr Ser Ile Leu Leu Lys Gln Lys Gly Gln Asp	775
70 75 80	
caa gat gct gct tcc att cct cca ttt gaa cct cca gga cct ggg agc Gln Asp Ala Ala Ser Ile Pro Pro Phe Glu Pro Pro Gly Pro Gly Ser	823
85 90 95	
tat gaa aat ctg tcc act ggc aca agg gaa tct aaa cca gat gct ctt Tyr Glu Asn Leu Ser Thr Gly Thr Arg Glu Ser Lys Pro Asp Ala Leu	871
100 105 110 115	
gca ggg aga cag gaa gcc agt gca gat tgt cag gat gtt att tct atg Ala Gly Arg Gln Glu Ala Ser Ala Asp Cys Gln Asp Val Ile Ser Met	919
120 125 130	
aca gct aac cgg cta agt gct gtc att caa gct ttt tac atg tgc tgt Thr Ala Asn Arg Leu Ser Ala Val Ile Gln Ala Phe Tyr Met Cys Cys	967
135 140 145	
tct tgt cag atg cct ccg gga atg act tca cct cgt ttc att gaa ttt Ser Cys Gln Met Pro Pro Gly Met Thr Ser Pro Arg Phe Ile Glu Phe	1015
150 155 160	
gtc tgc aaa cat gat gaa gtt tta aaa tgc ttt gtt aat aga aat ccc Val Cys Lys His Asp Glu Val Leu Lys Cys Phe Val Asn Arg Asn Pro	1063
165 170 175	
aaa att ata ttt gac cac ttt cac ttt ctc ctt gaa tgt cct gag ttg Lys Ile Ile Phe Asp His Phe His Phe Leu Leu Glu Cys Pro Glu Leu	1111
180 185 190 195	
atg tca aga ttc atg cat atc ata aaa gca cag cct ttt aaa gat cgc Met Ser Arg Phe Met His Ile Ile Lys Ala Gln Pro Phe Lys Asp Arg	1159
200 205 210	
tgt gaa tgg ttc tat gaa cat ttg cat tca gga cag cca gat tca gat Cys Glu Trp Phe Tyr Glu His Leu His Ser Gly Gln Pro Asp Ser Asp	1207
215 220 225	
atg gtg cac agg cca gtg aat gaa aat gat atc ctg ctg gtt cac aga Met Val His Arg Pro Val Asn Glu Asn Asp Ile Leu Leu Val His Arg	1255
230 235 240	
gat tct att ttt agg agt agc tgt gaa gtt gtg tca aaa gca aat tgt Asp Ser Ile Phe Arg Ser Ser Cys Glu Val Val Ser Lys Ala Asn Cys	1303
245 250 255	
gca aag cta aag caa ggg att gct gta cgg ttc cat gga gaa gaa ggc Ala Lys Leu Lys Gln Gly Ile Ala Val Arg Phe His Gly Glu Glu Gly	1351
260 265 270 275	
atg ggt caa ggt gtt gtg cgt gag tgg ttt gat att ctg tcc aat gag	1399

Met Gly Gln Gly Val Val Arg Glu Trp Phe Asp Ile Leu Ser Asn Glu	
280 285 290	
ata gtc aat cct gat tat gca ttg ttt acc cag tca gct gat gga aca	1447
Ile Val Asn Pro Asp Tyr Ala Leu Phe Thr Gln Ser Ala Asp Gly Thr	
295 300 305	
act ttt cag cct aat agc aac tct tat gta aat cct gat cac ttg aac	1495
Thr Phe Gln Pro Asn Ser Asn Ser Tyr Val Asn Pro Asp His Leu Asn	
310 315 320	
tat ttt cgg ttt gct ggg cag atc ttg gga tta gcg ttg aac cac agg	1543
Tyr Phe Arg Phe Ala Gly Gln Ile Leu Gly Leu Ala Leu Asn His Arg	
325 330 335	
cag ctg gtc aat att tac ttc aca cga tcc ttc tac aag cac att ctt	1591
Gln Leu Val Asn Ile Tyr Phe Thr Arg Ser Phe Tyr Lys His Ile Leu	
340 345 350 355	
ggt att cct gta aat tac caa gat gtg gca tcc att gat cca gaa tat	1639
Gly Ile Pro Val Asn Tyr Gln Asp Val Ala Ser Ile Asp Pro Glu Tyr	
360 365 370	
gcg aaa aat ttg caa tgg att tta gat aat gat ata agt gat ctg ggt	1687
Ala Lys Asn Leu Gln Trp Ile Leu Asp Asn Asp Ile Ser Asp Leu Gly	
375 380 385	
cta gaa cta act ttt tct gtt gag act gat gtg ttt gga gca atg gaa	1735
Leu Glu Leu Thr Phe Ser Val Glu Thr Asp Val Phe Gly Ala Met Glu	
390 395 400	
gag gtg cct ttg aaa cct ggg ggt ggg agt att ctt gtg aca caa aat	1783
Glu Val Pro Leu Lys Pro Gly Gly Gly Ser Ile Leu Val Thr Gln Asn	
405 410 415	
aat aaa gcg gag tac gtc cag ctt gtt act gaa ctt cga atg aca aga	1831
Asn Lys Ala Glu Tyr Val Gln Leu Val Thr Glu Leu Arg Met Thr Arg	
420 425 430 435	
gcc att cag cct cag atc aat gct ttt tta cag ggc ttt cat atg ttc	1879
Ala Ile Gln Pro Gln Ile Asn Ala Phe Leu Gln Gly Phe His Met Phe	
440 445 450	
att cca ccc tcc ctg ata cag ctt ttt gat gaa tat gaa ttg gag cta	1927
Ile Pro Pro Ser Leu Ile Gln Leu Phe Asp Glu Tyr Glu Leu Glu Leu	
455 460 465	
ctg ctt tct ggc atg cca gaa att gat gtg agt gat tgg ata aaa aat	1975
Leu Leu Ser Gly Met Pro Glu Ile Asp Val Ser Asp Trp Ile Lys Asn	
470 475 480	
aca gaa tac aca agt ggc tat gaa aga gaa gat cca gtt att cag tgg	2023
Thr Glu Tyr Thr Ser Gly Tyr Glu Arg Glu Asp Pro Val Ile Gln Trp	
485 490 495	
ttc tgg gaa gtt gta gaa gac att act caa gag gag aga gtt ctt ctg	2071
Phe Trp Glu Val Val Glu Asp Ile Thr Gln Glu Glu Arg Val Leu Leu	

500	505	510	515	
tta cag ttt gtt acg ggc agt tcc agg gtc cca cat ggt ggg ttt gct				2119
Leu Gln Phe Val Thr Gly Ser Ser Arg Val Pro His Gly Gly Phe Ala				
	520	525	530	
aat atc atg ggt gga agt gga ttg caa aac ttt aca atc gct gct gtg				2167
Asn Ile Met Gly Gly Ser Gly Leu Gln Asn Phe Thr Ile Ala Ala Val				
	535	540	545	
cca tat act cca aat ctt tta cca act tca agc aca tgc atc aac atg				2215
Pro Tyr Thr Pro Asn Leu Leu Pro Thr Ser Ser Thr Cys Ile Asn Met				
	550	555	560	
ctc aag tta cct gaa tac cca agt aaa gaa ata ctc aag gac aga ctt				2263
Leu Lys Leu Pro Glu Tyr Pro Ser Lys Glu Ile Leu Lys Asp Arg Leu				
	565	570	575	
ctt gtg gca cta cat tgt ggc agc tat ggt tac aca atg gca taa tga				2311
Leu Val Ala Leu His Cys Gly Ser Tyr Gly Thr Met Ala *				
	580	585	590	
agtctggaaa actcctctga ctactgatgc acaattcaga atggcagaag taatttgga				2371
aaatgtcaac aaaaaagcag cctaaatgca acccataggc agggctgatg cttccaattt				2431
ataaaggatc atcaggtttt ctgtttctct cttttccctt ttatgttttc tctgtttgta				2491
tacaattaga aaatataaaa tcacagtaga ttttattttt taaaatgcta actgaaagta				2551
atagagactg tccttttttca taattaattt tatccaagat tgtattaagg caaaatctga				2611
ttctacattc cacctctgct atgtaactgt cttgttaaaa ggggtgttttc tcctaatttc				2671
tgatatatta tatgagggtca tccagctggg gtgttctttt gcatgtaaac tgccatttat				2731
attttagaaa actattgtat agaatggatt tagattgtct ataaagccac aaatacgtat				2791
tttgccacag tgtattctat attgcaatga tttttttagc attttaatat tttaatatat				2851
attgtaaaat ttagactgat gatactaaca gttgatgaaa tgacatatataa tttatatatg				2911
aaagcttacg ctatatgtga tgaattattt gcatctttca gtggccagtt ttccatatgt				2971
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<400> 212

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tggctcctcc tccagcccct tggctctctg ctgctcccc cggggcagga gaaagaagga      180
aagagggcca ggggtcccct gccccaccac tttccatgat gacaagagat gggaaggtag      240
ccaggcagca acagtgtacg gcgacattgg agcggacctc acggcgacct caatttccac      300
tgcgcctcct ccagagcctt aagaagctgc aggcctgtgg tgcccagcac caagtgcaga      360
tggacacggg tcttcatccc cttccttggc accttccatt taagccaaac attagaaatg      420
taaagaaggg cttgtttctg gagtttccag tttgttccat tcatctactc agagcatctt      480
ctttggacaa cactgtctgc agctgtgggc ccactccaag gggaggcgat ggactgtagg      540
tctgtggagc tcagcacagg gctgtgccac ggacgcgggt gtcagtgaag tcacgcgcac      600
tttcagatgg aattctcctc cccgatgtga aca atg aac gac ggt gtc act ttc      654
                               Met Asn Asp Gly Val Thr Phe
                               1                               5

ata gga ttg tcc tgg agc cca cgg aga cgc ggg ctt ggg att caa cgt      702
Ile Gly Leu Ser Trp Ser Pro Arg Arg Arg Gly Leu Gly Ile Gln Arg
      10                               15                               20

gat gct gag cgg atc ttc tct gct tca gac cag gcc tca tgt ggc ttc      750
Asp Ala Glu Arg Ile Phe Ser Ala Ser Asp Gln Ala Ser Cys Gly Phe
      25                               30                               35

act att cat cca cac ata gat gct gca gag aca ctg agg gga ctc aca      798
Thr Ile His Pro His Ile Asp Ala Ala Glu Thr Leu Arg Gly Leu Thr
      40                               45                               50                               55

aat gca cct gtg cag aag gtg tca acg tgg aca aac aca ggc agg gaa      846
Asn Ala Pro Val Gln Lys Val Ser Thr Trp Thr Asn Thr Gly Arg Glu
      60                               65                               70

act ccc atg agc ccg tgt gcc aca tgc agt gag gga act ttg gtg gct      894
Thr Pro Met Ser Pro Cys Ala Thr Cys Ser Glu Gly Thr Leu Val Ala
      75                               80                               85

gag tct ggg cgg ggg tgg gct ggg ggc tca atc gat ttc cac cga gtg      942
Glu Ser Gly Arg Gly Trp Ala Gly Gly Ser Ile Asp Phe His Arg Val
      90                               95                               100

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tgt ctc caa atc ttt gct gga agt gca ggc aag ggg caa ggc ttg gac	990
Cys Leu Gln Ile Phe Ala Gly Ser Ala Gly Lys Gly Gln Gly Leu Asp	
105 110 115	
acc agc gtc gct gtt cct cca ggc tgg gct gat ccc ttt tta ttt cca	1038
Thr Ser Val Ala Val Pro Pro Gly Trp Ala Asp Pro Phe Leu Phe Pro	
120 125 130 135	
agt cac agg agc ctg ttc cct gaa atc ctg ggg aag tgt ggt gag gtg	1086
Ser His Arg Ser Leu Phe Pro Glu Ile Leu Gly Lys Cys Gly Glu Val	
140 145 150	
gcc ccg tgc cgt cga atc ccc atc ctg gtt tac tga agtg cagaagtgac	1136
Ala Pro Cys Arg Arg Ile Pro Ile Leu Val Tyr *	
155 160	
ataagtgcctt gtgaatcagc agggagctct tggccttgac tccctgtgca gatgagccca	1196
gggcgccagc tccttgctgg agaactcctt tgtccatttg cacgtatgga tctttcctca	1256
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tcttcttggc ctctatttca gccacgagct tccatggagg ggccaaactc tccatgcttc	1376
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atgtgtatatt caccacaatt taagaaatat gtaatttgag gcttggagaa ttttaattaag	180
tgatttatct gatgttaact tacagctgat acatggtaga gctgcatttt aatctcagtc	240
atctggctct ttttaaaaca attacagaga aaactttatt ttgggccatt taggaggttt	300
agatcatttt gatcatcttc agctgtcttc tcttcacata caggaaaggc cttggaaagc	360
agtcgttgcg ccagacagcc cagggaagag cggcagcctg aggacctagg gccacctgct	420
gttccctggg attcatgtcc ttctggggag gagggaggac ccaggaca atg gct gct	477
Met Ala Ala	

gtt cat gat ctg gag atg gag agc atg aat ctg aat atg ggg aga gag	525
Val His Asp Leu Glu Met Glu Ser Met Asn Leu Asn Met Gly Arg Glu	
5 10 15	
atg aaa gaa gag ctg gag gaa gag gag aaa atg aga gag gat ggg gga	573
Met Lys Glu Glu Leu Glu Glu Glu Glu Lys Met Arg Glu Asp Gly Gly	
20 25 30 35	
ggt aaa gat cgg gcc aag agt aaa aag gtc cac agg att gtc tca aaa	621
Gly Lys Asp Arg Ala Lys Ser Lys Lys Val His Arg Ile Val Ser Lys	
40 45 50	
tgg atg ctg ccc gaa aag tcc cga gga aca tac ttg gag aga gct aac	669
Trp Met Leu Pro Glu Lys Ser Arg Gly Thr Tyr Leu Glu Arg Ala Asn	
55 60 65	
tgc ttc ccg cct ccc gtg ttc atc atc tcc atc agc ctg gcc gag ctg	717
Cys Phe Pro Pro Pro Val Phe Ile Ile Ser Ile Ser Leu Ala Glu Leu	
70 75 80	
gca gtg ttt att tac tat gct gtg tgg aag cct cag aaa cag tgg atc	765
Ala Val Phe Ile Tyr Tyr Ala Val Trp Lys Pro Gln Lys Gln Trp Ile	
85 90 95	
acg ttg gac aca ggc atc ttg gag agt ccc ttt atc tac agt cct gag	813
Thr Leu Asp Thr Gly Ile Leu Glu Ser Pro Phe Ile Tyr Ser Pro Glu	
100 105 110 115	
aag agg gag gaa gcc tgg agg ttt atc tca tac atg ctg gta cat gct	861
Lys Arg Glu Glu Ala Trp Arg Phe Ile Ser Tyr Met Leu Val His Ala	
120 125 130	
gga gtt cag cac atc ttg ggg aat ctt tgt atg cag ctt gtt ttg ggt	909
Gly Val Gln His Ile Leu Gly Asn Leu Cys Met Gln Leu Val Leu Gly	
135 140 145	
att ccc ttg gaa atg gtc cac aaa ggc ctc cgt gtg ggg ctg gtg tac	957
Ile Pro Leu Glu Met Val His Lys Gly Leu Arg Val Gly Leu Val Tyr	
150 155 160	
ctg gca gga gtg att gca ggg tcc ctt gcc agc tcc atc ttt gac cca	1005
Leu Ala Gly Val Ile Ala Gly Ser Leu Ala Ser Ser Ile Phe Asp Pro	
165 170 175	
ctc aga tat ctt gtg gga gct tca gga gga gtc tat gct ctg atg gga	1053
Leu Arg Tyr Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Met Gly	
180 185 190 195	
ggc tat ttt atg aat gtt ctg gtg aat ttt caa gaa atg att cct gcc	1101
Gly Tyr Phe Met Asn Val Leu Val Asn Phe Gln Glu Met Ile Pro Ala	
200 205 210	
ttt gga att ttc aga ctg ctg atc atc atc ctg ata att gtg ttg gac	1149
Phe Gly Ile Phe Arg Leu Leu Ile Ile Ile Leu Ile Ile Val Leu Asp	
215 220 225	
atg gga ttt gct ctc tat aga agg ttc ttt gtt cct gaa gat ggg tct	1197

Met Gly Phe Ala Leu Tyr Arg Arg Phe Phe Val Pro Glu Asp Gly Ser
230 235 240

ccg gtg tct ttt gca gct cac att gca ggt gga ttt gct gga atg tcc 1245
Pro Val Ser Phe Ala Ala His Ile Ala Gly Gly Phe Ala Gly Met Ser
245 250 255

att ggc tac acg gtg ttt agc tgc ttt gat aaa gca ctg atg aaa gat 1293
Ile Gly Tyr Thr Val Phe Ser Cys Phe Asp Lys Ala Leu Met Lys Asp
260 265 270 275

cca agg ttt tgg ata gca att gct gca tat tta gct tgt gtc tta ttt 1341
Pro Arg Phe Trp Ile Ala Ile Ala Ala Tyr Leu Ala Cys Val Leu Phe
280 285 290

gct gtg ttt ttc aac att ttc cta tct cca gca aac tga cctgccccta 1390
Ala Val Phe Phe Asn Ile Phe Leu Ser Pro Ala Asn *

295 300

ttgtaagtca attaataaaa agagccatct ggaggaaata ataaaaaaaaa ggaagactct 1450

atgaagaaac agagaagtct cagcaaaggc taacaatttt atatagagga caaacagca 1510

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tcttaatgta gaaagggaaa aaaaaaaaaa 1600

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ttttggagtt gacatgcatg tggattggag gaaaaataat caacatatat tctcctttcg 180

tactgttttaa atcacaggaa gaagcggctt taagacaaag atcaaacc aa a atg aca 237
Met Thr
1

act gct cac ttt tac tgt caa tac tgc aca gca tca ctt ctt ggg aag 285
Thr Ala His Phe Tyr Cys Gln Tyr Cys Thr Ala Ser Leu Leu Gly Lys
5 10 15

aaa tat gta cta aag gat gac agt cca tac tgt gtt aca tgt tat gat 333
Lys Tyr Val Leu Lys Asp Asp Ser Pro Tyr Cys Val Thr Cys Tyr Asp
20 25 30

cgt gta ttt tct aac tat tgc gag gaa tgc aaa aaa cca att gaa tct	381
Arg Val Phe Ser Asn Tyr Cys Glu Glu Cys Lys Lys Pro Ile Glu Ser	
35 40 45 50	
gat tct aag gat ctt tgt tac aaa gac cgg cac tgg cat gaa gga tgc	429
Asp Ser Lys Asp Leu Cys Tyr Lys Asp Arg His Trp His Glu Gly Cys	
55 60 65	
ttc aag tgc acc aaa tgc aat cac tct ttg gtg gaa aag cct ttt gct	477
Phe Lys Cys Thr Lys Cys Asn His Ser Leu Val Glu Lys Pro Phe Ala	
70 75 80	
gcc aag gat gag cgc ctg ctg tgc acg gag tgc tat tct aac gag tgc	525
Ala Lys Asp Glu Arg Leu Leu Cys Thr Glu Cys Tyr Ser Asn Glu Cys	
85 90 95	
tcc tcc aag tgc ttc cac tgc aag agg acc atc atg cct ggt tcc cgc	573
Ser Ser Lys Cys Phe His Cys Lys Arg Thr Ile Met Pro Gly Ser Arg	
100 105 110	
aaa atg gaa ttt aag gga aac tac tgg cat gaa acc tgt ttt gtg tgt	621
Lys Met Glu Phe Lys Gly Asn Tyr Trp His Glu Thr Cys Phe Val Cys	
115 120 125 130	
gag aat tgc cga caa cct ata ggg aca aag cct ttg atc tcc aaa gag	669
Glu Asn Cys Arg Gln Pro Ile Gly Thr Lys Pro Leu Ile Ser Lys Glu	
135 140 145	
agt ggc aat tat tgt gtg cca tgt ttt gag aag gag ttt gct cac tac	717
Ser Gly Asn Tyr Cys Val Pro Cys Phe Glu Lys Glu Phe Ala His Tyr	
150 155 160	
tgc aac ttt tgt aag aag gtg ata act tca ggt ggg ata aca ttt tgt	765
Cys Asn Phe Cys Lys Lys Val Ile Thr Ser Gly Gly Ile Thr Phe Cys	
165 170 175	
gac cag cta tgg cat aaa gag tgt ttt ctg tgt agt ggc tgt agg aaa	813
Asp Gln Leu Trp His Lys Glu Cys Phe Leu Cys Ser Gly Cys Arg Lys	
180 185 190	
gat ctc tgt gaa gaa cag ttc atg tcc aga gac gac tat cca ttc tgc	861
Asp Leu Cys Glu Glu Gln Phe Met Ser Arg Asp Asp Tyr Pro Phe Cys	
195 200 205 210	
atg gac tgc tac aac cat ctt tat gcc aac aag tgt gta gcc tgt tcc	909
Met Asp Cys Tyr Asn His Leu Tyr Ala Asn Lys Cys Val Ala Cys Ser	
215 220 225	
aaa ccc att agt ggt ctc aca ggt gcc aag ttt atc tgc ttt caa gac	957
Lys Pro Ile Ser Gly Leu Thr Gly Ala Lys Phe Ile Cys Phe Gln Asp	
230 235 240	
agc cag tgg cat agc gaa tgc ttt aac tgc ggg aaa tgc tct gtc tcc	1005
Ser Gln Trp His Ser Glu Cys Phe Asn Cys Gly Lys Cys Ser Val Ser	
245 250 255	


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ttg gtg ggt aaa ggc ttc ctg acc cag aac aag gaa atc ttc tgc caa      1053
Leu Val Gly Lys Gly Phe Leu Thr Gln Asn Lys Glu Ile Phe Cys Gln
    260                      265                      270

aaa tgt ggc tcc gga atg gac act gac atc tag gagacagt ccttgcccac      1104
Lys Cys Gly Ser Gly Met Asp Thr Asp Ile *
    275                      280                      285

ctaaaaatcca ttttgccttc gttgtcacta aagccagaac tcaaaaaaaaa aaaa      1158

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<213> Homo sapiens

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<222> (1)..(1920)

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<400> 215

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    1                      5                      10                      15

ctc ctg ctg ctc ctg atg ctg gga tgc gtc ctg atg atg gtg gcg atg      96
Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met
    20                      25                      30

ttg cac cct ccc cac cac acc ctg cac cag act gtc aca gcc caa gcc      144
Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala
    35                      40                      45

agc aag cac agc cct gaa gcc agg tac cgc ctg gac ttt ggg gaa tcc      192
Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser
    50                      55                      60

cag gat tgg gta ctg gaa gct gag gat gag ggt gaa gag tac agc cct      240
Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro
    65                      70                      75                      80

ctg gag ggc ctg cca ccc ttt atc tca ctg cgg gag gat cag ctg ctg      288
Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu
    85                      90                      95

gtg gcc gtg gcc tta ccc cag gcc aga agg aac cag agc cag ggc agg      336
Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg
    100                      105                      110

aga ggt ggg agc tac cgc ctc atc aag cag cca agg agg cag gat aag      384
Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys
    115                      120                      125

gaa gcc cca aag agg gac tgg ggg gct gat gag gac ggg gag gtg tct      432
Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser

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130	135	140	
gaa gaa gag gag ttg acc ccg ttc agc ctg gac cca cgt ggc ctc cag			480
Glu Glu Glu Glu Leu Thr Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln			
145	150	155	160
gag gca ctc agt gcc cgc atc ccc ctc cag agg gct ctg ccc gag gtg			528
Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val			
	165	170	175
cgg cac cca ctg tgt ctg cag cag cac cct cag gac agc ctg ccc aca			576
Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr			
	180	185	190
gcc agc gtc atc ctc tgt ttc cat gat gag gcc tgg tcc act ctc ctg			624
Ala Ser Val Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu			
	195	200	205
cgg act gta cac agc atc ctc gac aca gtg ccc agg gcc ttc ctg aag			672
Arg Thr Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys			
	210	215	220
gag atc atc ctc gtg gac gac ctc agc cag caa gga caa ctc aag tct			720
Glu Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser			
	225	230	235
gct ctc agc gaa tat gtg gcc agg ctg gag ggg gtg aag tta ctc agg			768
Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu Arg			
	245	250	255
agc aac aag agg ctg ggt gcc atc agg gcc cgg atg ctg ggg gcc acc			816
Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly Ala Thr			
	260	265	270
aga gcc acc ggg gat gtg ctc gtc ttc atg gat gcc cac tgc gag tgc			864
Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His Cys Glu Cys			
	275	280	285
cac cca ggc tgg ctg gag ccc ctc ctc agc aga ata gct ggt gac agg			912
His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile Ala Gly Asp Arg			
	290	295	300
agc cga gtg gta tct ccg gtg ata gat gtg att gac tgg aag act ttc			960
Ser Arg Val Val Ser Pro Val Ile Asp Val Ile Asp Trp Lys Thr Phe			
	305	310	315
cag tat tac ccc tca aag gac ctg cag cgt ggg gtg ttg gac tgg aag			1008
Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg Gly Val Leu Asp Trp Lys			
	325	330	335
ctg gat ttc cac tgg gaa cct ttg cca gag cat gtg agg aag gcc ctc			1056
Leu Asp Phe His Trp Glu Pro Leu Pro Glu His Val Arg Lys Ala Leu			
	340	345	350
cag tcc ccc ata agc ccc atc agg agc cct gtg gtg ccc gga gag gtg			1104
Gln Ser Pro Ile Ser Pro Ile Arg Ser Pro Val Val Pro Gly Glu Val			
	355	360	365

gtg gcc atg gac aga cat tac ttc caa aac act gga gcg tat gac tct	1152
Val Ala Met Asp Arg His Tyr Phe Gln Asn Thr Gly Ala Tyr Asp Ser	
370 375 380	
ctt atg tcg ctg cga ggt ggt gaa aac ctc gaa ctg tct ttc aag gcc	1200
Leu Met Ser Leu Arg Gly Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala	
385 390 395 400	
tgg ctc tgt ggt ggc tct gtt gaa atc ctt ccc tgc tct cgg gta gga	1248
Trp Leu Cys Gly Gly Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly	
405 410 415	
cac atc tac caa aat cag gat tcc cat tcc ccc ctc gac cag gag gcc	1296
His Ile Tyr Gln Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala	
420 425 430	
acc ctg agg aac agg gtt cgc att gct gag acc tgg ctg ggg tca ttc	1344
Thr Leu Arg Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe	
435 440 445	
aaa gaa acc ttc tac aag cat agc cca gag gcc ttc tcc ttg agc aag	1392
Lys Glu Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys	
450 455 460	
gct gag aag cca gac tgc atg gaa cgc ttg cag ctg caa agg aga ctg	1440
Ala Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	
465 470 475 480	
ggt tgt cgg aca ttc cac tgg ttt ctg gct aat gtc tac cct gag ctg	1488
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu Leu	
485 490 495	
tac cca tct gaa ccc agg ccc agt ttc tct gga aag ctc cac aac act	1536
Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His Asn Thr	
500 505 510	
gga ctt ggg ctc tgt gca gac tgc cag gca gaa ggg gac atc ctg ggc	1584
Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp Ile Leu Gly	
515 520 525	
tgt ccc atg gtg ttg gct cct tgc agt gac agc cgg cag caa cag tac	1632
Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg Gln Gln Gln Tyr	
530 535 540	
ctg cag cac acc agc agg aag gag att cac ttt ggc agc cca cag cac	1680
Leu Gln His Thr Ser Arg Lys Glu Ile His Phe Gly Ser Pro Gln His	
545 550 555 560	
ctg tgc ttt gct gtc agg cag gag cag gtg att ctt cag aac tgc acg	1728
Leu Cys Phe Ala Val Arg Gln Glu Gln Val Ile Leu Gln Asn Cys Thr	
565 570 575	
gag gaa ggc ctg gcc atc cac cag cag cac tgg gac ttc cag gag aat	1776
Glu Glu Gly Leu Ala Ile His Gln Gln His Trp Asp Phe Gln Glu Asn	
580 585 590	

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ggg atg att gtc cac att ctt tct ggg aaa tgc atg gaa gct gtg gtg      1824
Gly Met Ile Val His Ile Leu Ser Gly Lys Cys Met Glu Ala Val Val
      595                      600                      605

caa gaa aac aat aaa gat ttg tac ctg cgt ccg tgt gat gga aaa gcc      1872
Gln Glu Asn Asn Lys Asp Leu Tyr Leu Arg Pro Cys Asp Gly Lys Ala
      610                      615                      620

cgc cag cag tgg cgt ttt gac cag atc aat gct gtg gat gaa cga tga      1920
Arg Gln Gln Trp Arg Phe Asp Gln Ile Asn Ala Val Asp Glu Arg *
      625                      630                      635                      640

atgtcaatgt cagaaggaaa agagaatttt ggccatcaaa atccagctcc aagtgaactt      1980

aaagagctta tataatttcat gaagctgata cttttgtgtg tgtgctcctg gtgttaggag      2040

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ccccactga agggcaaagt ccagcggatt ctacactgga ggtggacgga gccccctgcc      180

cccttc      atg gtg ggg ctg ccg ggg cct gac gtg gag ccc agc ctc cct      228
      Met Val Gly Leu Pro Gly Pro Asp Val Glu Pro Ser Leu Pro
      1                      5                      10

cca cct aag ccc ctg gag ggc atc cct gag aga gag ttc ttt gtc aag      276
Pro Pro Lys Pro Leu Glu Gly Ile Pro Glu Arg Glu Phe Phe Val Lys
      15                      20                      25                      30

tgg gca ggg ctg tcc tac tgg cat tgc tcc tgg gtg aag gag cta cag      324
Trp Ala Gly Leu Ser Tyr Trp His Cys Ser Trp Val Lys Glu Leu Gln
      35                      40                      45

ctg gag ctg tac cac acg gtg atg tat cgc aac tac caa aga aag aac      372
Leu Glu Leu Tyr His Thr Val Met Tyr Arg Asn Tyr Gln Arg Lys Asn
      50                      55                      60

gac atg gat gag ccg ccc ccc ttt gac tac ggc tct ggg gat gaa gac      420
Asp Met Asp Glu Pro Pro Pro Phe Asp Tyr Gly Ser Gly Asp Glu Asp

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65	70	75	
ggc aag agc gag aag agg aag aac aag gac ccc ctc tat gcc aag atg			468
Gly Lys Ser Glu Lys Arg Lys Asn Lys Asp Pro Leu Tyr Ala Lys Met			
80	85	90	
gag gag cgc ttc tac cgc tat ggc atc aag cca gag tgg atg atg att			516
Glu Glu Arg Phe Tyr Arg Tyr Gly Ile Lys Pro Glu Trp Met Met Ile			
95	100	105	110
cac cga atc ctg aac cat agc ttt gac aag aag ggg gat gtg cac tac			564
His Arg Ile Leu Asn His Ser Phe Asp Lys Lys Gly Asp Val His Tyr			
115	120	125	
ctg atc aag tgg aaa gac ctg ccc tat gac cag tgc acc tgg gag atc			612
Leu Ile Lys Trp Lys Asp Leu Pro Tyr Asp Gln Cys Thr Trp Glu Ile			
130	135	140	
gat gac atc gac atc ccc tac tac gac aac ctc aag cag gcc tac tgg			660
Asp Asp Ile Asp Ile Pro Tyr Tyr Asp Asn Leu Lys Gln Ala Tyr Trp			
145	150	155	
ggc cac agg gag ctg atg ctg gga gaa gac acc agg ctg ccc aag agg			708
Gly His Arg Glu Leu Met Leu Gly Glu Asp Thr Arg Leu Pro Lys Arg			
160	165	170	
ctg ctc aag aag ggc aag aag ctg agg gac gac aag cag gag aag ccg			756
Leu Leu Lys Lys Gly Lys Lys Leu Arg Asp Asp Lys Gln Glu Lys Pro			
175	180	185	190
ccg gac acg ccc att gtg gac ccc acg gtc aag ttc gac aag cag cca			804
Pro Asp Thr Pro Ile Val Asp Pro Thr Val Lys Phe Asp Lys Gln Pro			
195	200	205	
tgg tac atc gac tcc aca ggc ggc aca ctg cac ccg tac cag ctg gag			852
Trp Tyr Ile Asp Ser Thr Gly Gly Thr Leu His Pro Tyr Gln Leu Glu			
210	215	220	
ggc ctc aac tgg ctg cgc ttc tct tgg gcc cag ggc act gac acc atc			900
Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala Gln Gly Thr Asp Thr Ile			
225	230	235	
ctg gcc gat gag atg ggt ctg ggc aag acg gtg cag acc atc gtg ttc			948
Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Ile Val Phe			
240	245	250	
ctt tac tcc ctc tac aag gag ggc cac tcc aaa ggg ccc tac ctg gtt			996
Leu Tyr Ser Leu Tyr Lys Glu Gly His Ser Lys Gly Pro Tyr Leu Val			
255	260	265	270
agc gcg ccc ctc tcc acc atc atc aac tgg gaa cgc gag ttt gag atg			1044
Ser Ala Pro Leu Ser Thr Ile Ile Asn Trp Glu Arg Glu Phe Glu Met			
275	280	285	
tgg gcg ccc gac ttc tac gtg gtc acc tac acg ggg gac aag gag agc			1092
Trp Ala Pro Asp Phe Tyr Val Val Thr Tyr Thr Gly Asp Lys Glu Ser			
290	295	300	

cgc tcg gtg att cgg gag aac gag ttt tcc ttt gag gac aac gcc att	1140
Arg Ser Val Ile Arg Glu Asn Glu Phe Ser Phe Glu Asp Asn Ala Ile	
305 310 315	
cgg agt ggg aag aag gta ttc cgt atg aag aaa gaa gtg cag atc aaa	1188
Arg Ser Gly Lys Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys	
320 325 330	
ttc cac gtg ctg ctc acc tcc tat gag ctc atc acc atc gac cag gcc	1236
Phe His Val Leu Leu Thr Ser Tyr Glu Leu Ile Thr Ile Asp Gln Ala	
335 340 345 350	
atc ctg ggc tcc atc gag tgg gcc tgc ctg gtg gta gat gag gcc cac	1284
Ile Leu Gly Ser Ile Glu Trp Ala Cys Leu Val Val Asp Glu Ala His	
355 360 365	
cgc ctc aag aac aac cag tcc aag ttt ttt agg gtc tta aac agc tac	1332
Arg Leu Lys Asn Asn Gln Ser Lys Phe Phe Arg Val Leu Asn Ser Tyr	
370 375 380	
aag att gat tac aag ctg ctg ctg aca ggg acc ccc ctt cag aac aac	1380
Lys Ile Asp Tyr Lys Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn	
385 390 395	
ctg gag gag ctg ttc cat ctc ctc aac ttc ctg act cca gag agg ttc	1428
Leu Glu Glu Leu Phe His Leu Leu Asn Phe Leu Thr Pro Glu Arg Phe	
400 405 410	
aac aac ctg gag ggc ttc ctg gag gag ttt gct gac atc tcc aag gaa	1476
Asn Asn Leu Glu Gly Phe Leu Glu Glu Phe Ala Asp Ile Ser Lys Glu	
415 420 425 430	
gac cag atc aag aag ctg cat gac ctg ctg ggg ccg cac atg ctc agg	1524
Asp Gln Ile Lys Lys Leu His Asp Leu Leu Gly Pro His Met Leu Arg	
435 440 445	
cgg ctc aag gct gac gtg ttc aag aac atg ccg gcc aag acc gag ctc	1572
Arg Leu Lys Ala Asp Val Phe Lys Asn Met Pro Ala Lys Thr Glu Leu	
450 455 460	
att gtc cgg gtg gag ctg agc cag atg cag aag aag tac tac aag ttc	1620
Ile Val Arg Val Glu Leu Ser Gln Met Gln Lys Lys Tyr Tyr Lys Phe	
465 470 475	
atc ctc aca cgg aac ttt gag gca ctg aac tcc aag ggg ggc ggc aac	1668
Ile Leu Thr Arg Asn Phe Glu Ala Leu Asn Ser Lys Gly Gly Gly Asn	
480 485 490	
caa gta tcg ctg ctc aac atc atg atg gac ctg aaa aag tgc tgc aac	1716
Gln Val Ser Leu Leu Asn Ile Met Met Asp Leu Lys Lys Cys Cys Asn	
495 500 505 510	
cac ccc tac ctc ttc cct gtg gct gcc gtg gag gcc cct gtc ttg ccc	1764
His Pro Tyr Leu Phe Pro Val Ala Ala Val Glu Ala Pro Val Leu Pro	
515 520 525	

aat ggc tcc tac gat gga agc tcc ctg gtc aag tct tca ggg aag ctc	1812
Asn Gly Ser Tyr Asp Gly Ser Ser Leu Val Lys Ser Ser Gly Lys Leu	
530 535 540	
atg ctg cta cag aag atg ctg aag aaa ctg cgg gat gag ggg cac cgt	1860
Met Leu Leu Gln Lys Met Leu Lys Lys Leu Arg Asp Glu Gly His Arg	
545 550 555	
gtg ctc atc ttc tcc cag atg acc aag atg ctg gac ctc ctg gag gac	1908
Val Leu Ile Phe Ser Gln Met Thr Lys Met Leu Asp Leu Leu Glu Asp	
560 565 570	
ttc ctg gag tac gaa ggc tac aag tat gag cgg att gat ggt ggc atc	1956
Phe Leu Glu Tyr Glu Gly Tyr Lys Tyr Glu Arg Ile Asp Gly Gly Ile	
575 580 585 590	
acc ggg ggc ctc cgg cag gag gca atc gac aga ttc aat gcc ccc ggg	2004
Thr Gly Gly Leu Arg Gln Glu Ala Ile Asp Arg Phe Asn Ala Pro Gly	
595 600 605	
gcc cag cag ttc tgc ttc ctc ctc tca acc cgg gca ggt ggt ctg ggc	2052
Ala Gln Gln Phe Cys Phe Leu Leu Ser Thr Arg Ala Gly Leu Gly	
610 615 620	
atc aac ctg gcc acg gcg gac act gtc atc atc tac gac tcg gac tgg	2100
Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile Tyr Asp Ser Asp Trp	
625 630 635	
aac ccg cac aat gac atc cag gcc ttc agc cgc gcc cac cgc atc ggc	2148
Asn Pro His Asn Asp Ile Gln Ala Phe Ser Arg Ala His Arg Ile Gly	
640 645 650	
cag aac aag aag gtg atg atc tac cgc ttc gtg act cgg gcc tcg gtg	2196
Gln Asn Lys Lys Val Met Ile Tyr Arg Phe Val Thr Arg Ala Ser Val	
655 660 665 670	
gag gag cgc atc acg cag gtg gcc aag cgc aag atg atg ctc acc cac	2244
Glu Glu Arg Ile Thr Gln Val Ala Lys Arg Lys Met Met Leu Thr His	
675 680 685	
ctg gtg gtg cgg ccc ggc ctc ggc tcc aag tcg ggg tcc atg acc aag	2292
Leu Val Val Arg Pro Gly Leu Gly Ser Lys Ser Gly Ser Met Thr Lys	
690 695 700	
cag gag ctg gac gac atc ctc aag ttc ggc acg gag gaa ctc ttc aag	2340
Gln Glu Leu Asp Asp Ile Leu Lys Phe Gly Thr Glu Glu Leu Phe Lys	
705 710 715	
gac gac gtg gag ggc atg atg tct cag ggc cag agg ccg gtc aca ccc	2388
Asp Asp Val Glu Gly Met Met Ser Gln Gly Gln Arg Pro Val Thr Pro	
720 725 730	
atc cct gat gtc cag tcc tcc aaa ggg ggg aac ttg gcc gcc agt gca	2436
Ile Pro Asp Val Gln Ser Ser Lys Gly Gly Asn Leu Ala Ala Ser Ala	
735 740 745 750	
aag aag aag cac ggt agc acc ccg cca ggt gac aac aag gac gtg gag	2484

Lys	Lys	Lys	His	Gly	Ser	Thr	Pro	Pro	Gly	Asp	Asn	Lys	Asp	Val	Glu	
				755					760					765		
gac	agc	agt	gtg	atc	cac	tat	gac	gat	gcg	gcc	atc	tcc	aag	ctg	ctg	2532
Asp	Ser	Ser	Val	Ile	His	Tyr	Asp	Asp	Ala	Ala	Ile	Ser	Lys	Leu	Leu	
			770					775					780			
gac	cgg	aac	cag	gac	gct	aca	gat	gac	acg	gag	cta	cag	aac	atg	aac	2580
Asp	Arg	Asn	Gln	Asp	Ala	Thr	Asp	Asp	Thr	Glu	Leu	Gln	Asn	Met	Asn	
		785					790					795				
gag	tac	ctg	agc	tcc	ttc	aag	gtg	gcg	cag	tac	gtg	gtg	cgc	gag	gag	2628
Glu	Tyr	Leu	Ser	Ser	Phe	Lys	Val	Ala	Gln	Tyr	Val	Val	Arg	Glu	Glu	
	800					805					810					
gac	ggc	gtg	gag	gag	gtg	gag	cgg	gaa	atc	atc	aag	cag	gag	gag	aac	2676
Asp	Gly	Val	Glu	Glu	Val	Glu	Arg	Glu	Ile	Ile	Lys	Gln	Glu	Glu	Asn	
815					820					825					830	
gtg	gac	ccc	gac	tac	tgg	gag	aag	ctg	ctg	cgg	cac	cac	tat	gag	cag	2724
Val	Asp	Pro	Asp	Tyr	Trp	Glu	Lys	Leu	Leu	Arg	His	His	Tyr	Glu	Gln	
				835					840					845		
cag	cag	gag	gac	ctg	gcc	cgc	aac	ctg	ggc	aag	ggc	aag	cgc	atc	cgc	2772
Gln	Gln	Glu	Asp	Leu	Ala	Arg	Asn	Leu	Gly	Lys	Gly	Lys	Arg	Ile	Arg	
			850					855					860			
aag	cag	gtc	aac	tac	aac	gat	gcc	tcc	cag	gag	gac	cag	gag	tgg	cag	2820
Lys	Gln	Val	Asn	Tyr	Asn	Asp	Ala	Ser	Gln	Glu	Asp	Gln	Glu	Trp	Gln	
		865					870					875				
gat	gag	ctc	tct	gat	aac	cag	tca	gaa	tat	tcc	att	ggc	tct	gag	gat	2868
Asp	Glu	Leu	Ser	Asp	Asn	Gln	Ser	Glu	Tyr	Ser	Ile	Gly	Ser	Glu	Asp	
	880					885					890					
gag	gat	gag	gac	ttt	gaa	gag	agg	ccg	gaa	ggg	cag	agt	gga	cga	cga	2916
Glu	Asp	Glu	Asp	Phe	Glu	Glu	Arg	Pro	Glu	Gly	Gln	Ser	Gly	Arg	Arg	
895					900					905					910	
caa	tcc	cgg	agg	cag	ctg	aag	agt	gac	agg	gac	aag	ccc	ctg	ccc	ccg	2964
Gln	Ser	Arg	Arg	Gln	Leu	Lys	Ser	Asp	Arg	Asp	Lys	Pro	Leu	Pro	Pro	
				915					920					925		
ctt	ctc	gcc	cga	gtt	ggt	ggc	aac	atc	gag	gtg	ctg	ggc	ttc	aat	gcc	3012
Leu	Leu	Ala	Arg	Val	Gly	Gly	Asn	Ile	Glu	Val	Leu	Gly	Phe	Asn	Ala	
			930					935					940			
cga	cag	cgg	aag	gcc	ttt	ctg	aac	gcc	atc	atg	cgc	tgg	ggc	atg	ccc	3060
Arg	Gln	Arg	Lys	Ala	Phe	Leu	Asn	Ala	Ile	Met	Arg	Trp	Gly	Met	Pro	
		945					950					955				
ccg	cag	gac	gcc	ttc	aac	tcc	cac	tgg	ctg	gtg	cgg	gac	ctt	cga	ggg	3108
Pro	Gln	Asp	Ala	Phe	Asn	Ser	His	Trp	Leu	Val	Arg	Asp	Leu	Arg	Gly	
		960				965					970					
aag	agc	gag	aag	gag	ttt	aga	gcc	tat	gtg	tcc	ctc	ttc	atg	cgg	cac	3156
Lys	Ser	Glu	Lys	Glu	Phe	Arg	Ala	Tyr	Val	Ser	Leu	Phe	Met	Arg	His	

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Tyr Ser Asn Asn Phe Gly Pro Asn Phe Arg Gly Pro Gly Pro Gly Gly	
1440 1445 1450	
att gtc aac tac aac cag atg ccc ctg ggg ccc tat gtg acc gat atc	4596
Ile Val Asn Tyr Asn Gln Met Pro Leu Gly Pro Tyr Val Thr Asp Ile	
1455 1460 1465 1470	
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Met Ala Ser Pro Asp Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp	
1 5 10 15	
gtg ccc tcg ggg gtc gcg ctg ttc ctc acc atc cct ttc gcc ttc ttc	155
Val Pro Ser Gly Val Ala Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe	
20 25 30	
ctg ccc gag ctg ata ttt ggg ttc ttg gtc tgg acc atg gta gcc gcc	203
Leu Pro Glu Leu Ile Phe Gly Phe Leu Val Trp Thr Met Val Ala Ala	
35 40 45	
acc cac ata gta tac ccc ttg ctg caa gga tgg gtg atg tat gtc tcg	251
Thr His Ile Val Tyr Pro Leu Leu Gln Gly Trp Val Met Tyr Val Ser	
50 55 60	
ctc acc tcg ttt ctc atc tcc ttg atg ttc ctg ttg tct tac ttg ttt	299
Leu Thr Ser Phe Leu Ile Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe	
65 70 75	
gga ttt tac aaa aga ttt gaa tcc tgg aga gtt ctg gac agc ctg tac	347
Gly Phe Tyr Lys Arg Phe Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr	
80 85 90 95	
cac ggg acc act ggc atc ctg tac atg agc gct gcc gtc cta caa gta	395
His Gly Thr Thr Gly Ile Leu Tyr Met Ser Ala Ala Val Leu Gln Val	
100 105 110	

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cat gcc acg att gtt tct gag aaa ctg ctg gac cca aga att tac tac      443
His Ala Thr Ile Val Ser Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr
      115                      120                      125

att aat tcg gca gcc tcg ttc ttc gcc ttc atc gcc acg ctg ctc tac      491
Ile Asn Ser Ala Ala Ser Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr
      130                      135                      140

att ctc cat gcc ttc agc atc tat tac cac tga tgcacagg cgccaggcca      542
Ile Leu His Ala Phe Ser Ile Tyr Tyr His *
      145                      150

agggggaaat gctctttgaa agctccaatt attggtcccc aaaagcagct tccaacgttt      602

gccatctgga tgacaaacgg aagatccact aaaacgtcca cgggattaac agaacgtcct      662

tgcagactga gcgatgacac cacactttgt ttggacattt aaattcactc tgctgaatag      722

gaggaagctt ttctttttcc tgggaaaaca actgtctctt ggaattatct gaccatgaac      782

ttgtctttct agacaactca catcaaagcc ctcaactccac taatggagaa tcctagcccc      842

actaatgcca agtctgtttg gggattttgc ctcaactccac taatggagaa tcctagcccc      902

aggggaatac tcagtctgat cttttttttg tttgttttat tttgtttttt ttgagacgga      962

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gcctccgggg ttcccggcat                                                    1042

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ccaggcgcgc ccgctgctcg gtggcaggag ggccggcgga gcgcc      atg gcc tgc      174
                                     Met Ala Cys
                                     1

atc ctg aag aga aag tct gtg att gct gtg agc ttc ata gca gcg ttc      222
Ile Leu Lys Arg Lys Ser Val Ile Ala Val Ser Phe Ile Ala Ala Phe
      5                      10                      15

ctt ttc ctg ctg gtt gtg cgt ctt gta aat gaa gtg aat ttc cca ttg      270
Leu Phe Leu Leu Val Val Arg Leu Val Asn Glu Val Asn Phe Pro Leu

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Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile Pro Phe Ser	40	45	50	
tac aca tac agg cgg ccc ctt cga act cac tat gga tac ata aat gtg				366
Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr Ile Asn Val	55	60	65	
aag aca caa gag cct ttg caa ctg gac tgt gac ctt tgt gcc ata gtg				414
Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys Ala Ile Val	70	75	80	
tca aac tca ggt cag atg gtt ggc cag aag gtg gga aat gag ata gat				462
Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn Glu Ile Asp	85	90	95	
cga tcc tcc tgc att tgg aga atg aac aat gcc ccc acc aaa ggt tat				510
Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr Lys Gly Tyr	100	105	110	115
gaa gaa gat gtc ggc cgc atg acc atg att cga gtt gtg tcc cat acc				558
Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val Ser His Thr	120	125	130	
agc gtt cct ctt ttg cta aaa aac cct gat tat ttt ttc aag gaa gcg				606
Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe Lys Glu Ala	135	140	145	
aat act act att tgt gtt att tgg gga cct ttc cgc aat atg agg aaa				654
Asn Thr Thr Ile Cys Val Ile Trp Gly Pro Phe Arg Asn Met Arg Lys	150	155	160	
gat ggc aat ggc atc gtt tac aac atg ttg aaa aag aca gtt ggt atc				702
Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr Val Gly Ile	165	170	175	
tat ccg aat gcc caa ata tac gtg acc aca gag aag cgc atg agt tac				750
Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg Met Ser Tyr	180	185	190	195
tgt gat gga gtt ttt aag aag gaa act ggg aag gac agg ggg cat gca				798
Cys Asp Gly Val Phe Lys Lys Glu Thr Gly Lys Asp Arg Gly His Ala	200	205	210	
agg cga ctg ctg att tct aca gac act ttt taa gcgattac cagtgtctggc				849
Arg Arg Leu Leu Ile Ser Thr Asp Thr Phe *	215	220		
aagtggaact acctttccgg tcctcttaca agcatccagt cacttgctga aatgtcataa				909
gcgatataaa cctgctgaca ggccaggatc attgcatctc ctgcctcctc cttccacgta				969
acaaatctca ttgttgattg gcatatggca gcaagcatcc caacacccag agtggtgttc				1029
ttattttctga gggagcaggg tctgtgtgtg aattgcacac acagggagca atccccctgcc				1089

gaa aca ctt tgt cct cca aaa gga aga cag act tca cgt cat tca tct Glu Thr Leu Cys Pro Pro Lys Gly Arg Gln Thr Ser Arg His Ser Ser 120 125 130	557
gtt caa tac tct tcc gaa caa cag gaa att ttg cca gct aat gat tct Val Gln Tyr Ser Ser Glu Gln Gln Glu Ile Leu Pro Ala Asn Asp Ser 135 140 145 150	605
ctt gct tac agt gac tca gct ggt agc ttt tta aaa gaa gta gac cga Leu Ala Tyr Ser Asp Ser Ala Gly Ser Phe Leu Lys Glu Val Asp Arg 155 160 165	653
gac ata gaa caa ata gta aag tgt aca gac aat aag aga gag aac ctc Asp Ile Glu Gln Ile Val Lys Cys Thr Asp Asn Lys Arg Glu Asn Leu 170 175 180	701
aat gag gta gta tcg gcc tta aca gca caa caa atg cgt ttt gaa cct Asn Glu Val Val Ser Ala Leu Thr Ala Gln Gln Met Arg Phe Glu Pro 185 190 195	749
gat aac aaa aac act caa cgt aaa gac ccc tat tat gga gca gac tgg Asp Asn Lys Asn Thr Gln Arg Lys Asp Pro Tyr Tyr Gly Ala Asp Trp 200 205 210	797
gga ata ggg tgg tgg aca gct gta gtg ata atg ttg ata gta ggt ata Gly Ile Gly Trp Trp Thr Ala Val Val Ile Met Leu Ile Val Gly Ile 215 220 225 230	845
ata aca cca gtg ttt tat ttg ttg tat tat gaa att tta gct aag gtg Ile Thr Pro Val Phe Tyr Leu Leu Tyr Tyr Glu Ile Leu Ala Lys Val 235 240 245	893
gat gtt agt cat cat tca aca gtg gac tct tca cat tta cat tca aaa Asp Val Ser His His Ser Thr Val Asp Ser Ser His Leu His Ser Lys 250 255 260	941
atc aca ccc cca tca cag cag aga gaa atg gaa aat gga att gtg cca Ile Thr Pro Pro Ser Gln Gln Arg Glu Met Glu Asn Gly Ile Val Pro 265 270 275	989
act aaa gga ata cat ttc agc caa caa gat gat cat aaa ctg tat agt Thr Lys Gly Ile His Phe Ser Gln Gln Asp Asp His Lys Leu Tyr Ser 280 285 290	1037
caa gat tct cag tca cct gct gct caa cag gaa aca tag caattagctc Gln Asp Ser Gln Ser Pro Ala Ala Gln Gln Glu Thr *	1086
295 300 305	
ataatcaaat gttagtggtc aggtcacatg tgcacatctgga atgtgggtgaa tcagttatat	1146
ccaataatag cttcaaaggc agaatttaga gagattgagg atgccttttgt ttttaacaaa	1206
agggtttcac actttgaaaa ttttttgagc aactagttgt tgatgttgag agcagttgat	1266
ccataaatct ggtgtgtgaa tgtttcaagc agaaattaat ttaaattgtgt gtttaggaag	1326

tacttaactt ggaagatgta tcatttttct taaaatgcat gtttaaattt tattttttta	1386
agtaattttt aaaaagttaa ttaatgttaa atttatgatg cagaatgata gcatcagatg	1446
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attaaacgtg catattacca ttatttagga aataattcct tatatactgt gataaatcat	1926
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ccaaaggtgt atagattgct tgaaaggggg tggtagtgcc tctttttaag atctgttgag	2346
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agtctggatt gcctgttttg tatataatat atacttaaga tatataatac cacctcattt	2526
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tagttgtact ttgaaattgt tatgggttcg atttccaaaa tatgtaactt atttttttaa	3066

ggaataaggt gtgctgtgta tttgttgatt aaaaatcatt tgtcttgag agtatccttt 3126
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<220>
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 gccgagggat ccctccgagg acaccccagc agtggacggc agcacagaca cggacagg 178
 atg ccc ttg aag ctc tac ttg cct ggt ggt aat tcc agg atg acc cag 226
 Met Pro Leu Lys Leu Tyr Leu Pro Gly Gly Asn Ser Arg Met Thr Gln
 1 5 10 15
 gag agg ctg gaa aga gcg ttc aaa cgg cag ggc agc cag ccc gca cct 274
 Glu Arg Leu Glu Arg Ala Phe Lys Arg Gln Gly Ser Gln Pro Ala Pro
 20 25 30
 gtc agg aaa aat cag ttg ctg ccg tct gac aag gtg gat ggt gag ctg 322
 Val Arg Lys Asn Gln Leu Leu Pro Ser Asp Lys Val Asp Gly Glu Leu
 35 40 45
 ggt gcc ctg cgg ctc gag gat gtg gag gat gag ttg ata agg gaa gag 370
 Gly Ala Leu Arg Leu Glu Asp Val Glu Asp Glu Leu Ile Arg Glu Glu
 50 55 60
 gtc atc ctg tcg cca gtc cca tca gtg ctc aag ttg cag aca gca tca 418
 Val Ile Leu Ser Pro Val Pro Ser Val Leu Lys Leu Gln Thr Ala Ser
 65 70 75 80
 aaa cca att gac ctc tca gta gca aag gaa ata aag acc ctt ctg ttt 466
 Lys Pro Ile Asp Leu Ser Val Ala Lys Glu Ile Lys Thr Leu Leu Phe
 85 90 95

ggt tcc agc ttt tgc tgt ttc aat gaa gaa tgg aaa ctt cag agt ttt Gly Ser Ser Phe Cys Cys Phe Asn Glu Glu Trp Lys Leu Gln Ser Phe 100 105 110	514
tcc ttt agt aac aca gcc tca tta aaa tac ggc ata gtg cag aac aag Ser Phe Ser Asn Thr Ala Ser Leu Lys Tyr Gly Ile Val Gln Asn Lys 115 120 125	562
ggt ggt cct tgc gga gtc ctg gca gct gtc caa ggc tgt gtc cta cag Gly Gly Pro Cys Gly Val Leu Ala Ala Val Gln Gly Cys Val Leu Gln 130 135 140	610
aaa ctc ctg ttt gaa gga gat agc aaa gcc gac tgt gct cag gga ctg Lys Leu Leu Phe Glu Gly Asp Ser Lys Ala Asp Cys Ala Gln Gly Leu 145 150 155 160	658
cag cct tca gat gcc cac cgg acc cgc tgc ctc gtc ctg gcc ctc gca Gln Pro Ser Asp Ala His Arg Thr Arg Cys Leu Val Leu Ala Leu Ala 165 170 175	706
gac att gtg tgg cgg gca ggg ggc cga gag aga gcc gtt gtt gca ctg Asp Ile Val Trp Arg Ala Gly Gly Arg Glu Arg Ala Val Val Ala Leu 180 185 190	754
gct tcg aga aca cag cag ttc agt cca aca ggg aaa tac aaa gca gat Ala Ser Arg Thr Gln Gln Phe Ser Pro Thr Gly Lys Tyr Lys Ala Asp 195 200 205	802
gga gtc tta gaa aca ctt acg ctt cac agt ttg acc tgc tat gag gac Gly Val Leu Glu Thr Leu Thr Leu His Ser Leu Thr Cys Tyr Glu Asp 210 215 220	850
ctg gtg act ttt ctt caa caa agc att cat cag ttt gaa gtg ggc ccc Leu Val Thr Phe Leu Gln Gln Ser Ile His Gln Phe Glu Val Gly Pro 225 230 235 240	898
tat ggc tgc atc ctg ctc acc ctt tct gcc atc ctg tcc agg tct aca Tyr Gly Cys Ile Leu Leu Thr Leu Ser Ala Ile Leu Ser Arg Ser Thr 245 250 255	946
gag ctc atc cgc cag gac ttt gat gtc ccc acc agc cac ctg att gga Glu Leu Ile Arg Gln Asp Phe Asp Val Pro Thr Ser His Leu Ile Gly 260 265 270	994
gca cat ggc tac tgt aca cag gaa ctt gtc aat ctg ctc ctg act ggg Ala His Gly Tyr Cys Thr Gln Glu Leu Val Asn Leu Leu Leu Thr Gly 275 280 285	1042
aaa gct gtg tcc aac gtt ttc aac gat gtg gtt gag ctg gat tct ggg Lys Ala Val Ser Asn Val Phe Asn Asp Val Val Glu Leu Asp Ser Gly 290 295 300	1090
gat ggg aac atc aca ctt ctc aga ggc att gct gca cgc agt gat att Asp Gly Asn Ile Thr Leu Leu Arg Gly Ile Ala Ala Arg Ser Asp Ile 305 310 315 320	1138
ggc ttc tta tct ctc ttt gag cat tac aac atg tgc cag gtt ggc tgc	1186

Gly	Phe	Leu	Ser	Leu	Phe	Glu	His	Tyr	Asn	Met	Cys	Gln	Val	Gly	Cys		
				325					330					335			
ttc	ctg	aag	acc	ccg	agg	ttc	ccc	atc	tgg	gtg	gtt	tgc	agt	gag	agc	1234	
Phe	Leu	Lys	Thr	Pro	Arg	Phe	Pro	Ile	Trp	Val	Val	Cys	Ser	Glu	Ser		
			340					345					350				
cac	ttc	agc	atc	ctc	ttt	agc	ctg	cag	ccg	ggg	ctc	ctg	cgt	gac	tgg	1282	
His	Phe	Ser	Ile	Leu	Phe	Ser	Leu	Gln	Pro	Gly	Leu	Leu	Arg	Asp	Trp		
		355					360					365					
agg	act	gag	agg	ctc	ttt	gac	ttg	tac	tac	tac	gat	ggc	ctg	gcc	aac	1330	
Arg	Thr	Glu	Arg	Leu	Phe	Asp	Leu	Tyr	Tyr	Tyr	Asp	Gly	Leu	Ala	Asn		
	370					375					380						
cag	cag	gag	cag	atc	cgg	ctg	acc	att	gac	acc	acc	caa	acc	atc	tct	1378	
Gln	Gln	Glu	Gln	Ile	Arg	Leu	Thr	Ile	Asp	Thr	Thr	Gln	Thr	Ile	Ser		
385				390					395					400			
gag	gac	aca	gac	aac	gac	ctt	gtc	cca	ccc	ctc	gag	ctc	tgc	atc	aga	1426	
Glu	Asp	Thr	Asp	Asn	Asp	Leu	Val	Pro	Pro	Leu	Glu	Leu	Cys	Ile	Arg		
				405				410					415				
acc	aag	tgg	aag	ggg	gca	tca	gtg	aac	tgg	aac	ggc	tca	gac	ccc	atc	1474	
Thr	Lys	Trp	Lys	Gly	Ala	Ser	Val	Asn	Trp	Asn	Gly	Ser	Asp	Pro	Ile		
			420					425					430				
ctg	tga	ccgttgatg	tggtgtaaacc	ctgtggtcca	ccactcatca	cctcatcacc										1530	
Leu	*																
gaggatgaca	gctgaacccc	aagcctctgg	ggcaggtctc	atgtacccca	acctgggtca											1590	
gcatgactgc	agaagcatcc	agagcctccc	tgccccttcc	atgaagggcc	cacccaagac											1650	
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ctggaaggag	gttgccaggg	tctctgctac	ctttgtctgc	atccctccct	tgctccctgc											1770	
tggttggtcc	ctcaccagc	cctccaatgt	ggttggtccct	ggggactcat	tacttctggt											1830	
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 <212> DNA
 <213> Homo sapiens

<220>
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agaacagcta cccatctcaa accccaggag tcaccagccc ttggggccctc acatccctgg 180
agcctcagcc ccctccacac acgtgctgtg aatcataggg ggatcaggat actcctgctc 240
acagacaccc atctccccct accaaaaata acgctgggct cctccttcca ccttgactct 300
gcctctctgt ctgcaggagc ctggtcgggg tgctccacag aagctgtgcc tgggcttggg 360
agccaaggcc  atg tcc ctc tcc cgg cca ggg gag acg gag ccc atc cac 409
              Met Ser Leu Ser Arg Pro Gly Glu Thr Glu Pro Ile His
              1             5             10

agt gtc agc tat ggc cat gtg gcc gcc tgc cag cta atg ggc ccc cac 457
Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His
  15             20             25

acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc 505
Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Leu Gln Ser Pro
  30             35             40             45

cag gtg agt gag aag agg agt tgt ggg agg agg aga gaa ggg aag cga 553
Gln Val Ser Glu Lys Arg Ser Cys Gly Arg Arg Arg Glu Gly Lys Arg
          50             55             60

tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta 602
Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg  *
          65             70             75

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cagacaataa acaaggaatc ccaggctatg aagacagtga gaaatgctac aaaggaaaga 722
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gaaga 787

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<210> 222
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 <222> (66)..(425)

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aggag  atg ccc agc ctg gag gtg atc acg ctc agg tac ctc gct cct 107
        Met Pro Ser Leu Glu Val Ile Thr Leu Arg Tyr Leu Ala Pro
        1             5             10

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gct gtc atg ctc agc ctg ggg cct gga agc cgg ggc aga gcc tca cgt	155
Ala Val Met Leu Ser Leu Gly Pro Gly Ser Arg Gly Arg Ala Ser Arg	
15 20 25 30	
ccc tcc agt ggg acc cag cac tgt gac ata acc tgg aaa cct cca aca	203
Pro Ser Ser Gly Thr Gln His Cys Asp Ile Thr Trp Lys Pro Pro Thr	
35 40 45	
cag act gag ggc ggc ttc cag aag ggg agg ggc cgg gac agc gag agc	251
Gln Thr Glu Gly Gly Phe Gln Lys Gly Arg Gly Arg Asp Ser Glu Ser	
50 55 60	
tgg gcc tac cct gtg gcc ccc atg ttc agc cct cct tcc tca gag cct	299
Trp Ala Tyr Pro Val Ala Pro Met Phe Ser Pro Pro Ser Ser Glu Pro	
65 70 75	
cac ctg ggc ctc ctg atg gct cct gtc ccc tgc ctg ccc tgc tgt acg	347
His Leu Gly Leu Leu Met Ala Pro Val Pro Cys Leu Pro Cys Cys Thr	
80 85 90	
cct gcc cac cct tgg cct gtg tgc tcc gat aag cca ttg ctg tgt tca	395
Pro Ala His Pro Trp Pro Val Cys Ser Asp Lys Pro Leu Leu Cys Ser	
95 100 105 110	
ctg ggc cag tgc gtg gtg gag ccc tcc taa g gattcacggt ggccccgcct	446
Leu Gly Gln Ser Val Val Glu Pro Ser *	
115 120	
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ccccagtgcc accactgcct accagtttct ctgcaccccc tgacctgtgc ccgtcttctg	566
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 <213> Homo sapiens

<220>
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 <222> (74)..(1732)

<400> 223

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Met Thr Ser Glu Met Thr Arg Ser Pro Phe Ser Asp	
1 5 10	
tgg gaa tct ata tat gtg aca cag gaa tta cct ctg aag cag ttc atg	157
Trp Glu Ser Ile Tyr Val Thr Gln Glu Leu Pro Leu Lys Gln Phe Met	
15 20 25	
tat gat gat gca tgc atg gag gga att act agc tat gga ctt gag tgt	205
Tyr Asp Asp Ala Cys Met Glu Gly Ile Thr Ser Tyr Gly Leu Glu Cys	
30 35 40	
tcc act ttt gaa gaa aat tgg aaa tgg gaa gac ctt ttt gag aag cag	253
Ser Thr Phe Glu Glu Asn Trp Lys Trp Glu Asp Leu Phe Glu Lys Gln	
45 50 55 60	
atg gga agt cat gag atg ttt agc aag aaa gaa ata atc act cat aaa	301
Met Gly Ser His Glu Met Phe Ser Lys Lys Glu Ile Ile Thr His Lys	
65 70 75	
gaa acc atc act aag gaa aca gaa ttc aaa tat act aaa ttt ggg aaa	349
Glu Thr Ile Thr Lys Glu Thr Glu Phe Lys Tyr Thr Lys Phe Gly Lys	
80 85 90	
tgt atc cat ctg gaa aac ata gaa gag agt att tat aat cac aca tca	397
Cys Ile His Leu Glu Asn Ile Glu Glu Ser Ile Tyr Asn His Thr Ser	
95 100 105	
gat aaa aaa agc ttc tcc aaa aat tct att gta ata aaa cac aag aaa	445
Asp Lys Lys Ser Phe Ser Lys Asn Ser Ile Val Ile Lys His Lys Lys	
110 115 120	
gtc tat gta gga aag aag ctt ttt aaa tgt aat gaa tgt gac aaa acc	493
Val Tyr Val Gly Lys Lys Leu Phe Lys Cys Asn Glu Cys Asp Lys Thr	
125 130 135 140	
ttc acc cat agc tca tcc ctt act gtt cat ttt aga att cat act ggt	541
Phe Thr His Ser Ser Ser Leu Thr Val His Phe Arg Ile His Thr Gly	
145 150 155	
gaa aaa cca tat gca tgt gag gaa tgt gga aaa gcc ttc aag caa agg	589
Glu Lys Pro Tyr Ala Cys Glu Glu Cys Gly Lys Ala Phe Lys Gln Arg	
160 165 170	

aatgccagtg aaacagaacc gcttactccc ttgttaaggg ggctgaagcc ggggagccaa	2342
gtggttccca tgcccactga gcccagcaag ctaagatcca ctggcttgga attctccctg	2402
ccagcacagc agtctgaagt caacctggga tgatcaagct tgggtggggg aggggcgcca	2462
accattacca aagcttgaat aggtgggtttt cccctcacag cgtaaacaaa gccatgggga	2522
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tgctaaggga cagactgcct cctcaagtgg gtccctgacc cccatgcctc ctgacgggga	2822
gacacctccc agcaggggtc cacagacacc tcatacagga gagctctggc tggcatctgg	2882
tgggtgcccc tctgggacaa agcttccaga ggaaggaaca ggcagcaatc tttgctgttc	2942
tgcagcctcc actggtgata cccaggcaga cagggctctgg agtggacctc cagcaaactc	3002
cagcagacct gcagccgagg ggcctcactg ttagaaggaa aactaacagg aatataatca	3062
acatcaacaa aggacatcca cacagaaacc ccatctgaag gttaccagca tcaaagacca	3122
aaggtagata aattcacgaa gatgaggaga aaccagtgc aaaaagcctga aaattccaaa	3182
aaccagaatg cctcttctcc tccaaaggat cacaactcct tgccggcaag ggaacaaaac	3242
tggatagaga atgagtttga caaattgaca gaagtaggct tcagaagggtg ggaaataaca	3302
aactcctctg agctaaagga gcatgttcta acccaatgca aggaagctaa gaaccttgaa	3362
aaaaggttag aggaattgct aactagaata accagtttag agaagaacat aaatgacctg	3422
atggagctga aaaacacagc atgagaactt cgtgaagcat acagaagaaa aaccttcagc	3482
cagattgaat gctttacagg gaagaattca tactgcagag cggctttaac aatgtaaaga	3542
atgtgcaa atgtcctcagac aagatgcaca ccttgctcat cagtgagttc atttcaggca	3602
gccagctctt cctcaccac tacatcacca agtcctgtgg atatatctgc taaatatttt	3662
tggaatttat ccacttcttt tgggtcccca gtccaaaaca cagtcatttc acctggacta	3722
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aaaaaaaaag tctgtgcata gttttagtga tacaccacct ccaataagca aaaaagtcct	3902
cacattcaat gggttgcata cccatgaatt ctaaaacttc atcctctttt gtccctttcg	3962
agttaacatt acagccacag tgacctttca aaaatgcaaa ttaagttact cttaaaactc	4022

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tagttaaaat acttgatgta cataaagtgc ttagcaaaat gaccaactca tactaagtgc 4082
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gaaattaatt atgacttgat aaatagaaca tgttttaaga agtggctata tagctctgga 4502
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<210> 224
<211> 1026
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (578)..(916)

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<400> 224
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gactctcagg gccactgctg cacagggtga caaccgggca tggcacgcag tgtggctggt 120
gcagaggagg cttaaggctg gcctgggaga gattcttggc ctagctccca gcacggagcc 180
ttgcttgtgt cccagggcgg cactaaccag aaccagaaaa ggaaatcttt ggccctcggg 240
gagaattatg ccaattatct gtctgggtcc tgtctttgaa aatgcccgaga tgttggttta 300
caaatcagga agctgtcttg gggcaatctc tgttccctct ttgatgcaga gagcctttct 360
ctgtaaacac tggagagcag ggcttcactg tctggctccc ctccgcctc ttgcaggaag 420
gactagatgc tgctgatcag ctgatcatgg ctgagccggg tagagcttgg ggctctccta 480
agaggtcacc cactgggagg gagcttcaca gctgttcttt tgaccagga aggagctctt 540
tcaggactgt ggcaccagga gccgtggccc tctgcc atg cca ttg ttc cca ctt 595

```

Variable	Mean	SD	Min	Max
Age (years)	34.5	10.2	18	65
Gender (Male/Female)	15/15	-	-	-
Marital status (Married/Single)	10/5	-	-	-
Education (High school/College/Postgraduate)	10/5/0	-	-	-
Occupation (Student/Teacher/Other)	10/5/0	-	-	-
Religion (Hindu/Muslim/Other)	10/5/0	-	-	-
Family size (1-3/4-6/7-9/10-12)	10/5/0/0	-	-	-
Income (Monthly)	10/5/0	-	-	-
Health status (Good/Fair/Poor)	10/5/0	-	-	-
Smoking status (Smoker/Non-smoker)	10/5/0	-	-	-
Alcohol consumption (Yes/No)	10/5/0	-	-	-
Exercise frequency (Regular/Irregular/None)	10/5/0	-	-	-
Stress level (Low/Medium/High)	10/5/0	-	-	-
Sleep quality (Good/Fair/Poor)	10/5/0	-	-	-
Dietary habits (Vegetarian/Non-vegetarian)	10/5/0	-	-	-
Hydration status (Adequate/Inadequate)	10/5/0	-	-	-
Work-life balance (Good/Fair/Poor)	10/5/0	-	-	-
Overall well-being (Excellent/Good/Fair/Poor)	10/5/0/0	-	-	-

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<210> 225
<211> 1267
<212> DNA
<213> Homo sapiens
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<400> 225

503

gcc gcc cgc cga agc gag ttc ttc aag acc tat atc tgc ctc ccg ccg 204
Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu Pro Pro
30 35 40 45
gct caa ctg tat cac tgg gtg gag atg cgg acc aag atg cgc atc atg 252
Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met
50 55 60
ggc ttc cgg ggc acg gtc atc aag ccg ctg aac gag gag gcg gca gct 300
Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala
65 70 75
gag ctg ggc gca gag ctg ctg ggc gaa gcc acc atc ttc atc gtg ggc 348
Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly
80 85 90
ggc ggc tgc cta gtg ctg gag tac tgg cgc cac cag gcg cag cag cgc 396
Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg
95 100 105
cac aag gag gag gag gag cag cgt gct gcc tgg aac gcg ctg cgg gac gag 444
His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu
110 115 120 125
gtg ggc cac ctg gcg ctg gcg ctg gaa gcg ctg cag gcg cag gtg cag 492
Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln
130 135 140
gcg gcg ccg cca cag ggc gcc ctg gag gaa ctg cgc aca gag ctg caa 540
Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu Leu Gln
145 150 155
gag gtg cgc gcc cag ctc tgc aat ccc ggc cgg tcc gct tcc cac gca 588
Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser His Ala
160 165 170
gtg cct gcg tcc aag aaa tag ga gcttgctgga tggaacctga atttggacat 641
Val Pro Ala Ser Lys Lys *
175 180
ggcctatgta cctaacgtgg ccttcttccc gcaccaccct tgccctgcgct ggcccagtg 701
aaaccaccag gatcttgatg caacttggca tttggttacc cctgctgata agagcagcca 761
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tgggcactct ggcaaataaa aaaatggaac ctggtcttga gctgaatcaa tgtgttattg 941
ttacccccac ccccggttta cctgatcagt gttaaccttt actgggacac tcatctgtta 1001
cactggaaca ccttcttctt tttgtcaatc ggcacagacc actgtaagga aatgcagtgt 1061
gttgcagtggt ccttttctcc ccctcacctt ctaaggtcag ctctagctga gcatcagtcg 1121

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tctcttaagg aggaaaaaaaaa cgggtgcggtg gggagcggtg gctcacgcct gtaatcctag 1181
caccttggga ggccgaggcg ggcggatcac ttgaggtcag gagttccaga ccagcctggc 1241
caacatggtg aaactccgtc tttcta 1267
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<210> 226
<211> 1813
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (494)..(1126)
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agatcagcct caacaagatg atgagacccc ttctctacaa aagaaattat aaaaaattag 180
tcaggtgtgg tagtacacac ctatagcccc agctactcag gaggctgaag cgggaggatc 240
acttgaggcc aggagtttga ggccatagtg agcaaggatc atgccactgc cctccagcct 300
gggcaacaac gagaccctgt ctctaaaaaa taaataaaaa ctagttcctc gcccgcctggg 360
tgctgaagtt gggcggatgg cagcaaaccg gctccgctag aggaccgagc cgcccagccc 420
cgctcccccg gacccatcgg cgcgctgccc acacctccag gcgaccggcc aactgggtcc 480
tgaagtagct gaa atg cga aaa agg cag cag tcc caa aat gaa gga aca 529
Met Arg Lys Arg Gln Gln Ser Gln Asn Glu Gly Thr
1 5 10

cct gcc gtg tct caa gct cct gga aac cag agg ccc aac aac acc tgt 577
Pro Ala Val Ser Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys
15 20 25

tgc ttt tgt tgg tgc tgt tgt tgc agc tgc tcc tgc ctc act gtg agg 625
Cys Phe Cys Trp Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg
30 35 40

aat gaa gaa aga ggg gaa aat gcg gga aga ccc aca cac act aca aaa 673
Asn Glu Glu Arg Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys
45 50 55 60

atg gag agt atc cag gtc cta gag gaa tgc caa aac ccc act gca gag 721
Met Glu Ser Ile Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu
65 70 75

gaa gtc ttg tcc tgg tct caa aat ttt gac aag atg atg aag gcc cca 769
Glu Val Leu Ser Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro
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80	85	90	
gca gga aga aac ctt ttc aga gag ttc ctc cga aca gaa tac agt gaa			817
Ala Gly Arg Asn Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu			
95	100	105	
gag aac cta ctt ttc tgg ctt gct tgt gaa gac tta aag aag gag cag			865
Glu Asn Leu Leu Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln			
110	115	120	
aac aaa aaa gta att gaa gaa aag gct agg atg ata tat gaa gat tac			913
Asn Lys Lys Val Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr			
125	130	135	140
att tct ata cta tca cca aaa gag gtc agt ctt gat tct cga gtt aga			961
Ile Ser Ile Leu Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg			
145	150	155	
gag gtg atc aat aga aat ctg ttg gat ccc aat cct cac atg tat gaa			1009
Glu Val Ile Asn Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu			
160	165	170	
gat gcc caa ctt cag ata tat act tta atg cac aga gat tct ttt cca			1057
Asp Ala Gln Leu Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro			
175	180	185	
agg ttt ttg aac tct caa att tat aag tca ttt gtt gaa agt act gct			1105
Arg Phe Leu Asn Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala			
190	195	200	
ggc tct tct tct gaa tct taa tg ttcatttaaa aacaatcatt ttggagggct			1158
Gly Ser Ser Ser Glu Ser *			
205	210		
gagatgggaa ataaaagtag ttaaataaca tcagaaactg agttcctgga gaactacagt			1218
ttagcattcc tcaggctact gtgaaaacac aaccgttatg gtctttgtct ccatttttat			1278
caagggttttc catgggttaag tttggagaaa ataccacaca aaacaatgaa ttgccaaatt			1338
gtttgtttta ttcaagactc attctacttg caagcaaagt gtattttagtag tcctatgaac			1398
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atctaagacc caaaaaaag catttttact atggaacaat ggtattcaac aatctatata			1638
ctgtgttttag taccctaatt tttgagccaa tatttctgta ccttaaaaaa aactatttat			1698
ctttgtttgt tggaaaaacc taatggggaa tcctctggtg gtccttgcca aaactgtgga			1758
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<210> 227
 <211> 3404
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (170)..(2119)

<400> 227

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atccggcggc tcagcccggg gcggcgaggc tcggcacgga gatggcgggc cgctcggcgc      120

agacagagct gtgaaccaac cccgctcacg gctaacaagc ccacccacc      atg gcg      175
                                     Met Ala
                                     1

agc ccc act ctg agc ccc gac tcc tca tcc cag gag gcc ctg tcg gcc      223
Ser Pro Thr Leu Ser Pro Asp Ser Ser Ser Gln Glu Ala Leu Ser Ala
          5                      10                      15

ccc acc tgc tcc cca acc tct gac tcc gag aac ctc agc ccc gat gag      271
Pro Thr Cys Ser Pro Thr Ser Asp Ser Glu Asn Leu Ser Pro Asp Glu
          20                      25                      30

ctg gag ctg ctg gcc aag ctc gaa gag cag aac cgg ctc ctg gag gcc      319
Leu Glu Leu Leu Ala Lys Leu Glu Glu Gln Asn Arg Leu Leu Glu Ala
          35                      40                      45                      50

gac tcc aag tcc atg cgc tcc atg aat ggc tcg cgg cgg aac agt ggc      367
Asp Ser Lys Ser Met Arg Ser Met Asn Gly Ser Arg Arg Asn Ser Gly
          55                      60                      65

tcc tcg cta gtg tcc agc tcc tcg gcc tcc tcc aac ctg agc cac ctg      415
Ser Ser Leu Val Ser Ser Ser Ser Ala Ser Ser Asn Leu Ser His Leu
          70                      75                      80

gag gag gac acg tgg atc ctg tgg ggc cgg atc gcc aac gag tgg gag      463
Glu Glu Asp Thr Trp Ile Leu Trp Gly Arg Ile Ala Asn Glu Trp Glu
          85                      90                      95

gag tgg cgg cgc agg aag gag aag ctg ctc aag gag ctg atc cgc aag      511
Glu Trp Arg Arg Arg Lys Glu Lys Leu Leu Lys Glu Leu Ile Arg Lys
          100                      105                      110

ggc atc ccc cac cac ttc cgg gcc atc gtg tgg cag ctt ctg tgc agc      559
Gly Ile Pro His His Phe Arg Ala Ile Val Trp Gln Leu Leu Cys Ser
          115                      120                      125                      130

gcc acg gac atg ccc gtc aag aac cag tac tcc gag ctg ctc aag atg      607
Ala Thr Asp Met Pro Val Lys Asn Gln Tyr Ser Glu Leu Leu Lys Met
          135                      140                      145

tcc tcg ccg tgc gag aag ctg atc cgc agg gac atc gcc cgc acc tac      655

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375	380	385	
gag aac cgg ctc ctg aaa cag cgg att gaa acc cta gag aag gag agc Glu Asn Arg Leu Leu Lys Gln Arg Ile Glu Thr Leu Glu Lys Glu Ser 390 395 400			1375
gct gct ctg gct gat agg tta atc cag ggg caa gtg aca cgg gcg cag Ala Ala Leu Ala Asp Arg Leu Ile Gln Gly Gln Val Thr Arg Ala Gln 405 410 415			1423
gag gcg gag gag aac tac gtc atc aag cgg gag ctg gcg gtg gtg cgg Glu Ala Glu Glu Asn Tyr Val Ile Lys Arg Glu Leu Ala Val Val Arg 420 425 430			1471
cag cag tgc agc tcg gcg gcc gag gac ctg cag aag gca cag agc acc Gln Gln Cys Ser Ser Ala Ala Glu Asp Leu Gln Lys Ala Gln Ser Thr 435 440 445 450			1519
atc cgg cag cta cag gag cag cag gag aac ccc cgc ctc aca gaa gac Ile Arg Gln Leu Gln Glu Gln Gln Glu Asn Pro Arg Leu Thr Glu Asp 455 460 465			1567
ttc gtg tcc cac ctg gag acc gag ctg gag cag tcg agg ctg cgg gag Phe Val Ser His Leu Glu Thr Glu Leu Glu Gln Ser Arg Leu Arg Glu 470 475 480			1615
acg gag aca ctg ggg gcc ctt cgg gag atg cag gac aag gtt ctc gac Thr Glu Thr Leu Gly Ala Leu Arg Glu Met Gln Asp Lys Val Leu Asp 485 490 495			1663
atg gaa aag agg aac agc tcg ctg ccc gac gag aac aat gtg gcg cag Met Glu Lys Arg Asn Ser Ser Leu Pro Asp Glu Asn Asn Val Ala Gln 500 505 510			1711
ctg cag gag gag ctg aag gcg ctc aag gtg cgg gaa ggc cag gcg gtg Leu Gln Glu Glu Leu Lys Ala Leu Lys Val Arg Glu Gly Gln Ala Val 515 520 525 530			1759
gcc tcg acg cga gag ctt aaa ctg cag ctg cag gag ctc tcg gac acc Ala Ser Thr Arg Glu Leu Lys Leu Gln Leu Gln Glu Leu Ser Asp Thr 535 540 545			1807
tgg cag gac cag atc gag gag ctg aag acc gag gtg cgg ctg ctg aag Trp Gln Asp Gln Ile Glu Glu Leu Lys Thr Glu Val Arg Leu Leu Lys 550 555 560			1855
ggc ccg ccg ccc ttc gag gac ccg ctg gct ttc gat ggg ctg agc ctg Gly Pro Pro Pro Phe Glu Asp Pro Leu Ala Phe Asp Gly Leu Ser Leu 565 570 575			1903
gcg cgg cac ttg gac gag gac tcg ctg ccg tcg tcg gac gag gag cta Ala Arg His Leu Asp Glu Asp Ser Leu Pro Ser Ser Asp Glu Glu Leu 580 585 590			1951
ctt ggc gta ggc gtg ggc gct gcc ctg cag gac gca ttg tac cct ctg Leu Gly Val Gly Val Gly Ala Ala Leu Gln Asp Ala Leu Tyr Pro Leu 595 600 605 610			1999

tcc ccg cgc gat gcg cgc ttc ttc cgc cgt ctg gag cgg ccg gcc aag	2047
Ser Pro Arg Asp Ala Arg Phe Phe Arg Leu Glu Arg Pro Ala Lys	
615 620 625	
gac agc gag ggc agc tca gac agc gac gcc gat gag ctg gcc gcg ccc	2095
Asp Ser Glu Gly Ser Ser Asp Ser Asp Ala Asp Glu Leu Ala Ala Pro	
630 635 640	
tac agc cag ggt ctg gac aac tga ggccatgccc agcgcgcccc gagtcaggag	2149
Tyr Ser Gln Gly Leu Asp Asn *	
645 650	
gccgcagccg cgggggggcgc ccgggcagtc cgcgttctgc tccccacctg ccgcacttga	2209
caaaactacgc gccctctgtg gctcggccac ccctaaagcg agggcccggcg aggcagcgca	2269
gagggtaggg tccgacctgg gctcctcagg gccccggggc aggcctctctc tccccagcag	2329
tgtttacceca tcttgggtctg taccctccg ggccctctgg cgttccaggg gtgcctggag	2389
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cattgctggg aagtgtctag gaggtagccg aggcctgagg aaggagagcg ccagctctgg	2569
gctggacatc agcacccac aacactcctc gggatgaagt gacccttgac tagcccttgg	2629
ccatctctag gggagtcagg ccgctgggga cagatggcca ggccggcctc tcctgcctgg	2689
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cccagcgagc ggccctccct cacttctcc tgggtgtccc gttgtctctg ctgaatcaga	3049
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ttcctagctg cccacttttc agtggttacga agcctgggga ccggggcagg caccacggg	3289
gctctocaca cgcacctac actgcccgc accattttgc aactgcctg ttcacatgtc	3349
gcccaggcgg gaaaaatgga aaataaagtg tatttacaca gtcaaaaaaa aaaaa	3404

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (331)..(1167)

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 agcagcgagg acacctgcag aaatacattc ccaaagcaag gctgggcggc cgtgtgaagt 180
 aagcaatggc ctcagttttg cttctgtttt ggatgaacac caccacatag ggcttgaatg 240
 tgaaagaaga ccctctatctt gtctgttccg gggcagcctg gtagtaaaac actgttgaat 300
 gggccacagt ttcagcagac catcaggtga atg gga cca gtc tct ctt ctt 351
 Met Gly Pro Val Ser Leu Leu
 1 5
 cca aaa tat cag aag tta aac act tgg aac gga gat ttg gcc aag atg 399
 Pro Lys Tyr Gln Lys Leu Asn Thr Trp Asn Gly Asp Leu Ala Lys Met
 10 15 20
 acc cat tta cag gct gga ctc agt cca gag act ata gag aaa gct cgc 447
 Thr His Leu Gln Ala Gly Leu Ser Pro Glu Thr Ile Glu Lys Ala Arg
 25 30 35
 ctg gaa ctg aat gaa aac ccc gat gtt tta cat cag gat att cag caa 495
 Leu Glu Leu Asn Glu Asn Pro Asp Val Leu His Gln Asp Ile Gln Gln
 40 45 50 55
 gtc agg gac atg atc atc acc agg cct gac att gga ttt tta cgt aca 543
 Val Arg Asp Met Ile Ile Thr Arg Pro Asp Ile Gly Phe Leu Arg Thr
 60 65 70
 gat gat gcc ttc atc ctg aga ttt ctc cga gcc agg aag ttt cac caa 591
 Asp Asp Ala Phe Ile Leu Arg Phe Leu Arg Ala Arg Lys Phe His Gln
 75 80 85
 gcg gat gcc ttt aga ctc ctg gct cag tat ttc cag tac cgc cag cta 639
 Ala Asp Ala Phe Arg Leu Leu Ala Gln Tyr Phe Gln Tyr Arg Gln Leu
 90 95 100
 aac ctg gac atg ttc aaa aac ttc aag gca gat gat ccc ggc att aag 687
 Asn Leu Asp Met Phe Lys Asn Phe Lys Ala Asp Asp Pro Gly Ile Lys
 105 110 115
 agg gct ctg atc gat ggg ttc ccc ggg gtg ctg gaa aac cga gac cat 735
 Arg Ala Leu Ile Asp Gly Phe Pro Gly Val Leu Glu Asn Arg Asp His
 120 125 130 135

tac ggc agg aag att ctt ttg ctg ttt gca gcc aat tgg gat cag agt	783
Tyr Gly Arg Lys Ile Leu Leu Leu Phe Ala Ala Asn Trp Asp Gln Ser	
140 145 150	
agg aac tcc ttc aca gac atc ctt cgt gcc atc ctg ctg tca ttg gaa	831
Arg Asn Ser Phe Thr Asp Ile Leu Arg Ala Ile Leu Leu Ser Leu Glu	
155 160 165	
gtc cta atc gaa gat ccg gag ctt cag ata aat ggc ttc att tta att	879
Val Leu Ile Glu Asp Pro Glu Leu Gln Ile Asn Gly Phe Ile Leu Ile	
170 175 180	
ata gac tgg agt aat ttt tcc ttc aaa caa gcc tcc aaa ctg aca cct	927
Ile Asp Trp Ser Asn Phe Ser Phe Lys Gln Ala Ser Lys Leu Thr Pro	
185 190 195	
tca atc ctt aaa ctg gcc att gaa ggg ttg cag gac agc ttt cct gcc	975
Ser Ile Leu Lys Leu Ala Ile Glu Gly Leu Gln Asp Ser Phe Pro Ala	
200 205 210 215	
cgc ttt gga gga gtc cac ttt gtc aac cag ccc tgg tac att cat gcc	1023
Arg Phe Gly Gly Val His Phe Val Asn Gln Pro Trp Tyr Ile His Ala	
220 225 230	
ctc tac aca ctc atc aag cca ttt ctt aaa gac aag acc agg aaa cgg	1071
Leu Tyr Thr Leu Ile Lys Pro Phe Leu Lys Asp Lys Thr Arg Lys Arg	
235 240 245	
att ttc ctg cat gga aac aat tta aac agc ctt cac cag cta ata cac	1119
Ile Phe Leu His Gly Asn Asn Leu Asn Ser Leu His Gln Leu Ile His	
250 255 260	
cct gaa ttt ttg ccc tct gaa ttt gga gga act ctt cct ccc tta tga	1167
Pro Glu Phe Leu Pro Ser Glu Phe Gly Gly Thr Leu Pro Pro Leu *	
265 270 275	
catgggaact tgggcccgga cggttactcgg tcccgaactac agcgatgaaa atgactatac	1227
tcacacatcc tataatgcaa tgcacgtgaa gcatacgtcc tcgaatctgg agagagaatg	1287
ctcaccceaag ctgatgaaaa gatctcagtc tgtggtagaa gctggggaccc tgaaacatga	1347
ggagaaggga gagaatgaga acaccagcc actcctggct ctggactgaa ccctgagtca	1407
ccccaatgct cctgcacact ggccttcagt ggtatcagcc acccaggaag cacatgcaca	1467
actgacccat gcagacacgt gtgtttctgct tgacacaagg tcctccactc ctgaaccctt	1527
gcagtgactg tcaccagcca tcggtctgag cagccaaagt tggacaaaga cttgagagat	1587
gctttttttt tccccagtg aggggactgg aggatgatgc aaggcattta tgtaaaaaag	1647
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 agtcagattc tgactctgca taccctcca atg gct ttc gcc acc ccc aaa 171
 Met Ala Phe Ala Thr Pro Lys
 1 5
 tca ctt gga gta aaa gcc gaa gtc ctt cca gca gct tac cag gtg ctg 219
 Ser Leu Gly Val Lys Ala Glu Val Leu Pro Ala Ala Tyr Gln Val Leu
 10 15 20
 cat gat cca gac tcc ttc tta gcc ctc tgg ctc tcc tgc tgc tct cct 267
 His Asp Pro Asp Ser Phe Leu Ala Leu Trp Leu Ser Cys Cys Ser Pro
 25 30 35
 tct tca ttt ctc tct agc cac acc agc ttt ctt gct gag agc act ggg 315
 Ser Ser Phe Leu Ser Ser His Thr Ser Phe Leu Ala Glu Ser Thr Gly
 40 45 50 55
 tgc tct gtc tac act att ctc caa aat atc cat atg gtt tgt cct cct 363
 Cys Ser Val Tyr Thr Ile Leu Gln Asn Ile His Met Val Cys Pro Pro
 60 65 70
 tca ttt act ttc ttg aat tcc acg gtc tca gtg aga tta cct tgg cat 411
 Ser Phe Thr Phe Leu Asn Ser Thr Val Ser Val Arg Leu Pro Trp His
 75 80 85
 cct agt taa agctgct gcctgtcctc tcaccctgcg tcttgcagtc ccctttctag 467
 Pro Ser *
 90
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[illegible]

514

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190 195 200	
atc ggc gcg ttg cgg ggc cat gag gac aag atc cgc gtg gtg ctc aac	854
Ile Gly Ala Leu Arg Gly His Glu Asp Lys Ile Arg Val Val Leu Asn	
205 210 215	
aag gcc gac atg gtg gag acg cag cag ctg atg cgc gtc tac ggc gcg	902
Lys Ala Asp Met Val Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala	
220 225 230 235	
ctc atg tgg gcg ctg ggc aag gtg gtg ggc acg ccc gag gtg ctg cgc	950
Leu Met Trp Ala Leu Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg	
240 245 250	
gtc tac atc ggc tcc ttc tgg tcc cag ccc ctc ctc gtg ccc gac aac	998
Val Tyr Ile Gly Ser Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn	
255 260 265	
cgg cgc ctc ttc gag ctg gag gag cag gac ctc ttc cgc gac atc cag	1046
Arg Arg Leu Phe Glu Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln	
270 275 280	
ggc ctg ccc cgg cac gca gcc ttg cgc aag ctc aac gac ctg gtg aag	1094
Gly Leu Pro Arg His Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys	
285 290 295	
agg gcc cgg ctg gtg cga gtt cac gct tac atc atc agc tac ctg aag	1142
Arg Ala Arg Leu Val Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys	
300 305 310 315	
aag gag atg ccc tct gtg ttt ggg aag gag aac aag aag aag cag ctg	1190
Lys Glu Met Pro Ser Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu	
320 325 330	
atc ctc aaa ctg ccc gtc atc ttt gcg aag att cag ctg gaa cat cac	1238
Ile Leu Lys Leu Pro Val Ile Phe Ala Lys Ile Gln Leu Glu His His	
335 340 345	
atc tcc cct ggg gac ttt cct gat tgc cag aaa atg cag gag ctg ctg	1286
Ile Ser Pro Gly Asp Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu	
350 355 360	
atg gcg cac gac ttc acc aag ttt cac tcg ctg aag ccg aag ctg cta	1334
Met Ala His Asp Phe Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu	
365 370 375	
gag gca ctg gac gag atg ctg acg cac gac atc gcc aag ctc atg ccc	1382
Glu Ala Leu Asp Glu Met Leu Thr His Asp Ile Ala Lys Leu Met Pro	
380 385 390 395	
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Leu Leu Arg Gln Glu Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly	
400 405 410	

ggc gct ttt gag ggc acc cac atg ggc ccg ttt gtg gag cgg gga cct	1478
Gly Ala Phe Glu Gly Thr His Met Gly Pro Phe Val Glu Arg Gly Pro	
415 420 425	
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Asp Glu Ala Met Glu Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu	
430 435 440	
tgg gtg gtg acc aaa gac aag tcc aaa tac gac gag atc ttc tac aac	1574
Trp Val Val Thr Lys Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn	
445 450 455	
ctg gcg cct gcc gac ggc aag ctg agc ggc tcc aag gcc aag acc tgg	1622
Leu Ala Pro Ala Asp Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp	
460 465 470 475	
atg gtg ggg acc aag ctc ccc aac tca gtg ctg ggg cgc atc tgg aag	1670
Met Val Gly Thr Lys Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys	
480 485 490	
ctc agc gat gtg gac cgc gac ggc atg ctg gat gat gaa gag ttc gcg	1718
Leu Ser Asp Val Asp Arg Asp Gly Met Leu Asp Asp Glu Glu Phe Ala	
495 500 505	
ctg gcc agc cac ctc atc gag gcc aag ctg gaa ggc cac ggg ctg ccc	1766
Leu Ala Ser His Leu Ile Glu Ala Lys Leu Glu Gly His Gly Leu Pro	
510 515 520	
gcc aac ctg ccc cgt cgc ctg gtg cca ccc tcc aag cga cgc cac aag	1814
Ala Asn Leu Pro Arg Arg Leu Val Pro Pro Ser Lys Arg Arg His Lys	
525 530 535	
ggc tcc gcc gag tga gccggggcccc cctcccatgg ccttgcctgtg gctccccagc	1869
Gly Ser Ala Glu *	
540	
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tcattcaaatt atttattgag cacctactat gtgcccagcc ctgtttctagg cactgggcat	2169
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gggaccatgg ggggctcaga ggggagacac acctactgct tcttcagatg ggcccctccg	2469
cagccccttc ccttgctcgg ggaaagcccc caattctgcc cacacccatt tatttccttc	2529


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cttccttcc tcttttcttt ccttccttcc ttcttttttg tttttgcccc caattctgcc 2589
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ctgtccgctg ccaaggggaag tgacagccgc agccgggctc tcagccagcg gccgggcgcc 180
ccgcggaacc atg ctc tcc agt acg cag aac gcg ggc ggc tcc tat cag 228
          Met Leu Ser Ser Thr Gln Asn Ala Gly Gly Ser Tyr Gln
            1                   5                   10

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cgg gtc cgc ggg gcg ctt gat aca cag aaa tgc agt cca gag aaa agt	276
Arg Val Arg Gly Ala Leu Asp Thr Gln Lys Cys Ser Pro Glu Lys Ser	
15 20 25	
gcc tca ttt ttc agt aaa gtg aca tat tcc tgg ttt agc aga gta att	324
Ala Ser Phe Phe Ser Lys Val Thr Tyr Ser Trp Phe Ser Arg Val Ile	
30 35 40 45	
act tta ggc tat aag aga cct ttg gaa aga gag gat ctt ttt gaa cta	372
Thr Leu Gly Tyr Lys Arg Pro Leu Glu Arg Glu Asp Leu Phe Glu Leu	
50 55 60	
aag gaa agt gat tcc ttc tgc act gcg tgt ccc atc ttt gaa aaa caa	420
Lys Glu Ser Asp Ser Phe Cys Thr Ala Cys Pro Ile Phe Glu Lys Gln	
65 70 75	
tgg aga aag gaa gtt tta agg aat caa gag agg caa aaa gta aag gta	468
Trp Arg Lys Glu Val Leu Arg Asn Gln Glu Arg Gln Lys Val Lys Val	
80 85 90	
tct tgt tat aaa gag gca cat atc aag aaa cca tct cta ctc tat gca	516
Ser Cys Tyr Lys Glu Ala His Ile Lys Lys Pro Ser Leu Leu Tyr Ala	
95 100 105	
ttg tgg aac acc ttt aaa tcc atc ctg att caa gtt gcc tta ttc aaa	564
Leu Trp Asn Thr Phe Lys Ser Ile Leu Ile Gln Val Ala Leu Phe Lys	
110 115 120 125	
gtg ttt gct gat att ttg tcc ttc act agc cca ctc ata atg aag caa	612
Val Phe Ala Asp Ile Leu Ser Phe Thr Ser Pro Leu Ile Met Lys Gln	
130 135 140	
att atc att ttc tgt gaa cac agc tca gat ttt ggc tgg aat ggc tat	660
Ile Ile Ile Phe Cys Glu His Ser Ser Asp Phe Gly Trp Asn Gly Tyr	
145 150 155	
ggc tat gca gtg gca ctt ctt gtt gta gtc ttt ttg caa act ctg att	708
Gly Tyr Ala Val Ala Leu Leu Val Val Phe Leu Gln Thr Leu Ile	
160 165 170	
ctt cag caa tat caa cgt ttt aac atg ctc acc tca gca aaa gtt aag	756
Leu Gln Gln Tyr Gln Arg Phe Asn Met Leu Thr Ser Ala Lys Val Lys	
175 180 185	
aca gct gta aat gga ctg atc tac aaa aag gcc tta ctt tta tca aat	804
Thr Ala Val Asn Gly Leu Ile Tyr Lys Lys Ala Leu Leu Leu Ser Asn	
190 195 200 205	
gtt tct cga caa aag ttt tcc act ggg gaa att att aac ttg atg tca	852
Val Ser Arg Gln Lys Phe Ser Thr Gly Glu Ile Ile Asn Leu Met Ser	
210 215 220	
gca act cat gga ctt gac agc aaa cct caa tct cct ctg gtc tgc ccc	900
Ala Thr His Gly Leu Asp Ser Lys Pro Gln Ser Pro Leu Val Cys Pro	
225 230 235	

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ttt tca aat cct aat ggc cgt ata tct cct ttg gca aga gct ggg tcc      948
Phe Ser Asn Pro Asn Gly Arg Ile Ser Pro Leu Ala Arg Ala Gly Ser
      240                      245                      250

agc agt gtt agc agg ggt ggc agt cct tgt gtt tgt tat acc aat aaa      996
Ser Ser Val Ser Arg Gly Gly Ser Pro Cys Val Cys Tyr Thr Asn Lys
      255                      260                      265

tgc ttt agc tgc aac taa aataaa aaagttaaag gtaaaaaaat gactgcctca    1050
Cys Phe Ser Cys Asn  *
      270                      275

tgttacatgt gtcaaacagg agctgagttt tctgacttga gttaacaatc accatctcgc    1110

taattatata gagagagtta caaatggaag tcatcgaatt ttatcattta cttattcact    1170

caaccagtat tgaacaagca tgtatcttat gtcagccagt gtttcaggca caggaagtac    1230

agcagtgagg ggaaatgaca agtccagctc tcatgagggg tagtggagga gacaggcatt    1290

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Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys
      5                      10                      15

cac caa ccc cat aaa gtg aca cag tac aag aag ggc aag gat tct ctg      154
His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu
      20                      25                      30

tac gcc cag gga aag cgg cgt tat gac agg aag cag agt ggc tat ggt      202
Tyr Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly
      35                      40                      45

ggg caa act aag ccg att ttc cgg aaa aag gct aaa act aca aag aag      250
Gly Gln Thr Lys Pro Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys
      50                      55                      60                      65

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att gtg cta agg ctt gag tgc gtt gag ccc aac tgc aga tct aag aga      298
Ile Val Leu Arg Leu Glu Cys Val Glu Pro Asn Cys Arg Ser Lys Arg
              70                      75                      80

atg ctg gct att aaa aga tgc aag cat ttt gaa ctg gga gga gat aag      346
Met Leu Ala Ile Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp Lys
              85                      90                      95

aag aga aag gta tat aat tat ggg tgc gaa ggt gca atc ttt ctc ata      394
Lys Arg Lys Val Tyr Asn Tyr Gly Ser Glu Gly Ala Ile Phe Leu Ile
              100                     105                     110

gct tta tta ttt cga aaa ggt gaa cat cta ttc ctt gtg gca tag agc      442
Ala Leu Leu Phe Arg Lys Gly Glu His Leu Phe Leu Val Ala *
              115                     120                     125

tcaggggtaa tcctctaaaa atattagatc tatagctaaa gatatgtgag gtcttttgct      502

acaaggagga aaggaagaat gaggaagctt aacagcatgg tgactatttt aggaacagat      562

aatgtttctta atggggcagt agttcatggc aaaatacaaaa acaacttttt tctgttctgc      622

ttacagggcc aagtgatcca gttttaagtg tcattcttta ttatgaagac aataaaatct      682

tgagtttatg ttcaaaaaaa aaaaaa                                          707

<210> 233
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<220>
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<400> 233
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cgagctcgga tccactagtc cagtgtggtg gaattccata atg tat agt att tct      115
Met Tyr Ser Ile Ser
              1                      5

cct gcc aac tct gag gaa ggc cag gaa ctt tat gtc tgc aca gtc aag      163
Pro Ala Asn Ser Glu Glu Gly Gln Glu Leu Tyr Val Cys Thr Val Lys
              10                      15                      20

gat gat gtg aac ttg gat aca gta ctt ctc cta ccc ttt ttg aaa gaa      211
Asp Asp Val Asn Leu Asp Thr Val Leu Leu Leu Pro Phe Leu Lys Glu
              25                      30                      35

ata gca gta agc caa ctg gat caa ctg agc cca gag gaa cag ttg ctg      259
Ile Ala Val Ser Gln Leu Asp Gln Leu Ser Pro Glu Glu Gln Leu Leu
              40                      45                      50

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gtc aag tgt gct gca atc att ggt cac tcc ttc cat ata gat ttg ctg 307
Val Lys Cys Ala Ala Ile Ile Gly His Ser Phe His Ile Asp Leu Leu
55 60 65

cag cac ctg ctg cct ggc tgg gat aaa aat aag cta ctt cag gtc ttg 355
Gln His Leu Leu Pro Gly Trp Asp Lys Asn Lys Leu Leu Gln Val Leu
70 75 80 85

aga gct ctt gtg gat ata cat gtg ctg tgc tgg tct gac aag agc caa 403
Arg Ala Leu Val Asp Ile His Val Leu Cys Trp Ser Asp Lys Ser Gln
90 95 100

gag ctt cct gct gag ccc ata tta atg cct tcc tct atc gac atc att 451
Glu Leu Pro Ala Glu Pro Ile Leu Met Pro Ser Ser Ile Asp Ile Ile
105 110 115

gat gga acc aaa gag aag aag aca aag tta gat ggt ggg tca gcc tct 499
Asp Gly Thr Lys Glu Lys Lys Thr Lys Leu Asp Gly Gly Ser Ala Ser
120 125 130

ctt ctg agg cta caa gaa gaa tta tcc cta cca cag gca gca ctg aaa 547
Leu Leu Arg Leu Gln Glu Leu Ser Leu Pro Gln Ala Ala Leu Lys
135 140 145

cag aca ata gac agc ttc cac ccc act aca cgc ctg cag caa cac agc 595
Gln Thr Ile Asp Ser Phe His Pro Thr Thr Arg Leu Gln Gln His Ser
150 155 160 165

ccg gct gca cag gct ctg gta tgc gac cat cat gct tgc agt agc ccg 643
Pro Ala Ala Gln Ala Leu Val Cys Asp His His Ala Cys Ser Ser Pro
170 175 180

gtc ttt gca cgg cta cct cta gag cac ctt cag aaa tgc cct taa gca 691
Val Phe Ala Arg Leu Pro Leu Glu His Leu Gln Lys Cys Pro *
185 190 195

tgctgggggtc acgtgtcatg caaaccttgg acagatgact gaacctctct atgccttggt 751

ttcttcatct gtgtagacgc cagtgcgat gtctccttcc tcaggtcggg gactatctgg 811

gaccaaggt tct 824

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agctgggtcat	gctgagctca	taccctgatg	gctgctccat	gaggtcaaga	ctgggtctcc	180
tccctcctcc	cccttcacca	atgcctgggc	tcacggggct	agttttgacc	cccacgct	238
atg gca tca tgc acc tcc ctc cca gct cct ggc tct cgg cct aag aag	286					
Met Ala Ser Ser Thr Ser Leu Pro Ala Pro Gly Ser Arg Pro Lys Lys						
1 5 10 15						
cct cta ggc aag atg gct gac tgg ttc agg cag acc ctg ctg aag aag	334					
Pro Leu Gly Lys Met Ala Asp Trp Phe Arg Gln Thr Leu Leu Lys Lys						
20 25 30						
ccc aag aag agg ccc aac tcc cca gaa agc acc tcc agc gat gct tca	382					
Pro Lys Lys Arg Pro Asn Ser Pro Glu Ser Thr Ser Ser Asp Ala Ser						
35 40 45						
cag cct acc tca cag gac agc cca cta ccc cca agc ctc agc tca gtc	430					
Gln Pro Thr Ser Gln Asp Ser Pro Leu Pro Pro Ser Leu Ser Ser Val						
50 55 60						
acg tct ccc agc ctg cca ccc aca cat gcg agt gac agt ggc agt agt	478					
Thr Ser Pro Ser Leu Pro Thr His Ala Ser Asp Ser Gly Ser Ser						
65 70 75 80						
cgc tgg agc aaa gac tat gac gtc tgc gtg tgc cac agt gag gaa gac	526					
Arg Trp Ser Lys Asp Tyr Asp Val Cys Val Cys His Ser Glu Glu Asp						
85 90 95						
ctg gtg gcc gcc cag gac ctg gtc tcc tac ttg gaa ggc agc act gcc	574					
Leu Val Ala Ala Gln Asp Leu Val Ser Tyr Leu Glu Gly Ser Thr Ala						
100 105 110						
agc ctg cgc tgc ttc ctg caa ctc cgg gat gca acc cca ggc ggc gct	622					
Ser Leu Arg Cys Phe Leu Gln Leu Arg Asp Ala Thr Pro Gly Gly Ala						
115 120 125						
ata gtg tcc gag ctg tgc cag gca ctg agc agt agt cac tgc cgg gtg	670					
Ile Val Ser Glu Leu Cys Gln Ala Leu Ser Ser Ser His Cys Arg Val						
130 135 140						
ctg ctc atc acg ccg ggc ttc ctt cag gac ccc tgg tgc aag tac cag	718					
Leu Leu Ile Thr Pro Gly Phe Leu Gln Asp Pro Trp Cys Lys Tyr Gln						
145 150 155 160						
atg ctg cag gcc ctg acc gag gct cca ggg gcc gag ggc tgc acc atc	766					
Met Leu Gln Ala Leu Thr Glu Ala Pro Gly Ala Glu Gly Cys Thr Ile						
165 170 175						
ccc ctg ctg tgc ggc ctc agc aga gct gct tac cca cct gag ctc cga	814					
Pro Leu Leu Ser Gly Leu Ser Arg Ala Ala Tyr Pro Pro Glu Leu Arg						
180 185 190						
ttc atg tac tac gtc gat ggc agg ggc cct gat ggt ggc ttt cgt caa	862					
Phe Met Tyr Tyr Val Asp Gly Arg Gly Pro Asp Gly Gly Phe Arg Gln						
195 200 205						

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gtc aaa gaa gct gtc atg cgt tgt aag cta cta cag gag gga gaa ggg      910
Val Lys Glu Ala Val Met Arg Cys Lys Leu Leu Gln Glu Gly Glu Gly
    210                      215                      220

gaa cgg gat tca gct aca gta ttt gat cta ctt tga cttt taggagacag      960
Glu Arg Asp Ser Ala Thr Val Phe Asp Leu Leu *
    225                      230                      235

ccctgtagcc tagtagttca aagcgcagct tctggaagag gctgtcgggg tttgtatcct    1020

ggctcctgcc cttattaacc cataaaaagt aacttggtca agttaaaaaa aaaaaaa      1077

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<210> 235
<211> 916
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (169)..(738)

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<400> 235
agctggctag cgtttaaact taagcttggg accgagctcg gatccactag tccagtgtgg      60

tggaattcca cagccagta actttgctag tacctcttga gtgcaagggtg gagaattaag    120

atctggattt gagacggagc acggaacatt tcactcaggg gaagagct atg aac atg      177
                               Met Asn Met
                               1

ctg act gcc agc ctg ttg agg gca gtc ata gcc tcc atc tgt gtt gta      225
Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val
    5                      10                      15

tcc agc atg gct cag aag gta act caa gcg cag act gaa att tct gtg      273
Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val
    20                      25                      30                      35

gtg gag aag gag gat gtg acc ttg gac tgt gtg tat gaa acc cgt gat      321
Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp
                40                      45                      50

act act tat tac tta ttc tgg tac aag caa cca cca agt gga gaa ttg      369
Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu
                55                      60                      65

gtt ttc ctt att cgt cgg aac tct ttt gat gag caa aat gaa ata agt      417
Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser
    70                      75                      80

ggg cgg tat tct tgg aac ttc cag aaa tcc acc agt tcc ttc aac ttc      465
Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe
    85                      90                      95

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40	45	50	
gag agc tgg atg cac cat tgg ctc ctg ttt gaa atg agc agg cac tcc			247
Glu Ser Trp Met His His Trp Leu Leu Phe Glu Met Ser Arg His Ser			
55	60	65	70
ttg gag caa aag ccc act gac gct cca ccg aaa gta ctg acc aag tgc			295
Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys Val Leu Thr Lys Cys			
	75	80	85
cag gaa gag gtc agc cac atc cct gct gtc cac ccg ggt tca ttc agg			343
Gln Glu Glu Val Ser His Ile Pro Ala Val His Pro Gly Ser Phe Arg			
	90	95	100
ccc aag tgc gac gag aac ggc aac tat ctg cca ctc cag tgc tat ggg			391
Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro Leu Gln Cys Tyr Gly			
	105	110	115
agc atc ggc tac tgc tgg tgt gtc ttc ccc aac ggc acg gag gtc ccc			439
Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn Gly Thr Glu Val Pro			
	120	125	130
aac acc aga agc cgc ggg cac cat aac tgc agt gag tca ctg gaa ctg			487
Asn Thr Arg Ser Arg Gly His His Asn Cys Ser Glu Ser Leu Glu Leu			
	135	140	145
gag gac ccg tct tct ggg ctg ggt gtg acc aag cag gat ctg ggc cca			535
Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Leu Gly Pro			
	155	160	165
gtc ccc atg tga gag cagcagaggc ggtcttcaac atcctgccag cccacacag			590
Val Pro Met *			
	170		
ctacagcttt cttgctccct tcagcccca gccctcccc catctccac cctgtacctc			650
atcccatgag accctggtgc ctggctcttt cgtcaccctt ggacaagaca aaccaagtcg			710
gaacagcaga taacaatgca gcaaggccct gctgcccaat ctccatctgt caacaggggc			770
ggtcgacgcg gccgcgaatt cggatcctcg agagatctct ttttttgggt ttggtggggt			830
gtcttcatca tcggatatata taggtatata catcggccta tcaagg			876

<210> 237
 <211> 753
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (168)..(419)

 <400> 237

CCDS: CCDS10000.1

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gtccgtgcgc accgcccggc gtccaggtga gtctcccatc tgcagagacg cggacgcgcc      60
ggccccgcagt tggcctgcgg agcgcggtgg acggtttggc gcccaccagg cgatcaatac      120
tttggaatttt taattttctag atttggcaat tcttcgctga agtcatac  atg agc ttt      176
                                     Met Ser Phe
                                     1

ttc caa ctc ctg atg aaa agg aag gaa ctc att ccc ttg gtg gtg ttc      224
Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val Val Phe
      5                      10                      15

atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat tct ctt      272
Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr Ser Leu
      20                      25                      30                      35

tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa cct tgg      320
Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu Pro Trp
                      40                      45                      50

gaa act gtg gac cct act gta cct caa aag ctt ata aca atc aac caa      368
Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile Asn Gln
                      55                      60                      65

caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg acc aaa      416
Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val Thr Lys
                      70                      75                      80

tga cgag cctcgcctc tttcttctga agagtactct ataaatctag tggaaacatt      473
*

tctgcacaaa ctagattctg gacaccagtg tgcggaaatg cttctgctac attttttaggg      533

tttgtctaca ttttttgggc tctggataag gaattaaagg agtgcagcaa taactgcact      593

gtctaaaagt ttgtgcttat tttcttgtaa atttgaatat tgcataattga aatttttggt      653

tatgatctat gaatgttttt cttaaaattt acaaagcttt gtaaattaga ttttctttaa      713

taaaatgccca tttgtgcaag atttctcaaa aaaaaaaaaa      753

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<210> 238
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1060)

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<400> 238
gagtgggtgga attccgctgg cctcgcctcg tgcgcgcctc cctccccgc  atg cag      55
                                     Met Gln

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ccc gcc gag cgc tgc cgg gtc ccc agg atc gac ccg tac gga ttc gag	103
Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly Phe Glu	
5 10 15	
cgg cct gag gac ttc gac gac gcc gcc tac gag aag ttt ttc tcc agc	151
Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe Ser Ser	
20 25 30	
tac ctg gtc acg ctc acc cgc agg gcg atc aaa tgg tcc cgg ctg ctg	199
Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg Leu Leu	
35 40 45 50	
cag ggc ggg ggc gtc ccc agg agc cgg aca gtg aag cgc tat gtc cgg	247
Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr Val Arg	
55 60 65	
aaa ggg gtc ccg ctg gag cac cgt gcc cgc gtc tgg atg gtg ctg agt	295
Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val Leu Ser	
70 75 80	
ggg gcc cag gcg cag atg gac cag aat ccc ggc tac tac cac cag ctt	343
Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His Gln Leu	
85 90 95	
ctc cag gga gag aga aac ccc agg ctg gag gac gcc atc agg aca gac	391
Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg Thr Asp	
100 105 110	
ctg aac cgg acc ttc ccc gac aac gtg aag ttc cgg aag acc acg gac	439
Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr Thr Asp	
115 120 125 130	
ccc tgc tta cag agg acc ctg tac aat gtg ctg ctg gca tat ggg cac	487
Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr Gly His	
135 140 145	
cat aac cag gga gtg ggc tac tgc cag gga atg aat ttt ata gca gga	535
His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile Ala Gly	
150 155 160	
tat ctg att ctt ata aca aat aat gaa gaa gaa tct ttt tgg ctg tta	583
Tyr Leu Ile Leu Ile Thr Asn Asn Glu Glu Glu Ser Phe Trp Leu Leu	
165 170 175	
gat gct ctt gtt gga aga ata cta cca gat tac tac agc ccg gcc atg	631
Asp Ala Leu Val Gly Arg Ile Leu Pro Asp Tyr Tyr Ser Pro Ala Met	
180 185 190	
ctg ggc ctg aag acc gac cag gag gtc ctc ggg gag ctg gtg cgg gcg	679
Leu Gly Leu Lys Thr Asp Gln Glu Val Leu Gly Glu Leu Val Arg Ala	
195 200 205 210	
aag ctg ccg gct gtg ggg gcc ctg atg gag cgt ctc ggt gtg ctg tgg	727
Lys Leu Pro Ala Val Gly Ala Leu Met Glu Arg Leu Gly Val Leu Trp	
215 220 225	

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acg ctg ctg gtg tcc cgc tgg ttc atc tgc ctg ttt gtg gac atc ttg      775
Thr Leu Leu Val Ser Arg Trp Phe Ile Cys Leu Phe Val Asp Ile Leu
                230                235                240

ccc gtg gag aca gtg ctt cgg atc tgg gac tgt ttg ttt aac gaa ggc      823
Pro Val Glu Thr Val Leu Arg Ile Trp Asp Cys Leu Phe Asn Glu Gly
                245                250                255

tcg aag att atc ttc cgg gtg gcc ctg acc tta att aag cag cac cag      871
Ser Lys Ile Ile Phe Arg Val Ala Leu Thr Leu Ile Lys Gln His Gln
                260                265                270

gag ttg att ttg gaa gcc acc agc gtt cca gac att tgc gat aag ttt      919
Glu Leu Ile Leu Glu Ala Thr Ser Val Pro Asp Ile Cys Asp Lys Phe
275                280                285                290

aag cag ata acc aaa ggg agt ttc gtg atg gag tgt cac acg ttt atg      967
Lys Gln Ile Thr Lys Gly Ser Phe Val Met Glu Cys His Thr Phe Met
                295                300                305

cag aaa ata ttt tca gaa cct gga agc tta tcc atg gcc acc gtc gcc      1015
Gln Lys Ile Phe Ser Glu Pro Gly Ser Leu Ser Met Ala Thr Val Ala
                310                315                320

aag ctc cgc gag agc tgc agg gcc cgg ctg ctg gca cag ggg tga gcg      1063
Lys Leu Arg Glu Ser Cys Arg Ala Arg Leu Leu Ala Gln Gly *
                325                330                335

tgccgtgcc ctgcgttgct cgtctctaca ctgacgatgc ccctttccag agttgacact      1123

ggaccaactt tcaactgcttt ccttttttagt gttgtaaata cttgacatca ctacacttta      1183

gttgtgaatt ttttaaaaga gcagtttaaa atcaggtcat tctaccagct tttgatgatt      1243

agctatgaag tcatactttt taaagaaaac ttattttttac ctgagagatc aataatatat      1303

aaaatgtgag tgtggggttg tatctaataa agtatgccaa cacctgtggt tgtgatcagt      1363

ttctcagctg actggaaatt aaaaaaaaaa aa                                  1395

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<210> 239
<211> 767
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(326)

<220>
<221> misc_feature
<222> (1)...(767)
<223> n = a,t,c or g

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<400> 239
 ccgggtccgga attccccgggt cgacccacgc gtccgccctt ctctcttctt tggtgcttct 60
 ttttcttgct cggcatc atg gct gcc ctc aga tcc ctt gtg aag ccc aag 110
 Met Ala Ala Leu Arg Ser Leu Val Lys Pro Lys
 1 5 10
 atc gtc aaa aag aga acc aag aaa ttc atc cgg cac cag tca gac cga 158
 Ile Val Lys Lys Arg Thr Lys Lys Phe Ile Arg His Gln Ser Asp Arg
 15 20 25
 tat gtc aaa atc aag atg aga aga ata atg tct ggg gtg aag gtg aag 206
 Tyr Val Lys Ile Lys Met Arg Arg Ile Met Ser Gly Val Lys Val Lys
 30 35 40
 cac cca gcc caa gac tca gca gcc agg aag tgg ccc agc gct ctt tat 254
 His Pro Ala Gln Asp Ser Ala Ala Arg Lys Trp Pro Ser Ala Leu Tyr
 45 50 55
 acc acg ggt gca gga att cac aca gaa aag tgg agg cca agg cgt gag 302
 Thr Thr Gly Ala Gly Ile His Thr Glu Lys Trp Arg Pro Arg Arg Glu
 60 65 70 75
 aat tcc tca atg act gcc ctc taa aggaagagat ccaaagaaat cctgaggaag 356
 Asn Ser Ser Met Thr Ala Leu *
 80
 cacaacaaac aaaaacactc tggatcagaa cttcctgtgc cagcggttaca tcagggtttt 416
 ctagcagcaa gggcgggctc cacatggctg aagcaggcaa ccaggaggac caggcttctt 476
 gtcagagact gaggaccag gaagaaacat gtctcggccc ctgtccccct ccacaattca 536
 gaggccacat tctaacaggg gaggctgacc aattaaacag ataatgacac ctcttagagc 596
 taagagctct ccgactatga accagatgcc tggagaacac ggatgaatgg tctgagcatg 656
 agcaggggtg ggaggcagcg ttaaggagg catcagagtc agaacctagc aaacaagtgt 716
 ttgtgaagaa gaattcatag aanagggcaa tgcgggcatc acatgggcta a 767

<210> 240
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(324)

<400> 240
 gagtttttaa attcttttatt taaaaatctc taactgtaat gtttcataaa aaatatacac 60

gtttctatattt acatattcca ttaattctat tagtttgaat tagatttttaa gtccaatttt 120
gaaaagcttg cagaattttct tctgaaatta cttaaaatta ctgtatgcat aaacttacia 180
aaacat atg cta tac caa ggc aga gaa aag aaa aaa agt gaa gtg gct 228
Met Leu Tyr Gln Gly Arg Glu Lys Lys Lys Ser Glu Val Ala
1 5 10
aca aag gtc cct ggg gca tca cct gct cac cta gga acc agg agt act 276
Thr Lys Val Pro Gly Ala Ser Pro Ala His Leu Gly Thr Arg Ser Thr
15 20 25 30
gga tac tgt tcc gtt act ggt aac cta tct gga tgt aaa ggt tca taa 324
Gly Tyr Cys Ser Val Thr Gly Asn Leu Ser Gly Cys Lys Gly Ser *
35 40 45
gttacaatgc tttttttgtt taaaaaaaaa aaaaagtctg tacttttacia gccaaaagtg 384
aaaatgccac acatcctctt tacgctttca tgtacactaa gtcactccat ttggttgata 444
ccaataatga tagctcctgt gtataatatt ttcataaaatc atactcagta agcaaattctc 504
tcaagcagcc agcatatgca gc 526

<210> 241
<211> 3744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (27)..(3161)

<400> 241
aagagctgcc tcccaggagggt gtctac atg gtg cag ccc cag ggg tgc agc gat 53
Met Val Gln Pro Gln Gly Cys Ser Asp
1 5
gag gaa gac cac gcg gag gag ccc tcc aag gac ggc ggt gcc ctg gag 101
Glu Glu Asp His Ala Glu Glu Pro Ser Lys Asp Gly Gly Ala Leu Glu
10 15 20 25
gag aag gat tcg gac ggg gca gcc tcc aag gag gac agc ggc ccc agc 149
Glu Lys Asp Ser Asp Gly Ala Ala Ser Lys Glu Asp Ser Gly Pro Ser
30 35 40
acc agg cag gct tca gga gag gcc tcc tcg ctg cgg gac tac gcg gcc 197
Thr Arg Gln Ala Ser Gly Glu Ala Ser Ser Leu Arg Asp Tyr Ala Ala
45 50 55
tcc acc atg acc gag ttc ctc ggc atg ttt ggc tat gat gac cag aac 245
Ser Thr Met Thr Glu Phe Leu Gly Met Phe Gly Tyr Asp Asp Gln Asn
60 65 70

acg cgg gac gag ctg gcc agg aag atc agc ttt gag aag ctg cac gcg	293
Thr Arg Asp Glu Leu Ala Arg Lys Ile Ser Phe Glu Lys Leu His Ala	
75 80 85	
ggc tcc acc ccg gag gca gcc acc tcc tcc atg ctg ccc acc tcc gag	341
Gly Ser Thr Pro Glu Ala Ala Thr Ser Ser Met Leu Pro Thr Ser Glu	
90 95 100 105	
gat acc ctc agc aag cgg gcc cgg ttc tct aag tat gag gag tac atc	389
Asp Thr Leu Ser Lys Arg Ala Arg Phe Ser Lys Tyr Glu Glu Tyr Ile	
110 115 120	
cgc aag ctc aag gct gcc gag cag ctc tcc tgg ccg gcc ccc agc acc	437
Arg Lys Leu Lys Ala Gly Glu Gln Leu Ser Trp Pro Ala Pro Ser Thr	
125 130 135	
aag acc gag gag cgg gtg gcc aag gag gtg gtg gcc acc ctg ccc gcc	485
Lys Thr Glu Glu Arg Val Gly Lys Glu Val Val Gly Thr Leu Pro Gly	
140 145 150	
ctg cgg ctg ccc agc agc acg gcc cac ctg gag acc aag gcc acc atc	533
Leu Arg Leu Pro Ser Ser Thr Ala His Leu Glu Thr Lys Ala Thr Ile	
155 160 165	
ctg ccc ctg ccg tcg cac agc agt gtc cag atg cag aac ctg gta gcc	581
Leu Pro Leu Pro Ser His Ser Ser Val Gln Met Gln Asn Leu Val Ala	
170 175 180 185	
cgg gcc tcc aag tac gac ttc ttc atc caa aaa ctg aag acc gcc gag	629
Arg Ala Ser Lys Tyr Asp Phe Phe Ile Gln Lys Leu Lys Thr Gly Glu	
190 195 200	
aat ctg cgg ccc cag aac ggg agc acc tac aag aag cca tcc aag tac	677
Asn Leu Arg Pro Gln Asn Gly Ser Thr Tyr Lys Lys Pro Ser Lys Tyr	
205 210 215	
gac ctg gag aat gtc aag tac ctg cac ctc ttc aaa ccc ggg gag gcc	725
Asp Leu Glu Asn Val Lys Tyr Leu His Leu Phe Lys Pro Gly Glu Gly	
220 225 230	
agc ccc gac atg gcc ggg gcc atc gcc ttc aag aca gcc aag gtg ggg	773
Ser Pro Asp Met Gly Gly Ala Ile Ala Phe Lys Thr Gly Lys Val Gly	
235 240 245	
cgc cct tcc aag tac gac gtc cgg gcc atc cag aag cca gcc ccc gcc	821
Arg Pro Ser Lys Tyr Asp Val Arg Gly Ile Gln Lys Pro Gly Pro Ala	
250 255 260 265	
aag gtt ccg ccc acc ccc agc ctg gct ccc gca ccc ctc gcc agc gtg	869
Lys Val Pro Pro Thr Pro Ser Leu Ala Pro Ala Pro Leu Ala Ser Val	
270 275 280	
ccc agt gcc ccc aac gcc ccc ggg cca ggg cca gag cct cct gcc tcc	917
Pro Ser Ala Pro Asn Ala Pro Gly Pro Gly Pro Glu Pro Pro Ala Ser	
285 290 295	
ctg tcc ttc aac act ccc gag tac ctg aag tca acc ttc tcc aaa aca	965

Leu Ser Phe Asn Thr Pro Glu Tyr Leu Lys Ser Thr Phe Ser Lys Thr	
300 305 310	
gac tcc atc acc acg ggg acc gtc tcc act gtc aag aac gga ctg ccc	1013
Asp Ser Ile Thr Thr Gly Thr Val Ser Thr Val Lys Asn Gly Leu Pro	
315 320 325	
aca gat aaa cca gcc gtc act gaa gat gta aac att tac cag aaa tat	1061
Thr Asp Lys Pro Ala Val Thr Glu Asp Val Asn Ile Tyr Gln Lys Tyr	
330 335 340	
att gcc agg ttc tcg ggc agc cag cac tgt ggc cac atc cac tgt gcc	1109
Ile Ala Arg Phe Ser Gly Ser Gln His Cys Gly His Ile His Cys Ala	
350 355 360	
tac cag tac cgc gag cac tac cac tgc ctt gac cct gag tgt aac tac	1157
Tyr Gln Tyr Arg Glu His Tyr His Cys Leu Asp Pro Glu Cys Asn Tyr	
365 370 375	
cag agg ttc acg agt aag cag gac gtg atc cgc cac tac aac atg cac	1205
Gln Arg Phe Thr Ser Lys Gln Asp Val Ile Arg His Tyr Asn Met His	
380 385 390	
aag aag cgc gac aac tcc ctg cag cac ggc ttc atg cgt ttc agc ccg	1253
Lys Lys Arg Asp Asn Ser Leu Gln His Gly Phe Met Arg Phe Ser Pro	
395 400 405	
ctg gac gac tgc agc gtc tac tac cac ggc tgc cac ctc aat ggg aag	1301
Leu Asp Asp Cys Ser Val Tyr Tyr His Gly Cys His Leu Asn Gly Lys	
410 415 420 425	
agc acc cac tat cac tgc atg cag gtg ggc tgt aac aag gtg tac acg	1349
Ser Thr His Tyr His Cys Met Gln Val Gly Cys Asn Lys Val Tyr Thr	
430 435 440	
agc acg tct gac gtg atg acc cac gag aac ttc cac aag aag aat acc	1397
Ser Thr Ser Asp Val Met Thr His Glu Asn Phe His Lys Lys Asn Thr	
445 450 455	
cag ctc att aac gac ggc ttc cag cgc ttc cga gcc acc gaa gac tgt	1445
Gln Leu Ile Asn Asp Gly Phe Gln Arg Phe Arg Ala Thr Glu Asp Cys	
460 465 470	
ggc aca gcc gac tgc cag ttc tac gga cag aag acc acg cac ttc cac	1493
Gly Thr Ala Asp Cys Gln Phe Tyr Gly Gln Lys Thr Thr His Phe His	
475 480 485	
tgc agg cgc ccc ggc tgc aca ttc act ttc aag aac aag tgt gac atc	1541
Cys Arg Arg Pro Gly Cys Thr Phe Thr Phe Lys Asn Lys Cys Asp Ile	
490 495 500 505	
gag aag cac aag agc tac cac atc aag gac gat gcc tac gcc aag gac	1589
Glu Lys His Lys Ser Tyr His Ile Lys Asp Asp Ala Tyr Ala Lys Asp	
510 515 520	
ggc ttc aag aag ttc tac aag tac gag gag tgc aag tac gag ggc tgc	1637
Gly Phe Lys Lys Phe Tyr Lys Tyr Glu Glu Cys Lys Tyr Glu Gly Cys	

gcc ctc aag ccc tct gcc acc ttt gac cca gga agc ggg cag cag gtc Ala Leu Lys Pro Ser Ala Thr Phe Asp Pro Gly Ser Gly Gln Gln Val 765 770 775	2357
acc cca gcc agg ttc ccc ccg gcc caa gtg aag ccg gaa ccc ggt gag Thr Pro Ala Arg Phe Pro Pro Ala Gln Val Lys Pro Glu Pro Gly Glu 780 785 790	2405
agc acc ggc gcc cca ggc ccc cac gaa gcc tcc cag gac cgc agt cta Ser Thr Gly Ala Pro Gly Pro His Glu Ala Ser Gln Asp Arg Ser Leu 795 800 805	2453
gac ctg act gtg aag gag ccc agc aac gaa tca aat ggc cac gca gtc Asp Leu Thr Val Lys Glu Pro Ser Asn Glu Ser Asn Gly His Ala Val 810 815 820 825	2501
ccg gca aat tca tct ctt tta tcc tcg ctt atg aat aag atg tct cag Pro Ala Asn Ser Ser Leu Leu Ser Ser Leu Met Asn Lys Met Ser Gln 830 835 840	2549
ggc aac cct ggc ctg ggc agc ctg ctg aac atc aag gcg gaa gcg gag Gly Asn Pro Gly Leu Gly Ser Leu Leu Asn Ile Lys Ala Glu Ala Glu 845 850 855	2597
ggg agc ccc gct gcg gag ccc tcg ccc ttc cta ggc aag gcc gtg aag Gly Ser Pro Ala Ala Glu Pro Ser Pro Phe Leu Gly Lys Ala Val Lys 860 865 870	2645
gcg ctg gtt cag gag aag ttg gca gag ccc tgg aag gtg tac ctg cgc Ala Leu Val Gln Glu Lys Leu Ala Glu Pro Trp Lys Val Tyr Leu Arg 875 880 885	2693
agg ttt ggt aca aag gac ttc tgt gac ggc cag tgt gac ttc ctc cac Arg Phe Gly Thr Lys Asp Phe Cys Asp Gly Gln Cys Asp Phe Leu His 890 895 900 905	2741
aag gcc cac ttc cac tgc gtg gtg gag gaa tgc ggc gcg ctc ttc agc Lys Ala His Phe His Cys Val Val Glu Glu Cys Gly Ala Leu Phe Ser 910 915 920	2789
acc ttg gac ggg gcc atc aag cac gca aac ttc cac ttc cgg aca gag Thr Leu Asp Gly Ala Ile Lys His Ala Asn Phe His Phe Arg Thr Glu 925 930 935	2837
gga gga gca gca aaa gga aac aca gag gct gcc ttt ccg gcc tcg gcc Gly Gly Ala Ala Lys Gly Asn Thr Glu Ala Ala Phe Pro Ala Ser Ala 940 945 950	2885
gcc gag acc aaa cct ccc atg gcc ccc tcg tcc cct ccg gtc cct cct Ala Glu Thr Lys Pro Pro Met Ala Pro Ser Ser Pro Pro Val Pro Pro 955 960 965	2933
gtc acc acg gcc acg gtg tcc tct ctg gag ggg ccc gct ccc agc ccg Val Thr Thr Ala Thr Val Ser Ser Leu Glu Gly Pro Ala Pro Ser Pro 970 975 980 985	2981

gcc tcc gtg ccc tcc acc ccc acc ctg ctc gcc tgg aag cag ctg gct	3029
Ala Ser Val Pro Ser Thr Pro Thr Leu Leu Ala Trp Lys Gln Leu Ala	
990 995 1000	
tcc acc ata ccc cag atg cct cag atc cca gcg tca gtg cct cac ctg	3077
Ser Thr Ile Pro Gln Met Pro Gln Ile Pro Ala Ser Val Pro His Leu	
1005 1010 1015	
ccc gcc tcg ccc ttg gca acg act tct cta gag aac gcc aag ccc cag	3125
Pro Ala Ser Pro Leu Ala Thr Thr Ser Leu Glu Asn Ala Lys Pro Gln	
1020 1025 1030	
gtc aaa ccc gga ttc ctc cag ttc cag gag aag tga gtcc ctgatgagc	3175
Val Lys Pro Gly Phe Leu Gln Phe Gln Glu Lys *	
1035 1040 1045	
cgaggagtcgc gcgttcccct cgcgtctcgg gagtaggtgc tagcaagggc gctaggaggc	3235
cctgttcctc actgcggatg gtgctgctgt cccagcctc tctggggcat ggccatcggg	3295
tgatgtcctt ctagccaaag atgctgctgc tctacctca ctgcctgtcc cagagcaggc	3355
cagcccgcgt gggccgatgg tggcggcagt ggctactgct cctgcagggc atgtggtgat	3415
cctgccaggg ccaggtgggg tggactgggc gtggtggtcc tcagaggaca actcccagcc	3475
tgacaaggag ggctgcgtct cctccgagc ctccgtattg gcctcctctg tggctcacac	3535
ccatggctga atctctgcag ggcacgtgaa gtcacgggta ggggccaggc cctccaggc	3595
cgtcactggc ctgcacagtg gtctgagctc ttgggtggaa gggaccctcc tcaactggatg	3655
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ctcaataaaa gtaataaatt ggattatatt	3744

<210> 242
 <211> 2450
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 242	
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aaagctttta gagttctgat gcctatttaa gtaaatattc tcttttcccc ccaaaattct	180
taggcttgaa g atg cag tgg acg cca gag cat gcc cag tgg cca gaa cag	230
Met Gln Trp Thr Pro Glu His Ala Gln Trp Pro Glu Gln	

1	5	10	
cac ttt gac atc acc tca acc act cgg tct cct gcc cac aaa gtt gaa			278
His Phe Asp Ile Thr Ser Thr Thr Arg Ser Pro Ala His Lys Val Glu			
15	20	25	
gcc tac aga ggt cat ctg cag cgc acc tat cag tac gcc tgg gcg aat			326
Ala Tyr Arg Gly His Leu Gln Arg Thr Tyr Gln Tyr Ala Trp Ala Asn			
30	35	40	45
gat gac ata tct gct ctg act gca tcc aac cta cta aaa aaa tat gca			374
Asp Asp Ile Ser Ala Leu Thr Ala Ser Asn Leu Leu Lys Lys Tyr Ala			
50	55	60	
gag aag tat tcc ggc att ttg gaa ggt cct gtg gac cga ccc gta ctc			422
Glu Lys Tyr Ser Gly Ile Leu Glu Gly Pro Val Asp Arg Pro Val Leu			
65	70	75	
agc aac tat tcg gac aca cca tca gga cta gtg aac ggt cgg aaa aat			470
Ser Asn Tyr Ser Asp Thr Pro Ser Gly Leu Val Asn Gly Arg Lys Asn			
80	85	90	
gaa agt gaa ccc tgg cag cct tcc ttg aat tca gaa gct gtt tat ccc			518
Glu Ser Glu Pro Trp Gln Pro Ser Leu Asn Ser Glu Ala Val Tyr Pro			
95	100	105	
atg aac tgt gtt ccg gat gtt atc act gcc agc aaa gct gga gtc agt			566
Met Asn Cys Val Pro Asp Val Ile Thr Ala Ser Lys Ala Gly Val Ser			
110	115	120	125
tca gcc ctc cct cca gca gat gtc tct gcg agt ata gga agc tct cct			614
Ser Ala Leu Pro Pro Ala Asp Val Ser Ala Ser Ile Gly Ser Ser Pro			
130	135	140	
ggg gta gcc agc aac ctg aca gaa cct agt tat tca agt agt acc tgt			662
Gly Val Ala Ser Asn Leu Thr Glu Pro Ser Tyr Ser Ser Ser Thr Cys			
145	150	155	
gga agc cac act gta ccc agt ctt cat gca ggg ctc cca tct cag gaa			710
Gly Ser His Thr Val Pro Ser Leu His Ala Gly Leu Pro Ser Gln Glu			
160	165	170	
tat gcc cca gga tac aac gga tca tat ttg cat tct act tat agt agc			758
Tyr Ala Pro Gly Tyr Asn Gly Ser Tyr Leu His Ser Thr Tyr Ser Ser			
175	180	185	
cag cca gca cct gca ctt cct tca cct cat ccg tct cct ttg cat agc			806
Gln Pro Ala Pro Ala Leu Pro Ser Pro His Pro Ser Pro Leu His Ser			
190	195	200	205
tct ggg cta cta cag ccc cca cca cca cct cct ccg cca cca gcc ttg			854
Ser Gly Leu Leu Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu			
210	215	220	
gtc cca ggc tac aat ggg act tct aac ctc tcc agt tac agc tat ccg			902
Val Pro Gly Tyr Asn Gly Thr Ser Asn Leu Ser Ser Tyr Ser Tyr Pro			
225	230	235	

tct gct agc tat cct cct cag act gct gtg ggg tct ggg tac agc cct Ser Ala Ser Tyr Pro Pro Gln Thr Ala Val Gly Ser Gly Tyr Ser Pro 240 245 250	950
ggg ggg gca ccg cct ccg cct tca gcg tac ctg cct tca gga att cct Gly Gly Ala Pro Pro Pro Pro Ser Ala Tyr Leu Pro Ser Gly Ile Pro 255 260 265	998
gct ccc acc ccc cta ccc ccc acc act gtt cct ggc tac acc tac cag Ala Pro Thr Pro Leu Pro Pro Thr Thr Val Pro Gly Tyr Thr Tyr Gln 270 275 280 285	1046
ggc cat ggt ttg aca cct att gca ccg tcg gct ctg aca aac agt tca Gly His Gly Leu Thr Pro Ile Ala Pro Ser Ala Leu Thr Asn Ser Ser 290 295 300	1094
gca agt tct ctc aaa agg aaa gct ttc tac atg gca ggg caa gga gat Ala Ser Ser Leu Lys Arg Lys Ala Phe Tyr Met Ala Gly Gln Gly Asp 305 310 315	1142
atg gac tcc agt tat gga aat tac agc tat ggc caa cag aga tct aca Met Asp Ser Ser Tyr Gly Asn Tyr Ser Tyr Gly Gln Gln Arg Ser Thr 320 325 330	1190
cag agt cct atg tac aga atg ccc gac aac agc att tca aac aca aat Gln Ser Pro Met Tyr Arg Met Pro Asp Asn Ser Ile Ser Asn Thr Asn 335 340 345	1238
cgg ggg aat ggc ttt gac aga agt gct gaa aca tca tcc tta gca ttt Arg Gly Asn Gly Phe Asp Arg Ser Ala Glu Thr Ser Ser Leu Ala Phe 350 355 360 365	1286
aag cca acg aag cag cta atg tcc tct gaa cag caa agg aaa ttc agc Lys Pro Thr Lys Gln Leu Met Ser Ser Glu Gln Gln Arg Lys Phe Ser 370 375 380	1334
agc cag tcc agt agg gct ctg acc cct cct tcc tac agt act gct aaa Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr Ser Thr Ala Lys 385 390 395	1382
aat tca ttg gga tca aga tcc agt gaa tcc ttt ggg aag tac aca tcg Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly Lys Tyr Thr Ser 400 405 410	1430
cca gta atg agt gag cat ggg gac gag cac agg cag ctc ctc tct cac Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln Leu Leu Ser His 415 420 425	1478
cca atg caa ggc cct gga ctc cgt gca gct acc tca tcc aac cac tct Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser Ser Asn His Ser 430 435 440 445	1526
gtg gac gag caa ctg aag aat act gac acg cac ctc atc gac ctg gta Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu Ile Asp Leu Val 450 455 460	1574

acc aat gag att atc acc caa gga cct cca gtg gac tgg aat gac att	1622
Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp Trp Asn Asp Ile	
465 470 475	
gct ggt ctc gac ctg gtg aag gct gtc att aaa gag gag gtt tta tgg	1670
Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu Glu Val Leu Trp	
480 485 490	
cca gtg ttg agg tca gac gcg ttc agt gga ctg acg gcc tta cct cgg	1718
Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr Ala Leu Pro Arg	
495 500 505	
agc atc ctt tta ttt gga cct cgg ggg aca ggc aaa aca tta ttg ggc	1766
Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys Thr Leu Leu Gly	
510 515 520 525	
aga tgc atc gct agt cag ctg ggg gcc aca ttt ttc aaa att gcc ggt	1814
Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe Lys Ile Ala Gly	
530 535 540	
tct gga cta gtc gcc aag tgg tta gga gaa gca gag aaa att atc cat	1862
Ser Gly Leu Val Ala Lys Trp Leu Gly Glu Ala Glu Lys Ile Ile His	
545 550 555	
gcc tct ttt ctt gtg gcc agg tgt cgc cag ccc tcg gtg att ttt gtt	1910
Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser Val Ile Phe Val	
560 565 570	
agt gac att gac atg ctt ctc tcc tct caa gtg aat gag gaa cat agt	1958
Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn Glu Glu His Ser	
575 580 585	
cca gtc agt cgg atg aga acc gaa ttt ctg atg caa ctg gac act gta	2006
Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln Leu Asp Thr Val	
590 595 600 605	
cta act tcg gct gag gac caa atc gta gta att tgt gcc acc agt aaa	2054
Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys Ala Thr Ser Lys	
610 615 620	
cca gaa gaa ata gat gaa tcc ctt cgg agg tac ttc atg aaa cga ctt	2102
Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe Met Lys Arg Leu	
625 630 635	
tta atc cca ctt cct gac agc aca gcg agg cac cag ata ata gta caa	2150
Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln Ile Ile Val Gln	
640 645 650	
ctg ctc tca cag cac aat tac tgt ctc aat gac aag gag ttt gca ctg	2198
Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys Glu Phe Ala Leu	
655 660 665	
ctc gtc cag cgc aca gaa ggc ttt tct gga cta gat gtg gct cat ttg	2246
Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp Val Ala His Leu	
670 675 680 685	
tgt cag gaa gca gtg gtg ggc ccc ctc cat gcc atg cca gcc aca gac	2294

Cys Gln Glu Ala Val Val Gly Pro Leu His Ala Met Pro Ala Thr Asp	
690 695 700	
ctt tca gcc att atg ccc agc cag ttg agg ccc gtt aca tat caa gac	2342
Leu Ser Ala Ile Met Pro Ser Gln Leu Arg Pro Val Thr Tyr Gln Asp	
705 710 715	
ttt gaa aat gct ttc tgc aag att cag cct agc ata tct caa aag gag	2390
Phe Glu Asn Ala Phe Cys Lys Ile Gln Pro Ser Ile Ser Gln Lys Glu	
720 725 730	
ctt gat atg tat gtt gaa tgg aac aaa atg ttt ggt tgc agt cag tga	2438
Leu Asp Met Tyr Val Glu Trp Asn Lys Met Phe Gly Cys Ser Gln *	
735 740 745	
taactttcttt ag	2450

<210> 243
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(437)

<400> 243

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aagatgcctg taaatcaaata ttactataa ttgtaaagaa acctgaggca attagttaaa	120
aagttttaag tattcaggca attcatgata ccttgttgaa ataaagc atg cag act	176
Met Gln Thr	
1	
cat aaa aac ttg tat ata atc aaa ata aag ttc tac aaa tgg gaa aga	224
His Lys Asn Leu Tyr Ile Ile Lys Ile Lys Phe Tyr Lys Trp Glu Arg	
5 10 15	
gga tta tta tca ggg tat att aag gtg tta gac tta caa aag aag tgc	272
Gly Leu Leu Ser Gly Tyr Ile Lys Val Leu Asp Leu Gln Lys Lys Cys	
20 25 30 35	
ata att aat tac tca ttt aaa att aat tct ata ccc att agc ttg gca	320
Ile Ile Asn Tyr Ser Phe Lys Ile Asn Ser Ile Pro Ile Ser Leu Ala	
40 45 50	
aca gat aaa ata aaa gca tgc aac agt gct ttc tta gtc gac gcg gcc	368
Thr Asp Lys Ile Lys Ala Cys Asn Ser Ala Phe Leu Val Asp Ala Ala	
55 60 65	
gcg aat tcg gat cct cga gag atc tct ttt ttt ggg ttt ggt ggg gta	416
Ala Asn Ser Asp Pro Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val	
70 75 80	

tct tca tca tcg aat aga tag ttatatatcat catgctcttc aattaaaa	465
Ser Ser Ser Ser Asn Arg *	
85 90	

<210> 244
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (83)..(829)

<400> 244

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gcggcccggc ctcggggcag cc atg gac tcg cag gaa ttg aag act ttg att	112
Met Asp Ser Gln Glu Leu Lys Thr Leu Ile	
1 5 10	
aat tac tat tgt caa gag aga tat ttc cat cat gta tta ctg gtt gcc	160
Asn Tyr Tyr Cys Gln Glu Arg Tyr Phe His His Val Leu Leu Val Ala	
15 20 25	
agt gaa gga att aag agg tat gga agt gat cca gtc ttc agg ttt tat	208
Ser Glu Gly Ile Lys Arg Tyr Gly Ser Asp Pro Val Phe Arg Phe Tyr	
30 35 40	
cat gcc tat ggc aca tta atg gaa ggt aaa act caa gaa gct ctt cga	256
His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu Arg	
45 50 55	
gaa ttt gag gct att aaa aat aaa caa gat gta tca ctt tgt tct cta	304
Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser Leu	
60 65 70	
ctt gca ctg ata tat gcc cat aaa atg agt cct aat cca gat aga gaa	352
Leu Ala Leu Ile Tyr Ala His Lys Met Ser Pro Asn Pro Asp Arg Glu	
75 80 85 90	
gct att ctg gaa tca gat gcc aga gtg aag gaa caa cgt aaa gga gct	400
Ala Ile Leu Glu Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala	
95 100 105	
gga gag aaa gcc tta tac cat gca ggc tta ttt tta tgg cac att ggt	448
Gly Glu Lys Ala Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly	
110 115 120	
cgc cat gat aaa gca agg gaa tat att gac aga atg atc aaa ata tca	496
Arg His Asp Lys Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser	
125 130 135	

gat ggt agt aaa cag gga cac gtt ttg aaa gca tgg ctt gat att aca	544
Asp Gly Ser Lys Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr	
140 145 150	
aga gga aaa gag cct tac act aaa aaa gca ctg aag tat ttt gaa gag	592
Arg Gly Lys Glu Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu	
155 160 165 170	
gga ctc caa gat ggg aat gat act ttt gct ctg ctg ggt aag gca caa	640
Gly Leu Gln Asp Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Ala Gln	
175 180 185	
tgc ctt gag atg cgc cag aat tat tca ggt gcc ctg gag act gtg aac	688
Cys Leu Glu Met Arg Gln Asn Tyr Ser Gly Ala Leu Glu Thr Val Asn	
190 195 200	
cag ata atc gtg aat ttt ccg agc ttc ctt cct gct ttt gtt aag aaa	736
Gln Ile Ile Val Asn Phe Pro Ser Phe Leu Pro Ala Phe Val Lys Lys	
205 210 215	
atg aaa tta caa cta gcc ttg cag gat tgg gac cag aca gtt gag aca	784
Met Lys Leu Gln Leu Ala Leu Gln Asp Trp Asp Gln Thr Val Glu Thr	
220 225 230	
gca aaa ggt tgc tgc tcc aag ata gcc aaa atg tgg aag cac tga gaa	832
Ala Lys Gly Cys Cys Ser Lys Ile Ala Lys Met Trp Lys His *	
235 240 245	
tgcaggcact ctactatgtg tgtagagagg gggatataga gaaggcttcc accaagctgg	892
aaaacttggg aaatgcattg gatgccatgg aaccacagaa tgctcaactt ttctataaca	952
ttacactcgc cttcagcaga acttgtggac gtagtcaact tattcttcaa aaaattcaaa	1012
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taccaatt	1080

<210> 245
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(286)

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ttcaatattg tagttaattt tttggctttc aacagcagcc ctagta atg gtg gag	115
	Met Val Glu
	1

ttg tta att aat gtg tat att gta ctg aat ttc tgt cag tta agg ggt	163
Leu Leu Ile Asn Val Tyr Ile Val Leu Asn Phe Cys Gln Leu Arg Gly	
5 10 15	
tca ctg ctt tgg tgg aaa ttg gtg gaa att gct agc agg ttc cac gat	211
Ser Leu Leu Trp Trp Lys Leu Val Glu Ile Ala Ser Arg Phe His Asp	
20 25 30 35	
gtt tat ttt ttt ctc cat gtt gta tat cat tac cat ttc aca tac gcg	259
Val Tyr Phe Phe Leu His Val Val Tyr His Tyr His Phe Thr Tyr Ala	
40 45 50	
ttt cta ttt ttc ttc ctc tcc tcc tga tctcc ttaaaaatga atctagagtt	311
Phe Leu Phe Phe Phe Leu Ser Ser *	
55 60	
ggtaggctttt tccccctcct ctttggccag ttccacagtt cagttcttcc tgaaaacagg	371
gatgatgaac ttgtaggac aggacaaatg tgtgtttttc aaaaacttaa ggctgggtgt	431
gaaacacctt ctgtggacaa ggatttgtaa acttctctcc tccctccagc tgcggcccca	491
gcctaactga tagttacttg attcagtggtg ctagacactt aaatagcatc tatgtctctt	551
tcaaggggaat ttgtcaaata atgctgttta gctaattggt gcaagcaatt gcatattaac	611
agctgtgatt ttgttgga gcaagtatta tggccaaagc cagtttcttg gcatttcaaa	671
aataatgcaa taaaaactag ttgagggttag ctgaggctgg aaatgccttt ttcattggtaa	731
atgattcact tctatatattt tctttctttt tctttttttt tctttgggtt tcatcctgga	791
ttcatccctt gatcttaaat caaaacgtca gatcaatgaa ctatgaacta aagtattttt	851
cttaagccta ttgagtgatt aattttttta aaaatgttta aatgcatatg cttttctttc	911
agcacaaca acagcaaaaa cttttgtaat aactaactta cttttgcatg tatgaagaac	971
tgagtcattt atttccctaa ctactcctc tttcaagtaa caggtggcag atcataaaat	1031
gaattcttta ttgtatctac aactccaca ttctttactg tgtcctacta ctgtatcttg	1091
gtccctgct gtattaaaca ccatcttaag cacttggtcc tgcaggactc cttcttgaca	1151
ttttgtctcc ccttcaaag tcaactcaaag agtgggactt catcaaaaga aatgaattag	1211
tctctatcac accgaatact aagatttatt tcctctgatg gtacatagat ttctctctcc	1271
actaagaggg tcaactctcat agaggaatgt cttgtcagtt ttatacttgc tgaggctaga	1331
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ggatcaggtt gatgataata cctctaaaaa tatgcaataa taaaacaata gttatgaaag	1451
aaacttgaaa ggtttgcaag gtttctccta tcctgttaa aattatcatt tattatctct	1511
ttgtcagtg tagtaaggta acccatgaca gaataatttg agtgatagtt catcatgcag	1571

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aggatatgat caagatatta cctaattggtt ttatcctgaa aaaggtgtat acttttaggg 1631
cactgttaac aatgcgagtg aaaccaagat ggtgcaagtt ccctttgcag atggcgtggg 1691
cacacttgat ttttattatg agtgaatgta atctttctgt attttaccag agttacagca 1751
attacctgaa aagtttccta acattttaat aatggttaggg atttcgtttt ggtttttagtt 1811
gtcctcaaga gacaacaggt tcacagtaat ttccatgatg ttgggtgtgg ctaagctggg 1871
gattggttct gttccccctg ctcccggtga gagaaaagct atatttatac tgcattcttt 1931
ctcaactttc aggtaaaaca aactatgatt taaaaaaga aaaaagaaaa gacaggtact 1991
tttacttcaa agagtgtctt gctacatttt tatttaaacc aaaaatcaaa taaaataagg 2051
aggggggctg ggtatacttt aaacaaaacc agtcctgaaa tgctgttatt ctcaaagtac 2111
attccaaaaa aaaaaaa 2128

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<210> 246
<211> 3373
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (146)..(2254)

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<400> 246

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tttccccaca gggtgactta aatgtcccag gctggaaggt ggagcgagaa gtggatgccc 120
ccagggctct gggtcacact ccagg atg act tct cgg aac cag ctg gtg cag 172
Met Thr Ser Arg Asn Gln Leu Val Gln
1 5
aag gtg ctg cag gag ctg cag gaa gca gtg gag tgc gaa ggc ctg gag 220
Lys Val Leu Gln Glu Leu Gln Glu Ala Val Glu Cys Glu Gly Leu Glu
10 15 20 25
ggg ctc ata ggt gct tcc ttg gag gcc aag cag gtc ctg tct tcc ttc 268
Gly Leu Ile Gly Ala Ser Leu Glu Ala Lys Gln Val Leu Ser Ser Phe
30 35 40
act ctc ccc acc tgc cgg gag gga ggc cct ggc ctc cag gtg ctg gaa 316
Thr Leu Pro Thr Cys Arg Glu Gly Gly Pro Gly Leu Gln Val Leu Glu
45 50 55
gtg gac tcg gtg gcc ctg agc ctg tat cca gaa gat gct cca cgg aac 364
Val Asp Ser Val Ala Leu Ser Leu Tyr Pro Glu Asp Ala Pro Arg Asn
60 65 70

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atg ctg ccg ctg gtg tgc aag ggg gag ggc agc ctg ctg ttc gag gcg Met Leu Pro Leu Val Cys Lys Gly Glu Gly Ser Leu Leu Phe Glu Ala 75 80 85	412
gcc agc atg ctg ctg tgg ggt gac gca ggc ctc agc ctg gag ctg cgg Ala Ser Met Leu Leu Trp Gly Asp Ala Gly Leu Ser Leu Glu Leu Arg 90 95 100 105	460
gcc cgc acc gtg gta gag atg ctg ctg cac aga cac tac tac ctc cag Ala Arg Thr Val Val Glu Met Leu Leu His Arg His Tyr Tyr Leu Gln 110 115 120	508
ggc atg atc gac tcc aaa gtg atg ctg cag gcc gtg cgc tac tcc cta Gly Met Ile Asp Ser Lys Val Met Leu Gln Ala Val Arg Tyr Ser Leu 125 130 135	556
tgc tct gag gag tcc cct gag atg acc agc ttg ccc ccc gcc acg ctg Cys Ser Glu Glu Ser Pro Glu Met Thr Ser Leu Pro Pro Ala Thr Leu 140 145 150	604
gag gcc atc ttc gat gcc gac gtc aag gcc tcc tgt ttc ccc agc agc Glu Ala Ile Phe Asp Ala Asp Val Lys Ala Ser Cys Phe Pro Ser Ser 155 160 165	652
ttc tcc aac gtg tgg cac ttg tat gct ctc gcc tct gtc ctc cag cgg Phe Ser Asn Val Trp His Leu Tyr Ala Leu Ala Ser Val Leu Gln Arg 170 175 180 185	700
aac atc tac tcc atc tac ccc atg cgc aac ctc aag atc cgg ccc tac Asn Ile Tyr Ser Ile Tyr Pro Met Arg Asn Leu Lys Ile Arg Pro Tyr 190 195 200	748
ttc aac cgt gtc atc cgg ccc cgc cgc tgc gac cac gtg ccc tcc acg Phe Asn Arg Val Ile Arg Pro Arg Arg Cys Asp His Val Pro Ser Thr 205 210 215	796
ctg cac atc atg tgg gct ggc cag ccc ctc acc agc cac ttc ttc cgc Leu His Ile Met Trp Ala Gly Gln Pro Leu Thr Ser His Phe Phe Arg 220 225 230	844
cac cag tac ttt gcc cct gtg gtg ggg ctg gaa gag gtg gag gct gaa His Gln Tyr Phe Ala Pro Val Val Gly Leu Glu Glu Val Glu Ala Glu 235 240 245	892
ggt gcc cct ggc gtg gcc cca gct ctt cca gcc ctg gcc cca ctc tca Gly Ala Pro Gly Val Ala Pro Ala Leu Pro Ala Leu Ala Pro Leu Ser 250 255 260 265	940
tcg ccg gcc aag acc ctg gag ctg ctc aac cgt gaa cct ggc ctc agc Ser Pro Ala Lys Thr Leu Glu Leu Leu Asn Arg Glu Pro Gly Leu Ser 270 275 280	988
tac tct cac ctc tgt gag cgc tac agc gtc acc aaa agc acc ttc tac Tyr Ser His Leu Cys Glu Arg Tyr Ser Val Thr Lys Ser Thr Phe Tyr 285 290 295	1036

cgc tgg cgg cgg cag tcc cag gag cac cgg cag aag gtt gct gcc cgc Arg Trp Arg Arg Gln Ser Gln Glu His Arg Gln Lys Val Ala Ala Arg 300 305 310	1084
ttc tcc gcc aag cac ttc ctg cag gac agc ttc cac cgg ggg ggc gtc Phe Ser Ala Lys His Phe Leu Gln Asp Ser Phe His Arg Gly Gly Val 315 320 325	1132
gtg cca ctt cag cag ttc ctc cag cgg ttc ccg gag atc tcc cgc tca Val Pro Leu Gln Gln Phe Leu Gln Arg Phe Pro Glu Ile Ser Arg Ser 330 335 340 345	1180
acc tac tat gtc tgg aag cat gag ctg ctg ggc tct ggc acc tgc ccg Thr Tyr Tyr Val Trp Lys His Glu Leu Leu Gly Ser Gly Thr Cys Pro 350 355 360	1228
gcc ttg ccc ccc agg gag gtg ctg ggc atg gag gag cta gag aag ctg Ala Leu Pro Pro Arg Glu Val Leu Gly Met Glu Glu Leu Glu Lys Leu 365 370 375	1276
ccg gag gag cag gtg gct gag gag gag ctg gag tgc tcc gca ctg gcg Pro Glu Glu Gln Val Ala Glu Glu Glu Leu Glu Cys Ser Ala Leu Ala 380 385 390	1324
gtg tca agc cct gga atg gtc tta atg cag cgg gcc aag ttg tac ctg Val Ser Ser Pro Gly Met Val Leu Met Gln Arg Ala Lys Leu Tyr Leu 395 400 405	1372
gag cat tgc atc tcc ctg aac aca ctg gta ccc tat cgc tgc ttc aaa Glu His Cys Ile Ser Leu Asn Thr Leu Val Pro Tyr Arg Cys Phe Lys 410 415 420 425	1420
cgc agg ttc cct ggc atc tca cgg tcc act tat tat aat tgg cgg cga Arg Arg Phe Pro Gly Ile Ser Arg Ser Thr Tyr Tyr Asn Trp Arg Arg 430 435 440	1468
aag gcc ctc cgg agg aac ccc agc ttc aag ccg gca cca gcc ctc tct Lys Ala Leu Arg Arg Asn Pro Ser Phe Lys Pro Ala Pro Ala Leu Ser 445 450 455	1516
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cct tgg aag agt gag gcg gaa gag ggg gca ggg aat gcc aca ggt gag Pro Trp Lys Ser Glu Ala Glu Glu Gly Ala Gly Asn Ala Thr Gly Glu 475 480 485	1612
gac cct ccc gcc ccc ggg gag ctc ctg cca cta agg atg ccc ctg tcc Asp Pro Pro Ala Pro Gly Glu Leu Leu Pro Leu Arg Met Pro Leu Ser 490 495 500 505	1660
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Gln Glu Ala Glu Glu Lys Gln Glu Lys Glu Ala Gly Arg Asp Val Thr	
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Ala Val Met Ala Pro Pro Val Gly Ala Ser Ser Glu Asp Val Glu Gly	
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Gly Pro Ser Arg Glu Gly Ala Leu Gln Glu Gly Ala Thr Ala Gln Gly	
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Gln Pro His Ser Gly Pro Leu Leu Ser Gln Pro Val Val Ala Ala Ala	
620 625 630	
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Gly Gly Arg Asp Gly Arg Met Leu Val Met Asp Met Ile Ala Thr Thr	
635 640 645	
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Lys Phe Lys Ala Gln Ala Lys Leu Phe Leu Gln Lys Arg Phe Gln Ser	
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Lys Ser Phe Pro Ser Tyr Lys Glu Phe Ser Ala Leu Phe Pro Leu Thr	
670 675 680	
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Ala Arg Ser Thr Tyr Tyr Met Trp Lys Arg Ala Leu Tyr Asp Gly Leu	
685 690 695	
acc ctg gta gat ggc tga caggga ggtacaaaag gggctgggaa gaagggggac	2290
Thr Leu Val Asp Gly *	
700	
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atttgagtgg gttgggtggc ccccttgctg gagttggaag ccgtatgtat gtcagggggt	2590

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<213> Homo sapiens

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<222> (90)..(662)

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Met Gly Ala Thr Gly Ala Ala Glu
1 5

ccg ctg caa tcc gtg ctg tgg gtg aag cag cag cgc tgc gcc gtg agc 161
Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val Ser
10 15 20

ctg gag ccc gcg cgg gct ctg ctg cgc tgg tgg cgg agc ccg ggg ccc 209
Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly Pro
25 30 35 40

gga gcc ggc gcc ccc ggc gcg gat gcc tgc tct gtg cct gta tct gag 257
Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu

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atc atc gcc gtt gag gaa aca gac gtt cac ggg aaa cat caa ggc agt			305
Ile Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser			
60	65	70	
gga aaa tgg cag aaa atg gaa aag cct tac gct ttt aca gtt cac tgt			353
Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys			
75	80	85	
gta aag aga gca cga cgg cac cgc tgg aag tgg gcg cag gtg act ttc			401
Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe			
90	95	100	
tgg tgt cca gag gag cag ctg tgt cac ttg tgg ctg cag acc ctg cgg			449
Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg			
105	110	115	120
gag atg ctg gag aag ctg acg tcc aga cca aag cat tta ctg gta ttt			497
Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe			
125	130	135	
atc aac ccg ttt gga gga aaa gga caa ggc aag cgg ata tat gaa aga			545
Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg			
140	145	150	
aaa gtg gca cca ctg ttc acc tta gcc tcc atc acc act gac atc atc			593
Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile			
155	160	165	
gtt act gaa cat gct aat cag gcc aag gag act ctg tat gag att aac			641
Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn			
170	175	180	
ata gac aaa tac gac ggg tga gt aagccgtctt tcatcgccat caagtccatt			694
Ile Asp Lys Tyr Asp Gly *			
185	190		
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 <222> (526)..(1962)

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Phe	Thr	Asp	Pro	Asp	Leu	Leu	Leu	Asp	Leu	Val	Asp	Ala	Ala	Thr	Arg		
	165					170					175						
cgc	tgg	gta	cct	gtc	tac	ctg	ctc	ctg	gac	cgc	cag	cag	ctg	cct	gcc	1110	
Arg	Trp	Val	Pro	Val	Tyr	Leu	Leu	Leu	Asp	Arg	Gln	Gln	Leu	Pro	Ala		
	180				185					190					195		
ttc	ctg	gaa	ctg	gcc	cag	cag	ctg	ggg	gtg	aac	ccc	tgg	aac	acg	gag	1158	
Phe	Leu	Glu	Leu	Ala	Gln	Gln	Leu	Gly	Val	Asn	Pro	Trp	Asn	Thr	Glu		
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aac	gtg	gat	gtc	cgt	gtc	gtg	cgg	ggc	tgc	agc	ttc	cag	agc	cgc	tgg	1206	
Asn	Val	Asp	Val	Arg	Val	Val	Arg	Gly	Cys	Ser	Phe	Gln	Ser	Arg	Trp		
			215					220					225				
cga	cgg	cag	gtg	agc	ggc	acc	gtg	cgg	gag	aag	ttt	gtg	ctg	ctg	gac	1254	
Arg	Arg	Gln	Val	Ser	Gly	Thr	Val	Arg	Glu	Lys	Phe	Val	Leu	Leu	Asp		
		230					235					240					
ggc	gag	agg	gtc	atc	tca	gga	tcc	tac	agc	ttc	acg	tgg	agt	gac	gca	1302	
Gly	Glu	Arg	Val	Ile	Ser	Gly	Ser	Tyr	Ser	Phe	Thr	Trp	Ser	Asp	Ala		
	245					250					255						
cgc	ctg	cac	cga	ggc	ctg	gtg	acc	ctg	ctg	act	ggc	gaa	att	gtt	gac	1350	
Arg	Leu	His	Arg	Gly	Leu	Val	Thr	Leu	Leu	Thr	Gly	Glu	Ile	Val	Asp		
	260				265					270					275		
gcc	ttc	agc	ctt	gag	ttc	cgg	acg	ctg	tac	gcg	gcc	tcc	tgc	ccg	ctc	1398	
Ala	Phe	Ser	Leu	Glu	Phe	Arg	Thr	Leu	Tyr	Ala	Ala	Ser	Cys	Pro	Leu		
				280					285					290			
cca	cct	gcg	ccc	ccc	cag	aaa	ccc	tcg	gtc	ata	ggc	ggc	ctg	cag	cgg	1446	
Pro	Pro	Ala	Pro	Pro	Gln	Lys	Pro	Ser	Val	Ile	Gly	Gly	Leu	Gln	Arg		
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ggc	cgc	agc	ctg	cac	cgc	gtg	tcc	cgc	cgc	cgc	tcc	gtg	gcc	ccc	gcg	1494	
Gly	Arg	Ser	Leu	His	Arg	Val	Ser	Arg	Arg	Arg	Ser	Val	Ala	Pro	Ala		
	310						315					320					
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Ser	Pro	Pro	Pro	Pro	Asp	Gly	Pro	Leu	Ala	His	Arg	Leu	Ala	Ala	Cys		
	325					330					335						
cgc	gtc	tcc	cct	gct	acc	ccg	ggg	ccg	gca	ctc	agt	gac	att	cta	agg	1590	
Arg	Val	Ser	Pro	Ala	Thr	Pro	Gly	Pro	Ala	Leu	Ser	Asp	Ile	Leu	Arg		
	340				345				350						355		
agt	gtg	cag	cgc	gcc	cgg	acc	ccc	agc	ggc	ccc	ccg	gcc	cgg	ccc	agc	1638	
Ser	Val	Gln	Arg	Ala	Arg	Thr	Pro	Ser	Gly	Pro	Pro	Ala	Arg	Pro	Ser		
				360					365					370			
cgc	tcc	atg	tgg	gac	cta	agc	cgc	ctg	tcc	cag	ctg	tct	ggc	tcc	agt	1686	
Arg	Ser	Met	Trp	Asp	Leu	Ser	Arg	Leu	Ser	Gln	Leu	Ser	Gly	Ser	Ser		

375	380	385	
gat ggg gac aac gag ctc aag aaa tcc tgg ggc tcc aag gac act cca			1734
Asp Gly Asp Asn Glu Leu Lys Lys Ser Trp Gly Ser Lys Asp Thr Pro			
390	395	400	
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Ala Lys Ala Leu Met Arg Gln Arg Gly Thr Gly Gly Gly Pro Trp Gly			
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gaa gtg gac tcc cga cct ccg tgg ggc ggt gcc ctg ccc ctg ccc ccc			1830
Glu Val Asp Ser Arg Pro Pro Trp Gly Gly Ala Leu Pro Leu Pro Pro			
420	425	430	435
gcc cac cgc ctc cgc tat ctg tcc cca gcc cga agg cgg ttc ggt ggg			1878
Ala His Arg Leu Arg Tyr Leu Ser Pro Ala Arg Arg Arg Phe Gly Gly			
440	445	450	
gat gct aca ttc aaa ctt caa gag ccc aga ggc gtc agg ccg tca gac			1926
Asp Ala Thr Phe Lys Leu Gln Glu Pro Arg Gly Val Arg Pro Ser Asp			
455	460	465	
tgg gcc ccc cgg gca gga ctt ggg ggg caa ccc tga acag gagcccaagc			1976
Trp Ala Pro Arg Ala Gly Leu Gly Gly Gln Pro *			
470	475		
caaattctgct ggcccaccca aggagcagtg ccggacaact gtcggctcag agccctctgc			2036
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aaccagcgcg gccccctggc gctgaggtg ctccggcc atg gcc cct cgg ccc 413
Met Ala Pro Arg Pro
1 5
cgc gcc cgc cca ggg gtc gct gtc gcc tgc tgc tgg ctc ctc act gtt 461
Arg Ala Arg Pro Gly Val Ala Val Ala Cys Cys Trp Leu Leu Thr Val
10 15 20
gtt cta cgc tgc tgc gta tca ttc aat gtt gat gtg aaa aat tca atg 509
Val Leu Arg Cys Cys Val Ser Phe Asn Val Asp Val Lys Asn Ser Met
25 30 35
act ttc agc ggc ccg gtg gaa gac atg ttt gga tat act gtt caa caa 557
Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly Tyr Thr Val Gln Gln
40 45 50
tat gaa aat gaa gaa gga aaa tgg gtg ctt att ggt tct ccg tta gtt 605
Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile Gly Ser Pro Leu Val
55 60 65
ggc caa ccc aaa aac aga act gga gat gtc tat aag tgt cca gtt ggg 653
Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr Lys Cys Pro Val Gly
70 75 80 85
aga ggt gaa tca tta cct tgc gta aag ttg gat cta cca gtt aat aca 701
Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp Leu Pro Val Asn Thr
90 95 100
tca att ccc aat gtc aca gaa gta aag gag aac atg aca ttt gga tca 749
Ser Ile Pro Asn Val Thr Glu Val Lys Glu Asn Met Thr Phe Gly Ser
105 110 115
act tta gtc acc aac cca aat gga gga ttt ctg gct tgt ggg ccc tta 797
Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu Ala Cys Gly Pro Leu
120 125 130
tat gcc tat aga tgt gga cat ttg cat tac aca act gga atc tgt tct 845
Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr Thr Gly Ile Cys Ser
135 140 145
gac gtc agc ccc aca ttt caa gtc gtg aat tcc att gcc cct gta caa 893
Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser Ile Ala Pro Val Gln
150 155 160 165
gaa tgc agc act caa ctg gac ata gtc ata gtg ctg gat ggt tcc aac 941
Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val Leu Asp Gly Ser Asn
170 175 180

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Ser Ile Tyr Pro Trp Asp Ser Val Thr Ala Phe Leu Asn Asp Leu Leu	
185 190 195	
aaa aga atg gat att ggt cct aaa cag aca cag gtt gga att gta cag	1037
Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln Val Gly Ile Val Gln	
200 205 210	
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Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu Asn Lys Tyr Ser Ser	
215 220 225	
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Thr Glu Glu Val Leu Val Ala Ala Lys Lys Ile Val Gln Arg Gly Gly	
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Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val Lys Lys Val Met Val	
265 270 275	
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Ile Val Thr Asp Gly Glu Ser His Asp Asn His Arg Leu Lys Lys Val	
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Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg Phe Ser Ile Ala Ile	
295 300 305	
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gaa ata aaa tca att gca agt gaa ccc act gaa aag cat ttc ttc aat	1421
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330 335 340	
gtc tct gat gaa ttg gct cta gtc acc att gtt aaa act ctg gga gaa	1469
Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val Lys Thr Leu Gly Glu	
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Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln Ser Ala Ala Ser Phe	
360 365 370	
gaa atg gaa atg tct cag act ggc ttc agt gct cat tat tca cag gac	1565
Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala His Tyr Ser Gln Asp	
375 380 385	
tgg gtc atg ctt gga gca gta gga gcc tat gat tgg aat gga aca gtt	1613
Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp Trp Asn Gly Thr Val	
390 395 400 405	

gtc atg cag aag gct agt caa atc ata atc cct cga aac aca acc ttt	1661
Val Met Gln Lys Ala Ser Gln Ile Ile Ile Pro Arg Asn Thr Thr Phe	
410 415 420	
aat gtt gag tct acc aaa aag aat gaa ccg ctt gct tct tat tta ggt	1709
Asn Val Glu Ser Thr Lys Lys Asn Glu Pro Leu Ala Ser Tyr Leu Gly	
425 430 435	
tac act gta aac tct gct act gct tct tct gga gat gtg ctc tat att	1757
Tyr Thr Val Asn Ser Ala Thr Ala Ser Ser Gly Asp Val Leu Tyr Ile	
440 445 450	
gct gga cag cct cgg tac aat cat aca ggc cag gtc att atc tac agg	1805
Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val Ile Ile Tyr Arg	
455 460 465	
atg gaa gat gga aac atc aaa att ctc cag acg ctc agt gga gaa cag	1853
Met Glu Asp Gly Asn Ile Lys Ile Leu Gln Thr Leu Ser Gly Glu Gln	
470 475 480 485	
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Ile Gly Ser Tyr Phe Gly Ser Ile Leu Thr Thr Thr Asp Ile Asp Lys	
490 495 500	
gat tct aat act gac att ctt cta gtc gga gcc cct atg tac atg gga	1949
Asp Ser Asn Thr Asp Ile Leu Leu Val Gly Ala Pro Met Tyr Met Gly	
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aca gag aag gag gag caa gga aaa gtg tat gtg tat gct ctc aat cag	1997
Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr Ala Leu Asn Gln	
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gat cac ggg gga gct gtg tac att tat cat gga agt ggc aag act ata	2237
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600 605 610	
agg aaa gag tat gca caa cgt att cca tca ggt ggg gat ggt aag aca	2285
Arg Lys Glu Tyr Ala Gln Arg Ile Pro Ser Gly Gly Asp Gly Lys Thr	
615 620 625	
ctg aaa ttt ttt ggc cag tct atc cac gga gaa atg gat tta aat ggt	2333

Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met Asp Leu Asn Gly	
630 635 640 645	
gac ggt ctg aca gat gtg act att ggg ggc ctt ggt ggt gct gcc ctc	2381
Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly Gly Ala Ala Leu	
650 655 660	
ttc tgg tcc cga gat gtg gcc gta gtt aaa gtg acc atg aat ttt gag	2429
Phe Trp Ser Arg Asp Val Ala Val Val Lys Val Thr Met Asn Phe Glu	
665 670 675	
cca aat aaa gtg aat att caa aag aaa aac tgc cat atg gag gga aag	2477
Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys His Met Glu Gly Lys	
680 685 690	
gaa aca gta tgc ata aat gct aca gtg tgt ttt gag gtt aaa tta aag	2525
Glu Thr Val Cys Ile Asn Ala Thr Val Cys Phe Glu Val Lys Leu Lys	
695 700 705	
tct aaa gaa gac acg att tat gaa gct gat ttg cag tac cgt gtc acc	2573
Ser Lys Glu Asp Thr Ile Tyr Glu Ala Asp Leu Gln Tyr Arg Val Thr	
710 715 720 725	
cta gat tca cta aga caa ata tca cga agt ttt ttc tct gga act caa	2621
Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe Ser Gly Thr Gln	
730 735 740	
gag aga aag gtt caa agg aac atc aca gtt cga aaa tca gaa tgc act	2669
Glu Arg Lys Val Gln Arg Asn Ile Thr Val Arg Lys Ser Glu Cys Thr	
745 750 755	
aag cac tcc ttc tac atg ttg gac aag cat gac ttt cag gac tct gtg	2717
Lys His Ser Phe Tyr Met Leu Asp Lys His Asp Phe Gln Asp Ser Val	
760 765 770	
aga ata acg ttg gac ttt aat ctt acc gat cca gaa aat ggg cct gtt	2765
Arg Ile Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu Asn Gly Pro Val	
775 780 785	
ctt gat gat tct cta cca aac tca gta cat gaa tat att ccc ttt gcc	2813
Leu Asp Asp Ser Leu Pro Asn Ser Val His Glu Tyr Ile Pro Phe Ala	
790 795 800 805	
aaa gat tgt gga aat aag gaa aaa tgt atc tca gac ctc agc ctg cat	2861
Lys Asp Cys Gly Asn Lys Glu Lys Cys Ile Ser Asp Leu Ser Leu His	
810 815 820	
gtc gcc acc act gaa aag gac ctg ctg att gtc cga tcc cag aat gat	2909
Val Ala Thr Thr Glu Lys Asp Leu Leu Ile Val Arg Ser Gln Asn Asp	
825 830 835	
aag ttc aac gtt agc ctc aca gtc aaa aat aca aag gac agt gcc tat	2957
Lys Phe Asn Val Ser Leu Thr Val Lys Asn Thr Lys Asp Ser Ala Tyr	
840 845 850	
aac acc agg aca ata gtg cat tat tct cca aat cta gtt ttt tca gga	3005
Asn Thr Arg Thr Ile Val His Tyr Ser Pro Asn Leu Val Phe Ser Gly	

855	860	865	
att gag gct atc caa aaa gac agt tgt gaa tct aat cat aat atc aca Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser Asn His Asn Ile Thr 870 875 880 885			3053
tgt aaa gtt gga tat ccc ttc ctg aga aga gga gag atg gta act ttc Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly Glu Met Val Thr Phe 890 895 900			3101
aaa ata ttg ttt cag ttt aac aca tcc tat ctc atg gaa aat gtg acc Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu Met Glu Asn Val Thr 905 910 915			3149
att tat tta agt gca aca agt gac agc gaa gaa cct cct gaa acc ctt Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro Pro Glu Thr Leu 920 925 930			3197
tct gat aat gta gta aac att tct atc ccg gta aaa tat gaa gtt gga Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val Lys Tyr Glu Val Gly 935 940 945			3245
cta cag ttt tac agc tct gca agt gaa tac cac att tca att gct gcc Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His Ile Ser Ile Ala Ala 950 955 960 965			3293
aat gag aca gtc cct gaa gtt att aat tct act gag gac att gga aat Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr Glu Asp Ile Gly Asn 970 975 980			3341
gaa att aat atc ttc tac ttg att aga aaa agt gga tct ttt cca atg Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser Gly Ser Phe Pro Met 985 990 995			3389
cca gag ctt aag ctg tca att tca ttc ccc aat atg aca tca aat ggt Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn Met Thr Ser Asn Gly 1000 1005 1010			3437
tac cct gtg ctg tac cca act gga ttg tca tct tct gag aat gca aac Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser Ser Glu Asn Ala Asn 1015 1020 1025			3485
tgc aga ccc cat atc ttt gag gat cct ttc agt atc aac tct gga aag Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser Ile Asn Ser Gly Lys 1030 1035 1040 1045			3533
aaa atg act aca tca act gac cat ctc aaa cga ggc aca att ctg gac Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg Gly Thr Ile Leu Asp 1050 1055 1060			3581
tgc aat aca tgt aaa ttt gct acc atc aca tgt aat ctc act tct tct Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys Asn Leu Thr Ser Ser 1065 1070 1075			3629
gac atc agc caa gtc aat gtt tgc ctt atc ttg tgg aaa cca act ttt Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu Trp Lys Pro Thr Phe 1080 1085 1090			3677

ata aaa tca tat ttt tcc agc tta aat ctt act ata agg gga gaa ctt	3725
Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr Ile Arg Gly Glu Leu	
1095 1100 1105	
cgg agt gaa aat gca tct ctg gtt tta agt agc agc aat caa aaa aga	3773
Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser Ser Asn Gln Lys Arg	
1110 1115 1120 1125	
gag ctt gct att caa ata tcc aaa gat ggg cta ccg ggc aga gtg cca	3821
Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu Pro Gly Arg Val Pro	
1130 1135 1140	
tta tgg gtc atc ctg ctg agt gct ttt gcc gga ttg ttg ctg tta atg	3869
Leu Trp Val Ile Leu Leu Ser Ala Phe Ala Gly Leu Leu Leu Leu Met	
1145 1150 1155	
ctg ctc att tta gca ctg tgg aag att gga ttc ttc aaa aga cca ctg	3917
Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly Phe Phe Lys Arg Pro Leu	
1160 1165 1170	
aaa aag aaa atg gag aaa tga aa tattttatga aagaaaataa taacaattat	3970
Lys Lys Lys Met Glu Lys *	
1175 1180	
tcaataatct atcctcaggt ttgcctcaaa tatgtgacaa gaaatgtata attcatgaca	4030
tagtcatgta actatgtaat ccatcaggga ttcattactt ggaaaatgac aggtcatgca	4090
ttatccaaaa acaataccaa aaagacatat ttataaaaat gacaaaaaat attttacata	4150
attactcatt tttgttgagt aagcaaaatt acaaagtgtt tttaaaaaaa cctgtacaaa	4210
tatgtttatg tattaaatca ccatccaaaa tatttaagga atatataaaa agatttttat	4270
gatcatagaa acatctatct tcaaaacaat ataaattaag cttttcccct tgattcctgt	4330
tggatatcca tgttcagcat gacagtcagc actcgtaaat gccaaagaaa gaattacctg	4390
aaaaagatca tttctcccta ttcaaatgag aatattttcc ctcggtagaa tccatatata	4450
atatggattg aaaattaagt cacgaagaat acatttagca tctttgtgtt gggttctata	4510
cctaaaaatt ttccctcccg gcccaag	4537

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (608) .. (832)

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gagaaagagg ataactctga ccaggtttgg gtctgggtcag agcccccgcc tcttcagggc      180
aggtgctgag ttgtggaaat ttgaggagcc tattttcgtg tttagttttc aaactaagac      240
tgctgcttct gcttctctga cgggcttcag ctgggaacag attaactagg ttgctaaaagg      300
aacaatatatt tcttccgtgc actgaagaca ggcaggaaga caacagataa cgtacctgca      360
gtggagaggt taagctcctg tacggaagcg taattcataa atagataaat ataggaaagg      420
acaacaaaga aaatagggat agaataacgg gcagagaatt tagagatgat gtcaggtgat      480
tagttttctc atctaaaagc ttgaaaatcc tgcattgttg tggagtgggt aagcaggtgg      540
tgaagagggc aaactctttg attctacaat agctgatgag ggaacatgga ctttggagga      600
cagaaaa atg gtt cgt att gtt ctt aca aag aca aag aga gat gca gca      649
      Met Val Arg Ile Val Leu Thr Lys Thr Lys Arg Asp Ala Ala
      1             5             10

aat tgt tgg act tct cta cta gaa tct gaa tat gca gcg gat cct tgg      697
Asn Cys Trp Thr Ser Leu Leu Glu Ser Glu Tyr Ala Ala Asp Pro Trp
      15             20             25             30

gtg caa gac caa atg cag aga aag ctt aca tta gag aga ttc caa aaa      745
Val Gln Asp Gln Met Gln Arg Lys Leu Thr Leu Glu Arg Phe Gln Lys
      35             40             45

gaa aat cct ggt ttt gac ttc agt gga gca gaa atc tca gga aac tac      793
Glu Asn Pro Gly Phe Asp Phe Ser Gly Ala Glu Ile Ser Gly Asn Tyr
      50             55             60

act aaa ggt gga cca gat ttc tca aac ctt gag aaa taa ctgctttttt      842
Thr Lys Gly Gly Pro Asp Phe Ser Asn Leu Glu Lys *
      65             70             75

tcctgcattc tgtggatcct agcagatatt gccaaacttaa tcagataaac agattatgta      902
atggaagaaa aatgcggatg cctacagtta acagattgca aaatgtatct taaaatgggt      962
ctaaaaattg cattcaaaca taatttacat aggaaatgta ctgtgggaac tattctatgg      1022
atatatgggt aagttgtttt ggacttggtt ttgctcagca tgaagtttta tatgctgcat      1082
tttactaatt ccatatttaa ccatatgttt aatacaaaag aacattagag tatagatcat      1142
gtgaaatgaa ggggtgccttc ggggaaaatt aactttttct tttgatagta tgatattcac      1202
t                                                                                   1203

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<210> 251
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (36)..(362)

<400> 251

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                                         Met Thr Pro Ser Arg Leu
                                         1                               5

ccc tgg ttg ctt agc tgg gtc tcg gcc acg gcg tgg aga gcg gca aga   101
Pro Trp Leu Leu Ser Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg
                        10                        15                        20

tca ccc ctt ctg tgt cat tct ctg agg aaa aca agt tct tct caa gga   149
Ser Pro Leu Leu Cys His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly
                        25                        30                        35

gga aag tct gaa ctt gtc aaa cag tcc ctt aag aag ccg aag tta cca   197
Gly Lys Ser Glu Leu Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro
                        40                        45                        50

gaa ggt cgt ttt gat gca cca gag gat tcc cat tta gag aaa gaa cca   245
Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro
                        55                        60                        65                        70

ctg gaa aaa ttt cca gat gat gtt aat cca gtg acc aaa gaa aaa ggt   293
Leu Glu Lys Phe Pro Asp Asp Val Asn Pro Val Thr Lys Glu Lys Gly
                        75                        80                        85

gga ccc agg ggc cca gaa cct acc cga tat gga gat tgg gaa cga aaa   341
Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys
                        90                        95                        100

gga cgc tgt att gat ttt taa gt cgcataattct ttaacttcaa tattgttttc   394
Gly Arg Cys Ile Asp Phe *
                        105

tgaatatgta catctgaatt aacttatttc tgattatttt ctttctttat atcctttatg   454

tcgtgtagtt tgtataatgt gtttaaatat atatatatat atatatatat atatatatat   514

atgatggcctt tggaagaaaa tatgctgctg taaattagga aagggagacc agcctgacca   574

atatggagaa atctcgcctt tgctagagat acaaaattag ccaggcgtgg tggcatgcac   634

ctgtaatcag cctcctgagt agctgggatt acagacaccc accattgcgc ctggctaatt   694

tttgtatttt tagtaaagac aaggtttcac catgttagcc aggctgggtct cgaactcctg   754

acctcagttg atccacctgc ctcagcctcc caaagtgctg ggattgcagg tgtgagccac   814

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cacgcccagc ctagaaatga ttcttagagc tgtaggcctt tacttcatca tttttcagtt 874
 taaattaatc agttgcttat aaaatgcata cataaataaa ataattttta aaaaaaaaaa 934
 a 935

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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 252

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 Met Ser Cys Arg Gly
 1 5

cgg ggc gcg ggc gga cga tgg aac tcc aca tcc tgg agc acc ggc tgc 103
 Arg Gly Ala Gly Gly Arg Trp Asn Ser Thr Ser Trp Ser Thr Gly Cys
 10 15 20

aag ttg cca gcg tgc cca agg aga gta tcc cgc tgt tca cct acg ggc 151
 Lys Leu Pro Ala Ser Pro Arg Arg Val Ser Arg Cys Ser Pro Thr Gly
 25 30 35

ctg atc aaa ctt gcc ttc ctg ttc tcc aag acc agg tgc aag ttc ttc 199
 Leu Ile Lys Leu Ala Phe Leu Phe Ser Lys Thr Arg Cys Lys Phe Phe
 40 45 50

agt ctg act gag aca cca gag gat tac act atc att gtc gat gag gaa 247
 Ser Leu Thr Glu Thr Pro Glu Asp Tyr Thr Ile Ile Val Asp Glu Glu
 55 60 65

gga ttc cta gag ctg ccc tcc tca gag cac ctg agt gtg gcg gat gcc 295
 Gly Phe Leu Glu Leu Pro Ser Ser Glu His Leu Ser Val Ala Asp Ala
 70 75 80 85

acc tgg ctg gcc ctg aac gtg gtg tcc ggc ggt ggc agc ttc tcc agc 343
 Thr Trp Leu Ala Leu Asn Val Val Ser Gly Gly Gly Ser Phe Ser Ser
 90 95 100

tcc cag cct att ggc atg acc aag atc gcc aag tca gtc atc gcc cca 391
 Ser Gln Pro Ile Gly Met Thr Lys Ile Ala Lys Ser Val Ile Ala Pro
 105 110 115

ctg gct gac cag aac ata tcc gtg ttc atg ctg tcc acg tat cag aca 439
 Leu Ala Asp Gln Asn Ile Ser Val Phe Met Leu Ser Thr Tyr Gln Thr
 120 125 130

gac ttc atc ctg gtg ctc aag cgg gac ctg ccc ttt gtc acc cac acg 487
 Asp Phe Ile Leu Val Leu Lys Arg Asp Leu Pro Phe Val Thr His Thr

cag cca cct ctg cga gtc cca cag ctg gaa gga gca ccc agt cct ccc 327
Gln Pro Pro Leu Arg Val Pro Gln Leu Glu Gly Ala Pro Ser Pro Pro
25 30 35

aca cta gcc gga cag gcc cgc agc ctg cac tac tga gctg tcacggagga 377
Thr Leu Ala Gly Gln Ala Arg Ser Leu His Tyr *
40 45 50

ctctaccaag cccagtgcg gagccacaag tggaggacat cctg 421

<210> 254
<211> 636
<212> DNA
<213> Homo sapiens

<220>
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<400> 254
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ccctgcaggt tgggggacag ggaaggggga ataaggcctc gggagaagga agatgagcta 120

ggaggcctgg tgcactacac agctcctttg tgctccagg ccacctgccc aagctgggtgt 180

gcctcccttc taaggctctg tcccactggg cacaggaggc agatccagca gcgtggaatc 240

ccagataac atg tcc cac aga ctc tgg caa cgt cac aga tca cat gga 288
Met Ser His Arg Leu Trp Gln Arg His Arg Ser His Gly
1 5 10

gag gca agt gca ggc caa cga cat ccg cat ccg ggt cct aca gga gga 336
Glu Ala Ser Ala Gly Gln Arg His Pro His Pro Gly Pro Thr Gly Gly
15 20 25

gaa cgg gcg gct cca atc aat gct gtc caa aat ccg gga agt ggc cca 384
Glu Arg Ala Ala Pro Ile Asn Ala Val Gln Asn Pro Gly Ser Gly Pro
30 35 40 45

gca ggg tgg cct caa ggt ggg cct gag agg gcg ggc cct tgg gga cca 432
Ala Gly Trp Pro Gln Gly Gly Pro Glu Arg Ala Gly Pro Trp Gly Pro
50 55 60

gga gga agc ccc tat cca gca gca ggt ctt cag act ctg ccc cgg gaa 480
Gly Gly Ser Pro Tyr Pro Ala Ala Gly Leu Gln Thr Leu Pro Arg Glu
65 70 75

ctt gtg gag agc cca cct cat cac atg agg cct tag gctg tgcttttgtg 530
Leu Val Glu Ser Pro Pro His His Met Arg Pro *
80 85

aaacattttt cacatttcca gaaggcgtga ggatgttatg gattcgatgc cttccagttc 590

cataagccct ttgtagctgt cattccttta agtgcagcaa caagcc

636

<210> 255
 <211> 718
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (414)..(695)

<400> 255

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caccaccaag cctggactgg aagtgtgttg agccctggg tcaggctggc gagccagctc      120
ggccctgccc acccaggggt ttccgagatc acccctggtg aggcggcgtg ccagtccctt      180
gctttcttac ttgttctgca gagcggggag ctgaggctgc atgaggaag actcccgtac      240
cccagcacgg tggaggggtg gatgggggtca cgcctgtgcg acccaggagg tggccagcag      300
aaggaaacag tagtgtccac catggtctgc gtctccccac cacggattgt cttgggtccg      360
gatttgagac atggcagggc cagatgagga caacttgatg acagtttaca gag   atg      416
                                   Met
                                   1

gag gca ggg tgc cag gaa gcc acg ggg gag ccc cca ggg cac tca gca      464
Glu Ala Gly Cys Gln Glu Ala Thr Gly Glu Pro Pro Gly His Ser Ala
                    5                      10                      15

gtc cag gca ggg ctg ggc gtc ctg gca agg agc agg gac ctt ctg ccc      512
Val Gln Ala Gly Leu Gly Val Leu Ala Arg Ser Arg Asp Leu Leu Pro
                20                      25                      30

agg ggt gtg gcc agc ctg tgg gtg ctg tgt gca gga ccc cag gaa cca      560
Arg Gly Val Ala Ser Leu Trp Val Leu Cys Ala Gly Pro Gln Glu Pro
                35                      40                      45

agg ccg cag tct ctt ccc tcg ctc cag cat cct ccc aag gcc acc ctt      608
Arg Pro Gln Ser Leu Pro Ser Leu Gln His Pro Pro Lys Ala Thr Leu
                50                      55                      60                      65

ggc tgc act cag cca gag agc tgg ggc aca ggg acc cca cag gtt tcc      656
Gly Cys Thr Gln Pro Glu Ser Trp Gly Thr Gly Thr Pro Gln Val Ser
                    70                      75                      80

ctg gag gct gtc agg ggc tcc ggt ggg ggc ggg ggg tga gcccgtggg      705
Leu Glu Ala Val Arg Gly Ser Gly Gly Gly Gly Gly *
                    85                      90

ttcactgcac ctc      718
    
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<210> 256
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 <213> Homo sapiens

<220>
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 <222> (251)..(1609)

<400> 256

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gagtgagtgt cgtgggttggg gtgctggacc cagagtgcct accctcgctt gcctgggcct      120
cagtttccac atctgcacaa tgggggtgac catcctgcc ctgctggctg ccaggagcgg      180
ctgtgagtct tcaggcgtgg atgcagcctg ggggaagcca tagggcgctt tcacaggcct      240
ggccttcacc  atg gcg gga ggg aga ccg cat ctg aag agg agt ttc tcc      289
              Met Ala Gly Gly Arg Pro His Leu Lys Arg Ser Phe Ser
              1             5             10

atc atc ccc tgc ttt gtc ttc gtg gag tcg gtg ctg ctg ggc att gtg      337
Ile Ile Pro Cys Phe Val Phe Val Glu Ser Val Leu Leu Gly Ile Val
              15             20             25

atc ctg ctt gct tac cgc ctg gag ttc acg gac acc ttc cct gtg cac      385
Ile Leu Leu Ala Tyr Arg Leu Glu Phe Thr Asp Thr Phe Pro Val His
              30             35             40             45

acc cag gga ttc ttc tgc tat gac agt acc tac gcc aag ccc tac cca      433
Thr Gln Gly Phe Phe Cys Tyr Asp Ser Thr Tyr Ala Lys Pro Tyr Pro
              50             55             60

ggg cct gag gct gcc agc cga gtg cct cct gct ctt gtc tac gca ctg      481
Gly Pro Glu Ala Ala Ser Arg Val Pro Pro Ala Leu Val Tyr Ala Leu
              65             70             75

gtc act gcc ggg ccc acc ctg acg atc ctg ctg gga gag ctg gcg cgt      529
Val Thr Ala Gly Pro Thr Leu Thr Ile Leu Leu Gly Glu Leu Ala Arg
              80             85             90

gcc ttt ttc cct gca cca cct tca gcc gtc cca gtc atc ggg gag agc      577
Ala Phe Phe Pro Ala Pro Pro Ser Ala Val Pro Val Ile Gly Glu Ser
              95             100             105

acc atc gtg tct ggg gcc tgc tgc cgc ttc agc ccc cca gtg cgg agg      625
Thr Ile Val Ser Gly Ala Cys Cys Arg Phe Ser Pro Pro Val Arg Arg
              110             115             120             125

ctg gtc cgc ttc ctg ggg gtc tac tcc ttc ggc ctg ttc acc acg acc      673
Leu Val Arg Phe Leu Gly Val Tyr Ser Phe Gly Leu Phe Thr Thr Thr
              130             135             140
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atc ttc gcc aac gcg ggg cag gtg gtg acc ggc aat ccc acg cca cac Ile Phe Ala Asn Ala Gly Gln Val Val Thr Gly Asn Pro Thr Pro His 145 150 155	721
ttc ctg tcc gtg tgc cgc ccc aac tac acg gcc ctg ggc tgc ctg cca Phe Leu Ser Val Cys Arg Pro Asn Tyr Thr Ala Leu Gly Cys Leu Pro 160 165 170	769
cct tct ccg gat cgg cca ggt ccc gac cgc ttt gtc act gac cag ggt Pro Ser Pro Asp Arg Pro Gly Pro Asp Arg Phe Val Thr Asp Gln Gly 175 180 185	817
gcc tgc gct ggc agt ccc agc ctc gtg gcc gcc gcg cgc cgc gcc ttc Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala Arg Arg Ala Phe 190 195 200 205	865
ccc tgc aag gat gcg gcc ctc tgc gcc tac gcg gtc acc tac aca gcg Pro Cys Lys Asp Ala Ala Leu Cys Ala Tyr Ala Val Thr Tyr Thr Ala 210 215 220	913
atg tac gtg act ctc gtg ttc cgc gtg aag ggc tcc cgc ctg gtc aaa Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys 225 230 235	961
ccc tcg ctc tgc ctg gcc ttg ctg tgc ccg gcc ttc ctg gtg ggc gtg Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val 240 245 250	1009
gtc cgc gtg gcc gag tac cga aac cac tgg tcg gac gtg ctg gct ggc Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly 255 260 265	1057
ttc ctg aca ggg gcg gcc atc gcc acc ttt ttg gtc acc tgc gtt gtg Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val 270 275 280 285	1105
cat aac ttt cag agc cgg cca ccc tct ggc cga agg ctc tct ccc tgg His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp 290 295 300	1153
gag gac ctg ggc caa gcc ccc acc atg gat agc ccc ctc gaa aag tta Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Leu 305 310 315	1201
agt gtg gcg cag gaa ccc gag gtc tgc agg ccg cat tcg aca ccg gca Ser Val Ala Gln Glu Pro Glu Val Cys Arg Pro His Ser Thr Pro Ala 320 325 330	1249
cgg ctc acc cca tcc aag tcg cag aac tgc gcc cgc cgt ggc cac ctg Arg Leu Thr Pro Ser Lys Ser Gln Asn Cys Ala Arg Arg Gly His Leu 335 340 345	1297
atc ccc agc tgt gtc tcc tcc agg gcc cca gcc atg tgt tcg tcg ccc Ile Pro Ser Cys Val Ser Ser Arg Ala Pro Ala Met Cys Ser Ser Pro 350 355 360 365	1345
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Arg Val Pro Arg Pro Arg Leu Arg Ser Glu Pro Thr Pro Leu Pro Leu	
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Pro Leu Pro Leu Pro Ala Pro Thr Pro Ser Gln Gly Pro Ser Pro Ser	
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Leu Tyr Pro Ser Pro Phe His Arg Asp Asn Phe Ser Pro Tyr Leu Phe	
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Ala Ser Arg Asp His Leu Leu *	
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cggcctcgt gagtgcccag ccgcccggcg cccaggcctg gggcaccgcg agtgccgaac	360
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Asp Glu Gly Glu Glu Lys Tyr Glu Val Val Lys Leu Lys Ile Pro Met	
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Ala Arg Pro His Ala Cys Pro Asp Cys Gly Arg Ala Phe Ala Arg Arg	
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Ser Thr Leu Ala Lys His Ala Arg Thr His Thr Gly Glu Arg Pro Phe	
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Arg His Thr Gly Glu Lys Pro Tyr Ala Cys Ala His Cys Gly Arg Arg	
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ttc agg cat ggc gac ccg cct gag cca cct cca ggg gca aga gat gag      162
Phe Arg His Gly Asp Pro Pro Glu Pro Pro Gly Ala Arg Asp Glu
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Ile Thr Pro Val Ile His Cys Ser Ala Gln Asp Ser Ser Val Gly Ser
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[illegible]

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Variable	Mean	SD	Min	Max
Age	34.5	10.5	20	55
Gender	Male			
Marital status	Married			
Education	High school			
Occupation	Teacher			
Income	Low			
Health status	Good			
Stress level	High			
Life satisfaction	Low			
Depression	High			
Loneliness	High			
Self-esteem	Low			
Resilience	Low			
Optimism	Low			
Gratitude	Low			
Forgiveness	Low			
Empathy	Low			
Prosocial behavior	Low			
Aggression	High			
Conduct problems	High			
Academic achievement	Low			
Attendance	Low			
Engagement	Low			
Relationship quality	Low			
Parental involvement	Low			
Teacher-student relationship	Low			
Peer relationships	Low			
Family functioning	Low			
School climate	Low			
Teacher efficacy	Low			
Student motivation	Low			
Classroom management	Low			
Instructional quality	Low			
Assessment practices	Low			
Professional development	Low			
Leadership	Low			
Communication	Low			
Collaboration	Low			
Decision making	Low			
Problem solving	Low			
Conflict resolution	Low			
Emotional regulation	Low			
Self-regulation	Low			
Executive function	Low			
Attention	Low			
Memory	Low			
Language	Low			
Mathematics	Low			
Science	Low			
Reading	Low			
Writing	Low			
Art	Low			
Music	Low			
Physical education	Low			
Health education	Low			
Character education	Low			
Civics	Low			
History	Low			
Geography	Low			
Foreign languages	Low			
Technology	Low			
Environmental education	Low			
Arts integration	Low			
Interdisciplinary learning	Low			
Project-based learning	Low			
Flipped classroom	Low			
Blended learning	Low			
Distance learning	Low			
Hybrid learning	Low			
Microlearning	Low			
Personalized learning	Low			
Adaptive learning	Low			
Competency-based learning	Low			
Outcome-based learning	Low			
Standards-based learning	Low			
Common Core	Low			
Next Generation Science Standards	Low			
Common Core State Standards	Low			
International Baccalaureate	Low			
Advanced Placement	Low			
Gifted and talented	Low			
Special education	Low			
English language learners	Low			
Latino students	Low			
Hispanic students	Low			
Black students	Low			
White students	Low			
Asian students	Low			
Pacific Islander students	Low			
Native American students	Low			
Two-spirit students	Low			
Transgender students	Low			
Non-binary students	Low			
Gender-nonconforming students	Low			
Sexual orientation diverse students	Low			
Religious diverse students	Low			
Ethnically diverse students	Low			
Culturally diverse students	Low			
Linguistically diverse students	Low			
Socioeconomically diverse students	Low			
Disability diverse students	Low			
Ability diverse students	Low			
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High-achieving students	Low			
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At-risk students	Low			

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cgc	tgt	ctc	tgg	gat	cgg	ctg	cat	gcc	cag	cct	cgt	ttg	ggc	act	gtc	382							
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Ser	Pro	His	Pro	Val	Asp	Val	Leu	Gly	Val	Asp	Phe	Ser	Pro	Val	Ala	100	105	110					
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Ala	Gln	Asn	Leu	Gly	Ala	Val	Ala	Ser	Ser	Gly	Ser	Phe	Gln	Leu	Leu	145	150	155	160				
ctg	gac	aaa	ggc	aca	tgg	gat	gct	gtt	gcc	cgg	gga	ggt	ctg	cct	agg	766							
Leu	Asp	Lys	Gly	Thr	Trp	Asp	Ala	Val	Ala	Arg	Gly	Gly	Leu	Pro	Arg	165	170	175					
gct	tac	cag	ctt	cta	tca	gaa	tgc	ttg	agg	gtt	cta	aac	cct	cag	ggg	814							
Ala	Tyr	Gln	Leu	Leu	Ser	Glu	Cys	Leu	Arg	Val	Leu	Asn	Pro	Gln	Gly								

180	185	190	
acc ctg att cag ttc tca gat gag gac cct gat gtg cga ctg ccc tgc			862
Thr Leu Ile Gln Phe Ser Asp Glu Asp Pro Asp Val Arg Leu Pro Cys			
195	200	205	
ctg gaa caa ggg tcc tat ggc tgg act gtg act gtg cag gag cta ggc			910
Leu Glu Gln Gly Ser Tyr Gly Trp Thr Val Thr Val Gln Glu Leu Gly			
210	215	220	
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Pro Phe Arg Gly Ile Thr Tyr Phe Ala Tyr Leu Ile Gln Gly Ser His			
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taa agac atttttagtag tcctgaccct agtattttctg tgggcaagga gagggctgaa			1015
*			
gaactgtctt tgcaagctat ctggctgcaa agtgagaatt tgagtcctgg cttccacatt			1075
tactagctgg gtgccatatt gctgaatggt tctgttcccc agtttactca tctgcagagt			1135
gagaataact tggagttacg gagattacat acaatgatgt gcgcaatatt tagcacaaaa			1195
tgaatgctga aaagagaagg tacaattggg tcattcccca gtttcaacta actggagctc			1255
ctaaaagcag cagacaggaa ctgaatcaaa acccctgcgc tgactgactt gtataatcta			1315
gtggcctaac ctgtaagcct cattnttgtc acctgtaaaa ggagattgta agaggatggg			1375
tataacgagc ttcataaacc tcgatgagat atttgagggg gagggaacaa tacttaccct			1435
caaagctatt aggaggccgg agatgggaat atttccacaa gcccg			1480
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<211> 1645			
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<213> Homo sapiens			
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<222> (389)..(1030)			
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ttgaagatcg tgacgtcttg taactagcag tgtgtgcaca gaatcctact caaggaacgt			180
cttggcccag cgatgcaaag aactgaagtt tcaagctgga agagcctgta ttgtcctcac			240
aatagtatag aagaattcaa gagaggagag agagacagca ccgaatgaag actgtaaaag			300

aaaagaagga atgccagaga ttgagaaaat ctgccaagac taggagggta acccagagga 360
 aaccgtcttc agggcctgtt tgctggct atg ctt cga gaa cct ggg gat ccc 412
 Met Leu Arg Glu Pro Gly Asp Pro
 1 5
 gaa aaa tta ggg gaa ttt ctt cag aaa gac aat atc agc gtg cat tat 460
 Glu Lys Leu Gly Glu Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr
 10 15 20
 ttc tgt ctt atc tta tct agt aag ctg cct cag agg ggc cag tcc aac 508
 Phe Cys Leu Ile Leu Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn
 25 30 35 40
 aga ggt ttc cat gga ttt ctg cct gaa gac atc aaa aag gag gca gcc 556
 Arg Gly Phe His Gly Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala
 45 50 55
 cgg gct tct agg aag atc tgc ttt gtg tgc aag aaa aag gga gct gct 604
 Arg Ala Ser Arg Lys Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala
 60 65 70
 atc aac tgc cag aag gat cag tgc ctc aga aac ttc cat ctg cct tgt 652
 Ile Asn Cys Gln Lys Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys
 75 80 85
 ggc caa gaa agg ggt tgc ctt tca caa ttt ttt gga gag tac aaa tca 700
 Gly Gln Glu Arg Gly Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser
 90 95 100
 ttt tgt gac aaa cat cgc cca aca cag aac atc caa cat ggg cat gtg 748
 Phe Cys Asp Lys His Arg Pro Thr Gln Asn Ile Gln His Gly His Val
 105 110 115 120
 ggg gag gaa agc tgc atc tta tgt tgt gaa gac tta tcc caa cag agt 796
 Gly Glu Glu Ser Cys Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser
 125 130 135
 gtt gag aac atc cag agc ccg tgt tgt agt caa gcc atc tac cac cgc 844
 Val Glu Asn Ile Gln Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg
 140 145 150
 aag tgc ata cag aaa tat gcc cac aca tca gca aag cat ttc ttc aaa 892
 Lys Cys Ile Gln Lys Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys
 155 160 165
 tgt cca cag tgt aac aat cga aaa gag ttt cct caa gaa atg ctg aga 940
 Cys Pro Gln Cys Asn Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg
 170 175 180
 atg gga att cat att cca gac agg agg tgg tgc ctc att ctg tgt gct 988
 Met Gly Ile His Ile Pro Asp Arg Arg Trp Cys Leu Ile Leu Cys Ala
 185 190 195 200
 act gcg gat ccc acg gaa ccc aca gga ctg ctc ctc tct tag atctaac 1037
 Thr Ala Asp Pro Thr Glu Pro Thr Gly Leu Leu Leu Ser *
 205 210

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agtaagaaat gggagtgtga ggagtgttca cctgctgcag ccacagacta catacctgaa 1097
aactcagggg acatcccttg ctgcagcagc accttccacc ctgaggaaca tttctgcaga 1157
gacaacacct tggaagagaa tccgggcctt tcttggactg attggccaga accttcctta 1217
ttagaaaagc cagagtcctc tcgtggcagg aggagctact cctggaggtc caaggggtgc 1277
agaatcacta acagctgcaa aaaatccaag taacaccttc tgagtagctg ctgtcccaca 1337
caatagggta tgaagctgcg ctccctccatc gggtttgggg agggagcact ctgggactgt 1397
gagacaagga agcagggcca gcagtgcagc tatgagccaa gcaaagagaa gtctcagtgg 1457
agcatgagga gggagcagtc cagatgccaa caaggaaatg cgtttatggc tacaagagtg 1517
cctctgcttt ctctctctct cctcccacca aggattcttc caccttaatc ttgttttcat 1577
atgcctcttc ttacttcacc catgtttgtt gttatgcaaa taaaggtttt ctctccaaaa 1637
aaaaaaaaa 1645

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<210> 262
<211> 694
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (166)..(672)

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atcagattag ctgctcctgt gtgttcttct aagactctgc aggctgaggt ccctttgtca 120
gactgtgtcc aaaaagcaag taaaccact tcaagcacac aaatc atg gtg aag 174
Met Val Lys
1
acc aac atg tat cat aat gaa aag gtg aac ttt cat gtt gaa tgt aaa 222
Thr Asn Met Tyr His Asn Glu Lys Val Asn Phe His Val Glu Cys Lys
5 10 15
gac tat gta aaa aag gca aag gta aag atc aac cca gtg caa cag agc 270
Asp Tyr Val Lys Lys Ala Lys Val Lys Ile Asn Pro Val Gln Gln Ser
20 25 30 35
cgg ccc ttg ttg agc cag att cac aca gat gca gca aag gag aac acc 318
Arg Pro Leu Leu Ser Gln Ile His Thr Asp Ala Ala Lys Glu Asn Thr
40 45 50
tgc tac tgt ggt gca gtg gca aag aga caa gag aaa aaa ggg atg gag 366

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Cys Tyr Cys Gly Ala Val Ala Lys Arg Gln Glu Lys Lys Gly Met Glu	
55 60 65	
cct ctt caa ggt cat gcc act ccc gct ttg cct ttt aaa gaa acc cag	414
Pro Leu Gln Gly His Ala Thr Pro Ala Leu Pro Phe Lys Glu Thr Gln	
70 75 80	
gaa cta tta cta agt ccc ctg ccc cag gaa ggt cct ggg tca ctt gca	462
Glu Leu Leu Leu Ser Pro Leu Pro Gln Glu Gly Pro Gly Ser Leu Ala	
85 90 95	
gca gga gag agc agc agt ctt tct gcc agt aca tca gtc tca gat tca	510
Ala Gly Glu Ser Ser Ser Leu Ser Ala Ser Thr Ser Val Ser Asp Ser	
100 105 110 115	
tcc cag aaa aaa gaa gag cac aat tat tct ctt ttt gtc tcc gac aac	558
Ser Gln Lys Lys Glu Glu His Asn Tyr Ser Leu Phe Val Ser Asp Asn	
120 125 130	
ttg ggt gaa cag cca act aaa tgc agt cct gaa gaa gat gag gag gac	606
Leu Gly Glu Gln Pro Thr Lys Cys Ser Pro Glu Glu Asp Glu Glu Asp	
135 140 145	
gag gag gat gtt gat gat gag gac cat gat gaa gga ttc ggc agt gag	654
Glu Glu Asp Val Asp Asp Glu Asp His Asp Glu Gly Phe Gly Ser Glu	
150 155 160	
cat tac atc att ata taa tgggtacttcc tcaagttgct gg	694
His Tyr Ile Ile Ile *	
165	

<210> 263
 <211> 1540
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1033)..(1188)

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tccagatctc cactcttatg cgccagctgc agcagggttaa ggacagccag caggatgagc	120
tggatgacct cggtgagatg cgcagaaagg tcctggaatc cttgtctgac aagattcaga	180
agaagaagaa aaaaattctg agttctgtgg tggcggaac ccagcgtccc tatgaagagg	240
ctctctaca gaagatgtgg gaaagccagg acttcctgaa atgcatgcaa aggttcagag	300
aagtgcgtgg gcaaggaagg tgggtggtccc tgtagggaag cagtggatgg gcagtcccca	360

cggcctgtgg	gaatgagtc	ggcttctcct	gatctggcgc	tcaggaggtc	tctgattctg	420
gtgttggcct	ccctccttgc	cgggtgccatt	actgtcactt	gtctttcctc	tgggaaggcg	480
attggcactg	acctaggcct	tgcctcatta	gccagcaatg	ctggctaata	accattttac	540
aaccatcacc	aaacatcacc	tattcagcca	ttaaccaccg	tgcattcttta	ccccttgatt	600
cttgttactg	cccaccaccc	attatcagtg	ttaatgaact	tcaccatcac	tgccttcttg	660
aattaatttt	cattatcttg	cctcttcact	ggtttttaat	gtgcatgccc	ttcactatct	720
ctgccagcct	ccattcattc	ccacgattga	gcattccccg	ccactttgta	acctgtctcc	780
attctccatg	atccctcacc	tgtttcagca	ccactgaata	ttgtcactaa	cttgggaagcc	840
agccgcaccc	tgcattggga	agtcacctct	ctggagtcca	gcaagtccca	gtgacagaac	900
ccataccatt	tcccagata	gctttgctcc	tcgttcattt	tggcctttct	ccctttgggt	960
ggggggccatt	tgcctctccc	ttctccccctg	ctgtgccttt	cctctcagtt	tattgaccag	1020
tttgaggaga	ac	atg cct gta tta	agg gcc gag gtg	gaa gag ctc caa		1068
		Met Pro Val Leu	Arg Ala Glu Val	Glu Glu Leu Gln		
		1	5	10		
gcc cag acc	cgg gaa ccc	cga gag gtc	ata ttt gag	gat gtt ctg	ctt	1116
Ala Gln Thr	Arg Glu Pro	Arg Glu Val	Ile Phe Glu	Asp Val Leu	Leu	
	15	20	25			
cgg aga ccc	aag tgc acc	cca gac atg	gat gtc atc	ctc aac att	cct	1164
Arg Arg Pro	Lys Cys Thr	Pro Asp Met	Asp Val Ile	Leu Asn Ile	Pro	
	30	35	40			
gtg gaa gag	cca cta ccc	ttc tag atg	gcagctgc	catgggcgc	cctccccctc	1218
Val Glu Glu	Pro Leu Pro	Phe *				
	45	50				
tgtctctctc	ccagcacctg	gagccttgga	tcatttactt	ccaggaccgg	atctccattc	1278
agaccctgat	ctacagtctc	cctgctccct	ctgcccttcc	tccctctttc	tttccctccc	1338
tccctccctc	ccttcttccc	cccttccctt	ccctcctcct	tccttccctc	tctccctccc	1398
tccctccttt	ctttcttcc	gtgggttttt	cctctcttct	tcccttcttt	ctgggttggtg	1458
ctgctggggc	aggtgggaat	ttctgattaa	atctgctatt	cctttttttac	caataaagct	1518
ggattttacat	ttaaaaaaaaa	aa				1540

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<210> 264
<211> 583
<212> DNA
<213> Homo sapiens
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<220>
 <221> CDS
 <222> (216)..(464)

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 ggaatctgca gcaagcattt ccagaatatc tagataaatg gcagaggtag ctctactaga 180
 gttttaacag agacaaaaca gccttacttc aggag atg cca ttt agg act ttc 233
 Met Pro Phe Arg Thr Phe
 1 5
 aca gct cta ggt aag cta ata tct gac ttc aaa gat tca aag gac ggg 281
 Thr Ala Leu Gly Lys Leu Ile Ser Asp Phe Lys Asp Ser Lys Asp Gly
 10 15 20
 ctg act ctt tac ttt gta gag aca gcg tca cgc tct gtt gtg ctg gct 329
 Leu Thr Leu Tyr Phe Val Glu Thr Ala Ser Arg Ser Val Leu Ala
 25 30 35
 ggt ctt gaa ctc ttg acc tca agt gat cct cca acc tca gcc tcc caa 377
 Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Thr Ser Ala Ser Gln
 40 45 50
 agc act gga att aca ggt gta agc cac ttt tcc cag cct ggg ctg gct 425
 Ser Thr Gly Ile Thr Gly Val Ser His Phe Ser Gln Pro Gly Leu Ala
 55 60 65 70
 ttc ttg tta gag gtc aat gca gtt ggt gac ttt aaa tga atgctaatat 474
 Phe Leu Leu Glu Val Asn Ala Val Gly Asp Phe Lys *
 75 80
 tcaattacca ttccaaaaat ccaagagcca gttaagaatt atgctacatc ctctgtgccga 534
 attcattgcc tcgagggcca aattccctat agtgatcgta ttaaattca 583

<210> 265
 <211> 2077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (154)..(834)

<400> 265
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 ctgcccactc cagccagtac ccggattctt agaaaatatt ccaatattcg aggaaagctc 120

agagcccagc aacgtttaat caagaatgag aaa atg gaa tgc cca gat gct ctg	174
Met Glu Cys Pro Asp Ala Leu	
1 5	
gct gtg gaa agt aag cca agt cgt aag agc gta tgc atc aac cct ctg	222
Ala Val Glu Ser Lys Pro Ser Arg Lys Ser Val Cys Ile Asn Pro Leu	
10 15 20	
atg tcc ccc aag ctt gcc ctg caa gtg gat gca gat ggg ttt cct gtt	270
Met Ser Pro Lys Leu Ala Leu Gln Val Asp Ala Asp Gly Phe Pro Val	
25 30 35	
aag ccc aag agt act gaa gga atg aag gga agg aag ggg aag cag gtg	318
Lys Pro Lys Ser Thr Glu Gly Met Lys Gly Arg Lys Gly Lys Gln Val	
40 45 50 55	
tct gaa atc ttg cct aaa gca gaa gtt cag agt aaa cgc aag aga aca	366
Ser Glu Ile Leu Pro Lys Ala Glu Val Gln Ser Lys Arg Lys Arg Thr	
60 65 70	
gaa ggc agc agc cct cca gat agt aag aac aag ggg cct acg gtg aaa	414
Glu Gly Ser Ser Pro Pro Asp Ser Lys Asn Lys Gly Pro Thr Val Lys	
75 80 85	
gcc agc aaa gaa aag cat gct gat gga gcc acc aaa acc cct gct gcc	462
Ala Ser Lys Glu Lys His Ala Asp Gly Ala Thr Lys Thr Pro Ala Ala	
90 95 100	
aag agg cca gct gca agg gac aga agc agc caa ccc ccc aaa aag acg	510
Lys Arg Pro Ala Ala Arg Asp Arg Ser Ser Gln Pro Pro Lys Lys Thr	
105 110 115	
tct ttg aaa gag aat aaa gtg aag atc cct aaa aag tcc gct ggg aag	558
Ser Leu Lys Glu Asn Lys Val Lys Ile Pro Lys Lys Ser Ala Gly Lys	
120 125 130 135	
agc tgc cct ccc tcc agg aaa gaa aaa gag aat aca aac aaa agg cct	606
Ser Cys Pro Pro Ser Arg Lys Glu Lys Glu Asn Thr Asn Lys Arg Pro	
140 145 150	
tcc cag tct att gcc tcg gaa aca ctg acg aaa cct gca aaa cag aag	654
Ser Gln Ser Ile Ala Ser Glu Thr Leu Thr Lys Pro Ala Lys Gln Lys	
155 160 165	
ggg gcc ggt gaa tcc tct tca agg cct cag aaa gcc acg aat agg aag	702
Gly Ala Gly Glu Ser Ser Ser Arg Pro Gln Lys Ala Thr Asn Arg Lys	
170 175 180	
cag agt agt gga aag act cgg gcc aga ccc tca acg aaa acc cca gag	750
Gln Ser Ser Gly Lys Thr Arg Ala Arg Pro Ser Thr Lys Thr Pro Glu	
185 190 195	
agc agt gca gct cag aga aag cga aag ctg aag gca aag ctg gac tgt	798
Ser Ser Ala Ala Gln Arg Lys Arg Lys Leu Lys Ala Lys Leu Asp Cys	
200 205 210 215	
tcg cac ggc aaa cgg agg cgg ctg gat gca aag tga ttgg aaagatggta	848

Ser His Gly Lys Arg Arg Arg Leu Asp Ala Lys *

220

225

gccaagagta aaactgttct atagaagtaa ccttttatct tgcattaact aaatctgctt 908
 ttataagctt atcaagcctt tcaaatttac agttaatgga gaacaccgta atttgagatg 968
 tcagaaaatg catctcagat ggagaaggga acttgcagag tccttctctg aggctaaggg 1028
 aagttatata ttatatctg gttgttcctt ggggttttaa cttggaacca agcagttttc 1088
 gtttttaaaa gtacagtgcc ttatttatcc tttttgtttt taaatttaca aaagctaaaa 1148
 agctgatcta tgtgattaaa ggcttgattt ttatacttga tgcacaagca cttgtactgt 1208
 agccgagaag accaccatca tgcacataaa aggagctttt cagcagccac cctgcagcat 1268
 ctgcccacga acagatgccc ttctttgcaa accccagcag tgaacttccc tctctgtctt 1328
 gtttggttgt ttagatgatg tttgaaagct aaaccaaata attttatggg atgcagagga 1388
 ttataatta taaaagatta ctatttctgt taccctctt taaaaaagat catgttcatt 1448
 gttggctcct cctctcacct ttgatgtttt gtcatttgag agcatgtatt ctaaattatg 1508
 tgcccatggg acaagagata tgcacaagt gtttaatttt gtttacaac tctaaaaaat 1568
 catttgcac cccaaactgt attactaatt ctccaccatct tcttcatttc tggctctgct 1628
 agcactcctg caaggcttcc atcctacttc gggaggaaaa agcctaggat tttttttttc 1688
 catcttgtag ctgtaatttg atgattagga tgaaaatgac tcttattttc tttcttacct 1748
 agagtacttc catattcaaa gaaagccgaa ctattatttc cagtaataga aaggtttaag 1808
 aatatgtatg tccatgtgtg tttgggtgca tttgcatgtg gttatcagcc acaaattgtct 1868
 cccaatccca attttacagt aaaatttttt ccctatgcag tgtgcttggg tgtccctgag 1928
 ttgagtaatt agcaaaggac agatggttta aaagtagccc agtgtctctg tgagcatccc 1988
 caataccact ttggtaccag actcagaaag atctaaaaca gcatggagtt atgtaaaggt 2048
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<210> 266
 <211> 1175
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (116) .. (685)

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cgcaggcagg actctgggac agacgcaggc cagctgcca gagcccagac caagc atg 118
Met
1
gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc 166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
5 10 15
cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta 214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
20 25 30
gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt 262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
35 40 45
ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg 310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
50 55 60 65
tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag 358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
70 75 80
ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc 406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
85 90 95
atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg 454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val
100 105 110
acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag 502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys
115 120 125
gtg cgc agt ggg gag tgg acc gag gac gag gtg ctg cgc cgc ttc ctg 550
Val Arg Ser Gly Glu Trp Thr Glu Asp Glu Val Leu Arg Arg Phe Leu
130 135 140 145
gac aac ttc gac tcc tct gag aag gac ggg cag gtc aca ctg gcg gaa 598
Asp Asn Phe Asp Ser Ser Glu Lys Asp Gly Gln Val Thr Leu Ala Glu
150 155 160
ttc cag gac tac tac agc ggc gtg agt gcc tcc atg aac acg gat gag 646
Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser Met Asn Thr Asp Glu
165 170 175
gag ttc gtg gcc atg atg acc agt gcc tgg cag ctg tga gcagctccgg 695
Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln Leu *
180 185 190
ctcagccctg ctgcctggc ctgtcactcc ccaccctgc cggagacctc ccttccctgg 755


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gcccccttctc tcctgggcag ccacaccaca gagcggggag gggcaggtgg gggaatggag      815
gctgcaggac tggctagacc aggtccctgc cgggccacca ggcggaggtg ggacaaaggt      875
cctaacagga gtcactggct caggaccca gggagaaacg ctctccccac ccacgccatg      935
ctgaccagag gtcttgacgc cctgtggat gccccgcgcg aggtcccccg atccccgcac      995
ccggactgct gtcacctgcc cctcccttgc gggcccccca ggaagccagg tgacccagg      1055
tgggaggctg tgtgtggagg ccactctgga aggaagttaa gacctgcca ggtgtggagc      1115
gaggggcaca ggggcacctt aacctcagaa actgaaataa agcctttgaa aaaaaaaaaa      1175

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<210> 267
<211> 1094
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (116)..(604)

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cgcaggcagg actctgggac agacgcaggc cagctgcca gagcccagac caagc atg      118
                                         Met
                                         1

gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc      166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
                    5                      10                      15

cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta      214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
                    20                      25                      30

gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt      262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
                    35                      40                      45

ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg      310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
                    50                      55                      60                      65

tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag      358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
                    70                      75                      80

ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc      406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
                    85                      90                      95

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CCDS: CDS: 1-387

atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg	454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val	
100 105 110	
acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag	502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys	
115 120 125	
gtc aca ctg gcg gaa ttc cag gac tac tac agc ggc gtg agt gcc tcc	550
Val Thr Leu Ala Glu Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser	
130 135 140 145	
atg aac acg gat gag gag ttc gtg gcc atg atg acc agt gcc tgg cag	598
Met Asn Thr Asp Glu Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln	
150 155 160	
ctg tga gcagctccgg ctcagccctg ctgccctggc ctgtcactcc ccacccctgc	654
Leu *	
cgagacctc ccttccttg gccccttctc tcctgggcag ccacaccaca gagcggggag	714
gggcaggttg gggaatggag gctgcaggac tggctagacc aggtccctgc cgggtccacca	774
ggcggaggtg ggacaaaggt cctaacagga gtcactggct caggacccca gggagaaacg	834
ctctccccac ccacgccatg ctgaccagag gtcttgacgc ccctgtggat gccccgcgcg	894
aggtcccccg atccccgcac ccggactgct gctccctgcc cctcccttgc ggggtcccca	954
ggaagccagg tgaccccagg tgggaggctg tgtgtggagg ccatcctgga aggaagttaa	1014
gacctgcca ggtgtggagc gaggggcaca ggggcatcct aacctcagaa actgaaataa	1074
agcctttgaa aaaaaaaaaa	1094

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ggttatgtgt gcacttcaca cctctgactt ttttcagggt tcctattg atg gtt agg	177
Met Val Arg	
1	

gag cgg cag gag gcg ctg cgc cag gcg gag gag gag cgc aag gcc aag	320
Glu Arg Gln Glu Ala Leu Arg Gln Ala Glu Glu Glu Arg Lys Ala Lys	
40 45 50	
tac gcc aag atg gag gcg gag cgc gag gcc gtg cgc cag ggc atc cga	368
Tyr Ala Lys Met Glu Ala Glu Arg Glu Ala Val Arg Gln Gly Ile Arg	
55 60 65	
gac aag tac ggc atc aag aag aag gag gag cgc gag gcc gag gcc cag	416
Asp Lys Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln	
70 75 80	
gcc gcc atg gag gcc aac tcc gag ggg agc ttg acg cgg ccc aag aag	464
Ala Ala Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys	
85 90 95	
gcc atc ccg ccg ggc tgc ggg gac gag gtg gag gag gag gac gag agc	512
Ala Ile Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser	
100 105 110 115	
atc ctg gac acc gtc atc aag tac ctg ccc ggg ccg ctg cat gac atg	560
Ile Leu Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu His Asp Met	
120 125 130	
ctc aag atg tat ccc cgc gcg gga cag ctg ccc cgc gga gcc ggc cat	608
Leu Lys Met Tyr Pro Arg Ala Gly Gln Leu Pro Arg Gly Ala Gly His	
135 140 145	
tga acac tgcaccctcc acaggagccg cagaggccct gaggcaccgg actgcttgga	665
*	
gaccctgcgc ccctgcccag cacctcctcc gtgggcagct cctcggtgtg gggcctgcgg	725
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cggcatccga gccctgttt ctctccatt catgtttatt ttgcatcaca atttgttgaa	845
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caatactaac gaccgacgcc cctccggaca gagaccaccg cgccctctg cgcccatcg	1085
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tcccgggtcg tgtcttatta aaact	1170

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<213> Homo sapiens

<220>

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<222> (497)..(766)

<400> 270

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ctcggcctct tgcttgagag acagattgga gcagagtctt tgtggatgca aagccacctg      180
ggccactgcc gtgtgtgcca cctgaactt caagctgccc tgaaccgcgt gcgttttctca      240
gtgtcacgta cagctcggcc tgaccgtttg ccttttagtg ttctcttctt tctcgggtgtc      300
ctcctcctct tcctcactaa cattcatcca gagcctttca gtgcagaaat caggtagctg      360
ctgaactcgg cagctgcgtc ctttttccca tcattctctt tgtcctttgc tagctgtcat      420
ttcttccttc ttggcttcaa ctgcacatcc ctgggtttgt cctaataaggg aatttttccc      480
acttgagtag acaagc      atg aga ata tca tta ttt tta tat gtt ata tgt      529
                        Met Arg Ile Ser Leu Phe Leu Tyr Val Ile Cys
                        1          5          10

tat att ttt agc aga gaa aaa agt gga aaa tgt gtg caa act tgc aga      577
Tyr Ile Phe Ser Arg Glu Lys Ser Gly Lys Cys Val Gln Thr Cys Arg
                        15          20          25

agg ccc ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc      625
Arg Pro Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly
                        30          35          40

ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc ccc gga      673
Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly Pro Gly
                        45          50          55

gga ggg tcg tcc ctg tgc cca tgc ggt cag aaa ggc ccc gga gga ggg      721
Gly Gly Ser Ser Leu Cys Pro Cys Gly Gln Lys Gly Pro Gly Gly Gly
                        60          65          70          75

tca tct ctg tgc cca tgc ggt cag gtt ggg gct gag gca ctt tga tca      769
Ser Ser Leu Cys Pro Cys Gly Gln Val Gly Ala Glu Ala Leu *
                        80          85          90

ttgctcctcc tcagagtgtt cttttcctgc cctctcagat tataataacg aggtagttac      829
agagtgagct ccagcctaga tcgtctgggt ttgaatccag ctccatgact gtggccgtgt      889
tgccaatctt ctctgagtct cagcttcctt ttctgtaaag tgggtataat agtagagtct      949
aactgtggg gctgtggtgg gattcattgt gttcacacgt gtgcagggct gagaacaggg      1009
cccaaacag ggtaggcaca atgaagcatg agtcagaata ataatacaga tgacagtttc      1069
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tctatcacta atttgaacat tgcagacagt gcaaagaaga aaattag 1116

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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 271
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 Met Asp Ala Val Val Pro Asp Arg Asn Ser Arg Val
 1 5 10

gac cca cgc gtc cgg ttt ccc agc gcg gtg ccc gcc cct cat cct cct 98
 Asp Pro Arg Val Arg Phe Pro Ser Ala Val Pro Ala Pro His Pro Pro
 15 20 25

cca gtc tcc ctc ccc tcg ccg act gcc gcc cca ggc tcc gcc atg ggg 146
 Pro Val Ser Leu Pro Ser Pro Thr Ala Ala Pro Gly Ser Ala Met Gly
 30 35 40

aat gtg cca tcc gcg gtg aag cac tgc ctc agc tac cag cag ctt ctc 194
 Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln Leu Leu
 45 50 55 60

cgg gag cat ctc tgg atc ggg gat tca gtg gca ggg gcg ctc gac ccc 242
 Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu Asp Pro
 65 70 75

gcg cag gaa aca tcc cag tta tct gga ctc cct gag ttt gtt aaa ata 290
 Ala Gln Glu Thr Ser Gln Leu Ser Gly Leu Pro Glu Phe Val Lys Ile
 80 85 90

gta gaa gtt ggg cct agg gat gga ttg cag aat gaa aag gtt ata gtt 338
 Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val
 95 100 105

cct aca gat ata aaa att gaa ttt atc aat cga ctt tcc caa act ggc 386
 Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly
 110 115 120

ttg tct gta ata gaa gtg act agc ttt gtg tct tcc aga tgg gta cca 434
 Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro
 125 130 135 140

cag gtt gct gct gga gct act gag ata tca gtt ttt gga gct gca tct 482
 Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser
 145 150 155

gaa tcc ttt agc aag aag aat att aac tgt tcc att gaa gaa agt atg 530
 Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met

160	165	170	
gga aaa ttt gag gag gtt gtt aag tct gca aga cac atg aat att cca			578
Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro			
175	180	185	
gca cga ggg tac tta tga aatccc acaaattctg ttttggttaat gtttattggt			632
Ala Arg Gly Tyr Leu *			
190			
aaagcttact caaaaattat ctagagattc ttatatcatt tataaaaata tacatagaat			692
atcatatttc tattttgttt aatcagggtg atcactatat agttacatct cattaacatc			752
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gccctcttat ctcagcctac atgtgctgat aagttggtat aaactcaca cagcttttgg			932
aaaagaatca cctaattgtgg ttttcaaatt ttttttaaaa catgactttt tcttcaaaga			992
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caagatccac aaacctaat ttctctctca ggagtttaga aatgggtatac caaacatggg			1412
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gaaacctata atgcattttt gtgtgtgttt gtttcttaag gaagaatttg tttctaagac			1712
attagctact ttttctatta attttataaa tatggagata tgatgaacac acatcttaac			1772
aagttaaagt gcatagcgat tggtaataga aggttgaaag ctggggatgg atttgggtgc			1832
aggctgtact tcccttagtt gaggtgagca aagttcatgg tagcgggaaa gattcaacag			1892
ttaatgagaa agataagtga gtcaattgtg actgaaaata ttagtgaaat gattggaatt			1952
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tagtttggtt tctatttata tttttcctgt cctccatagt aagtctacat gagtttctaa			2072

aatttgaaat tacttttgta attaagatag atgcatatca tgtaaggact atatgagaaa 2132
aattttaaatt ccaaggcaat gtacttccaa agacataaaa taaaggatat ttattttttca 2192
ggcaaaagtt acaaaaccac aatcaaaaag gagagatata ctattgggtt ctcaattcga 2252
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ctcttaaaaa aaaaaaa 2569

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<211> 1204
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (64)..(630)

<400> 272
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Met Ala Pro Pro Trp Ala Gly Gly Glu Arg Arg Gly Pro Gly Thr
1 5 10 15
acg tgc ctg cac tct ccc tgg atg ctg gag gct gct ccg ccg tgg gca 156
Thr Cys Leu His Ser Pro Trp Met Leu Glu Ala Ala Pro Pro Trp Ala
20 25 30
gga gga gaa gga aga gaa ctg ggt gcc gcc tgc ctg cac tct ctc cgg 204
Gly Gly Glu Gly Arg Glu Leu Gly Ala Ala Cys Leu His Ser Leu Arg
35 40 45
atg ctg gag gct gga ggc agt gag gca gca aca gcg cga ggg cga ggc 252
Met Leu Glu Ala Gly Gly Ser Glu Ala Ala Thr Ala Arg Gly Arg Gly
50 55 60
gac ttt gga gct gcc tca tgc agc gac ctc gcc ttc cgc tgc gcc tcc 300
Asp Phe Gly Ala Ala Ser Cys Ser Asp Leu Ala Phe Arg Cys Ala Ser
65 70 75
tcc cag aac cca aga agc ctg gaa cct gtg gcg tcc agc cct gaa agg 348
Ser Gln Asn Pro Arg Ser Leu Glu Pro Val Ala Ser Ser Pro Glu Arg
80 85 90 95


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agg aga cgg caa ccc agc cgc gct ttt gcc tgc act ctc cct gga tgc      396
Arg Arg Arg Gln Pro Ser Arg Ala Phe Ala Cys Thr Leu Pro Gly Cys
                100                105                110

tgg agg ctg gag gca gtg acg cag caa cag cgc gag gcg act ttg gag      444
Trp Arg Leu Glu Ala Val Thr Gln Gln Gln Arg Glu Ala Thr Leu Glu
                115                120                125

cgg cct cat ata gcg acc tcg cct tcc gct gcg cgt cct ccc aga gcc      492
Arg Pro His Ile Ala Thr Ser Pro Ser Ala Ala Arg Pro Pro Arg Ala
                130                135                140

caa gaa gcc cgg aac ctg tgg cat cca tct ctg aaa gga gaa gac ggc      540
Gln Glu Ala Arg Asn Leu Trp His Pro Ser Leu Lys Gly Glu Asp Gly
                145                150                155

aac cca gcc gag gca cta ctg ggt tgg ggt ctc cac gac cga gct ggt      588
Asn Pro Ala Glu Ala Leu Leu Gly Trp Gly Leu His Asp Arg Ala Gly
                160                165                170                175

ctc atc aag tgg cgt cca aca agg ggc tca aac ccg ggt tga ggggttg      637
Leu Ile Lys Trp Arg Pro Thr Arg Gly Ser Asn Pro Gly *
                180                185

ctggagcgcac ggagaacgtg gaactacact ggaggacacc agagtactct taagcaatcc      697

cttggccaaa accagcaact gatttgata ccatcaagac acctgaaatc ttgtcatgag      757

ccagatactg aggaagagat tttgggaaga acccaaggac cccccagttg cagccatgtc      817

aagactgaca ataaggaaga catcagtccc agcaagcaac attcatcggg cacagccacc      877

catgtggggc cagatcaaga agttgacaca gacggcggaa gaaaatctga agaaagcgga      937

tgaccagcta caatgagtaa tctaattgta gctatgatgg ctgtgctcac cattgccatg      997

agtattcccc cagcacctgc tgaaacaaaa aacattatac ttattgggca tatattcctt     1057

ttccaccagt ttcattggcca gtgacatggt tagaccccc agtggaggta tacactaatg     1117

atagcttttg gatacctggt tctacagatg atagaggccc atctcacccc caaaaggagg     1177

gaacattatg aatatttcgt tgggatt                                           1204

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<210> 273
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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acacgaggag cctccactcc gggcagctgt tcgggttcgt ctcagttgcc aaacggaata 180
atttcacact ctgataacct gattgttttt taagccttgt ggtattctta attgcccggt 240
gttagataaa ctgtgattta aagagcacia acccagatag cagacacaca aaacactggc 300
ttgggaatag caaggagtga cttatttact ttagcaaagc cttttataag gtttt atg 358
Met
1
gct gca cta tca gag tgt cac cca gaa gtc act ctg gga ggt gaa cgc 406
Ala Ala Leu Ser Glu Cys His Pro Glu Val Thr Leu Gly Gly Glu Arg
5 10 15
aca ggg cag gac caa ggt agc acc agg cag aca caa gcc tcc ctg tgg 454
Thr Gly Gln Asp Gln Gly Ser Thr Arg Gln Thr Gln Ala Ser Leu Trp
20 25 30
gga gcc tct ctc atc tgt cgg ggg cct gcg ggc agg gga gag gag gtg 502
Gly Ala Ser Leu Ile Cys Arg Gly Pro Ala Gly Arg Gly Glu Glu Val
35 40 45
ccc cta cag gca agc ctg tgg ggg cgg cac cca gac ctc tgg aga cca 550
Pro Leu Gln Ala Ser Leu Trp Gly Arg His Pro Asp Leu Trp Arg Pro
50 55 60 65
agc acc act gcc acc cag tgc tgg gga gaa ggg atg gag aga atc aaa 598
Ser Thr Thr Ala Thr Gln Cys Trp Gly Glu Gly Met Glu Arg Ile Lys
70 75 80
agc cag cac tag gaa ggctgttgc tctgcatgac ccatggcggg gcaggtggag 653
Ser Gln His *
85
gggaagccgg acacaggaga gctcctgggg ccagacacgc cacctctgcc aggtgagccc 713
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tggtcacttc ccagcctcct gaccacact caggccagc tcttccag actgtcatcc 833
tctttctaga aggaaacagg gaccccttg ggtccgggat ggccctgagc tcccctgtgt 893
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<212> DNA
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<220>
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 <222> (27) .. (488)

<400> 274

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1 5	
ctt gga tcc tct aga gcg gcc gct gtc gtt gtt ctg agg aga aac ctt	101
Leu Gly Ser Ser Arg Ala Ala Val Val Val Leu Arg Arg Asn Leu	
10 15 20 25	
aca agt gta ata aat gtg cga agg ttt tta atc aaa aag gaa tcc ttg	149
Thr Ser Val Ile Asn Val Arg Arg Phe Leu Ile Lys Lys Glu Ser Leu	
30 35 40	
cac aac atc aga gag ttc ata ctg gag aga aac ctt aca agt gta atg	197
His Asn Ile Arg Glu Phe Ile Leu Glu Arg Asn Leu Thr Ser Val Met	
45 50 55	
aat gtg gca agg ttt tta atc aaa aag caa gcc ttg caa aac atc aga	245
Asn Val Ala Arg Phe Leu Ile Lys Lys Gln Ala Leu Gln Asn Ile Arg	
60 65 70	
gag ttc ata ctg cag aga aac ctt aca agt gta atg agt gtg gca aag	293
Glu Phe Ile Leu Gln Arg Asn Leu Thr Ser Val Met Ser Val Ala Lys	
75 80 85	
cct tta ctg gac agt caa cac tta ttc acc atc aag caa tcc atg ggt	341
Pro Leu Leu Asp Ser Gln His Leu Phe Thr Ile Lys Gln Ser Met Gly	
90 95 100 105	
gta ggg aaa ctt tac aaa tgt aat gat tgt cac aaa gtc ttc agt aat	389
Val Gly Lys Leu Tyr Lys Cys Asn Asp Cys His Lys Val Phe Ser Asn	
110 115 120	
gct aca acc att gca aat cat tac aga atc cat att gaa gag aga tct	437
Ala Thr Thr Ile Ala Asn His Tyr Arg Ile His Ile Glu Glu Arg Ser	
125 130 135	
aca agt gta ata aat gtg gca aat ttt tca gac gtc att cat aac ttg	485
Thr Ser Val Ile Asn Val Ala Asn Phe Ser Asp Val Ile His Asn Leu	
140 145 150	
tag ttca tcagtgaact catactggag agaaacctta caaatatcat gactgtgaca	542
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aggtcttcag tcaagcttca tcctatgcaa aacatagaat tcatacagga gagaaacctc	602
acaagtgtga tgattgtggc aaagccttta cttcatgttc acacctcatt agacatcaga	662
gaattcatac tggacagatg ccttacaaat gtaaggggtgg caaggtcttc actctgtggg	722
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<210> 275
 <211> 1078
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (357)..(713)

<220>
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 <223> n = a,t,c or g

<400> 275

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cagactccca gggatcatcaa cctcctcggg tcactaacc tccccagtgt ctgtctaccc    180
ctaagtccag agaacacgtc ctctctaggg tcgagccgga atcaatatag gctacaaggg    240
catcagttca ggctgcgcgg aggagagaag gaagtgctga tgtggagtcc tccctcccc    300

ttctccttca cccccaagtg tctcccacga ctgccctccc cgacctctag ctgacc      356
atg gca tca gag gca gaa aaa aca ttc cat cgg ttt gct gcg ttt gga      404
Met Ala Ser Glu Ala Glu Lys Thr Phe His Arg Phe Ala Ala Phe Gly
  1             5             10             15

gaa tca tca agc agt ggc act gaa atg aac aac aag aac ttc tcc aag      452
Glu Ser Ser Ser Ser Gly Thr Glu Met Asn Asn Lys Asn Phe Ser Lys
          20             25             30

ctg tgc aaa gac tgt ggc atc atg gat ggc aag aca gtc acc tcc acg      500
Leu Cys Lys Asp Cys Gly Ile Met Asp Gly Lys Thr Val Thr Ser Thr
          35             40             45

gac gtg gac atc gtg ttc agc aaa gtc aag gcc aag aac gcc cga acc      548
Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala Lys Asn Ala Arg Thr
          50             55             60

atc acg ttt caa cag ttc aaa gag gca gtg aag gaa ctg ggc cag aag      596
Ile Thr Phe Gln Gln Phe Lys Glu Ala Val Lys Glu Leu Gly Gln Lys
          65             70             75             80

cgc ttc aaa ggg aag agt cca gat gaa gtc ctg gag aac att tat gga      644
Arg Phe Lys Gly Lys Ser Pro Asp Glu Val Leu Glu Asn Ile Tyr Gly
          85             90             95

ctc atg gag ggc aaa gac cca gcc acc act ggc gct act ttt ccc tgg      692
Leu Met Glu Gly Lys Asp Pro Ala Thr Thr Gly Ala Thr Phe Pro Trp

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100	105	110	
tta cct atg caa gaa acc tga aa gtgacccag acccctccac ctccccaatc			745
Leu Pro Met Gln Glu Thr *			
115			
ccagctacgg ggaggcgggc ctgcatgggtg gttaagatca aggcttttga gtgaaacaga			805
ccaggaattg aatcctgcct ctgcagctta caaactgcac accatctatc tgtttacgaa			865
accactgaaa gcttccttgt ttcattctgtt catgaggata gtatttttta ctcacggcag			925
tatgaggatc cattaagatg tatatcaaga gtttttagac cagtgcccg cacaatgtgga			985
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 <213> Homo sapiens

<220>
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 <222> (74)..(223)

<400> 276	
aaaaatgaaa catttaccct agtgtctaag tgtctaataa ggaagaactt aaaatgtggg	60
cacctatgta aaa atg tca aaa ttg aaa atg cgg agg ggg cat ctg gaa	109
Met Ser Lys Leu Lys Met Arg Arg Gly His Leu Glu	
1 5 10	
tca aac tgg tgg cct ctc ggt ctg cag tct tat gct cta acc ctg agc	157
Ser Asn Trp Trp Pro Leu Gly Leu Gln Ser Tyr Ala Leu Thr Leu Ser	
15 20 25	
tat acc cct tcc tgc tgc tgt ggg ggt caa tta atg cct ttg act tgt	205
Tyr Thr Pro Ser Cys Cys Cys Gly Gly Gln Leu Met Pro Leu Thr Cys	
30 35 40	
gcg gtc aca ccc aga tga ccagtc acctgtgtgt tgccacttca caatggaagc	259
Ala Val Thr Pro Arg *	
45 50	
tcctaggagc tgccaggtct acctcagtga aaactcattg accttgtgca tagcaagagg	319
cagtccccgc tcctcagata acccccgtgc ctgtgtcttc cctgccttga gtccttagtt	379
atgggcagca ggctggaaaa gcactgccag cagccactag aatggccttg agagtcatcc	439
tcacagtaact gtttatgggtg ggcacatata agagaaactt tgtgtgactg aggtgtctgt	499

tctaaaacac ttaatgacag agttgggcct ggctctcctg gtccagtgtt ccattcaggg 559
cagattcagc acaactgcag tctaggacaa aagatgattc tttcaacttt tactttttca 619
gttaatacaa atgaagaatg ttagagaagg agcaactcca agaaatagtg agaagtgtgt 679
agctgagtag atttcccaaa agcattaata gggccagtgt tacca 724

<210> 277
<211> 1007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(682)

<400> 277
tttcgtcagt tcgcggcagt tcgcgcggga gcggggcgcc tgggtggatg ggcgcttggg 60
cgctgggct gccggacggt gggaacggaa gtcgctgtgg gacgctgagg aagccagg 118
atg gcg act ccg agc aag aag acg tca act cca agc ccc cag cct tcc 166
Met Ala Thr Pro Ser Lys Lys Thr Ser Thr Pro Ser Pro Gln Pro Ser
1 5 10 15
aag aga gct ctc ccg aga gac cct tcg tcg gag gtc ccg agc aag agg 214
Lys Arg Ala Leu Pro Arg Asp Pro Ser Ser Glu Val Pro Ser Lys Arg
20 25 30
aag aat tcg gcc ccg cag ctg ccg ctg ttg cag tcg tcc ggg cct ttc 262
Lys Asn Ser Ala Pro Gln Leu Pro Leu Leu Gln Ser Ser Gly Pro Phe
35 40 45
gtg gaa ggc tct atc gtc cgc atc tcg atg gag aac ttc cta aca tat 310
Val Glu Gly Ser Ile Val Arg Ile Ser Met Glu Asn Phe Leu Thr Tyr
50 55 60
gat att tgt gaa gta tct cct gga ccc cac ttg aat atg atc gtt gga 358
Asp Ile Cys Glu Val Ser Pro Gly Pro His Leu Asn Met Ile Val Gly
65 70 75 80
gcc aat gga aca ggg aag tcg agc att gtg tgt gcc att tgc ctt ggt 406
Ala Asn Gly Thr Gly Lys Ser Ser Ile Val Cys Ala Ile Cys Leu Gly
85 90 95
tta gct gga aaa cct gct ttc atg gga cga gca gat aag gtt ggg ttt 454
Leu Ala Gly Lys Pro Ala Phe Met Gly Arg Ala Asp Lys Val Gly Phe
100 105 110
ttt gtg aag aga gga tgt tct aga ggc atg gtt gaa att gaa ttg ttc 502
Phe Val Lys Arg Gly Cys Ser Arg Gly Met Val Glu Ile Glu Leu Phe
115 120 125
agg gct tct gga aat ctt gta atc acc cgt gag att gat gtg gca aaa 550

Arg Ala Ser Gly Asn Leu Val Ile Thr Arg Glu Ile Asp Val Ala Lys
130 135 140

aat cag tcc ttt tgg ttc atc aac aaa aaa tct aca acc cag aaa ata 598
Asn Gln Ser Phe Trp Phe Ile Asn Lys Lys Ser Thr Thr Gln Lys Ile
145 150 155 160

gtg gaa gag aaa gtt gca gcc tta aat att cag tgg gga atc ttt gcc 646
Val Glu Glu Lys Val Ala Ala Leu Asn Ile Gln Trp Gly Ile Phe Ala
165 170 175

agt ttc tcc tca gga caa gtt gga gga att tgc taa actc agcaaattgg 696
Ser Phe Ser Ser Gly Gln Val Gly Gly Ile Cys *
180 185

actcctcgaa gcaactggaaa gttcaatggg ccccagaaa ttgcgcaata tcctgtgtac 756

tccaaactgt ggagaagaag aacagtcccg acccctgcgc agagaaactg ctgtctctcg 816

cgaaatggtg tgcccgttc gaggattata ccccgggtgg gagggcttct agcagggccg 876

cacatattcg agctgccacc cacagcacgc tggacaaaag ctgcgcctc agagacatat 936

tgacgcgag cgcatcacag gcaactccact catgcacagg agccctgcgg cgcggaacgg 996

cgcacacacc g 1007

<210> 278
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18)..(131)

<400> 278

cgacgatttc gtccaaa atg gcg gca gcg atg gat gtg gat acc ccg agc 50
Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser
1 5 10

ggc acc aac agc ggc gcg ggc aag aag cgc ttt gaa gtg aaa aag gtt 98
Gly Thr Asn Ser Gly Ala Gly Lys Lys Arg Phe Glu Val Lys Lys Val
15 20 25

ggg tct cgc cag cgc ctt cct cag gga agc tag agaggcgc ggatctggct 149
Gly Ser Arg Gln Arg Leu Pro Gln Gly Ser *
30 35

ggcaggcccg aggatggtcg aggcgcggag taaagggttt catttcaggg cgttcctggg 209

accgggtacc acgaaaggaa gccggggggc gggctctaga gttgatcggc gtgacggcgg 269

cccactgttg ggggaagtgt tggtttcgct gtgaggctaa ggggccaatc acagagctgc 329

ttattgagat acgcgggggtt gcgacttggc ggcgggagcc aagcgcttga gctgtcactg 389
gagtgggttga gaggtggggg aaggacaggg tatggtggag tgggggtgggt 439

<210> 279
<211> 1771
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24)..(1049)

<400> 279
tttcgtcacg ggccttggtc acc atg tcg gtg ctg gat gcg ctt tgg gag 50
Met Ser Val Leu Asp Ala Leu Trp Glu
1 5

gat cgg gat gtc cgt ttc gac ctg tcc gcg cag caa atg aaa aca aga 98
Asp Arg Asp Val Arg Phe Asp Leu Ser Ala Gln Gln Met Lys Thr Arg
10 15 20 25

cct gga gaa gtc ctt att gat tgt tta gat tcc att gaa gac acc aaa 146
Pro Gly Glu Val Leu Ile Asp Cys Leu Asp Ser Ile Glu Asp Thr Lys
30 35 40

gga aat aat gga gat aga ggt aga ctc ttg gta aca aat tta aga att 194
Gly Asn Asn Gly Asp Arg Gly Arg Leu Leu Val Thr Asn Leu Arg Ile
45 50 55

ctc tgg cac tct ttg gca tta tca aga gtc aat gtt tct gtc ggt tac 242
Leu Trp His Ser Leu Ala Leu Ser Arg Val Asn Val Ser Val Gly Tyr
60 65 70

aat tgc ata ttg aat att aca aca agg act gct aac tct aaa tta cga 290
Asn Cys Ile Leu Asn Ile Thr Thr Arg Thr Ala Asn Ser Lys Leu Arg
75 80 85

ggc caa act gaa gct ctc tat ata cta aca aaa tgt aac agt act cgt 338
Gly Gln Thr Glu Ala Leu Tyr Ile Leu Thr Lys Cys Asn Ser Thr Arg
90 95 100 105

ttt gaa ttt ata ttt aca aat ttg gtt cct gga agc cct aga ctt ttt 386
Phe Glu Phe Ile Phe Thr Asn Leu Val Pro Gly Ser Pro Arg Leu Phe
110 115 120

act tct gtg atg gca gta cac aga gct tat gaa act tct aaa atg tat 434
Thr Ser Val Met Ala Val His Arg Ala Tyr Glu Thr Ser Lys Met Tyr
125 130 135

cgt gat ttt aaa tta aga agt gca cta att cag aac aag caa cta aga 482
Arg Asp Phe Lys Leu Arg Ser Ala Leu Ile Gln Asn Lys Gln Leu Arg
140 145 150

ctg ttg cca caa gaa cat gta tat gat aaa ata aat gga gtt tgg aat	530
Leu Leu Pro Gln Glu His Val Tyr Asp Lys Ile Asn Gly Val Trp Asn	
155 160 165	
tta tcc agt gat cag ggc aat tta gga acc ttt ttt att acc aat gtg	578
Leu Ser Ser Asp Gln Gly Asn Leu Gly Thr Phe Phe Ile Thr Asn Val	
170 175 180 185	
aga att gtg tgg cat gca aat atg aat gat agt ttt aat gtc agt ata	626
Arg Ile Val Trp His Ala Asn Met Asn Asp Ser Phe Asn Val Ser Ile	
190 195 200	
cca tat ctg caa att cgt tca ata aag att aga gat tca aaa ttt ggt	674
Pro Tyr Leu Gln Ile Arg Ser Ile Lys Ile Arg Asp Ser Lys Phe Gly	
205 210 215	
tta gct ctt gtc ata gaa agc tct cag cag agt ggt gga tat gtt ctt	722
Leu Ala Leu Val Ile Glu Ser Ser Gln Gln Ser Gly Gly Tyr Val Leu	
220 225 230	
ggc ttt aaa ata gat cct gtg gaa aaa cta caa gaa tca gtt aag gaa	770
Gly Phe Lys Ile Asp Pro Val Glu Lys Leu Gln Glu Ser Val Lys Glu	
235 240 245	
atc aat tca ctt cac aaa gtc tat tct gcc agt ccc ata ttt gga gtt	818
Ile Asn Ser Leu His Lys Val Tyr Ser Ala Ser Pro Ile Phe Gly Val	
250 255 260 265	
gat tat gag atg gaa gaa aag ccc cag ccg ctc gaa gct ctg aca gtc	866
Asp Tyr Glu Met Glu Glu Lys Pro Gln Pro Leu Glu Ala Leu Thr Val	
270 275 280	
gaa caa att caa gat gat gta gaa ata gac tct gat ggt cac acg gat	914
Glu Gln Ile Gln Asp Asp Val Glu Ile Asp Ser Asp Gly His Thr Asp	
285 290 295	
gct ttt gtg gct tat ttt gct gat ggc aat aag caa caa gat cgt gaa	962
Ala Phe Val Ala Tyr Phe Ala Asp Gly Asn Lys Gln Gln Asp Arg Glu	
300 305 310	
cct gta ttt tca gaa gaa ctg ggg ctt gca ata gag aaa ttg aag gat	1010
Pro Val Phe Ser Glu Glu Leu Gly Leu Ala Ile Glu Lys Leu Lys Asp	
315 320 325	
gga ttc acc cta cag gga ctt tgg gaa gta atg agt tga ttgaccttga	1059
Gly Phe Thr Leu Gln Gly Leu Trp Glu Val Met Ser *	
330 335 340	
gttgagatgg atttctatta aagatatctc tagttttaaag atactagtca cctgccataa	1119
gtcatggaat agtttttata ttacagctt ttatatattaa aacttgtaag agttttttta	1179
atgattgagg aaaaagtcac ttagaaaact tcagtttttcg gccagcgcgt cgagggaggg	1239
gccagcgaca catggcctag taaccgtccg gccgcggcgc tggcttaagc catggctgag	1299

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ggtagccgga ttcctcaggc cggggcgctc ctacagcagt gcctgcacgc cgggctgcaa 1359
attcgcccag ccgatgggga cgtcgcggcc cagtgggtgg aggtccaaag aggactggtg 1419
atctacgtgt gctttttcaa gggagctgat aaagaacttc ttcccaaat ggatctacga 1479
ctctggctcc actgattacc ttaaccatat tacatggaat gatgtaaggg agaaacagaa 1539
gactcttggt gaacagctcc tgtctttggt gaacagctcc ccagggcctc ctacccgcaa 1599
actgcttgct aagaatctag ccatacttta tagtattgga gacacattct ccgttcatga 1659
agcaatcgat aaatgtaatg atcttattcg tagcaaagat gattctccaa gttatcttcc 1719
cactaagctg taagtgaaac attaaaacag aacagaaaac aaaaaaaaaa aa 1771

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<210> 280
<211> 1109
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (162)..(1064)

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<400> 280
gtttgggccc tttggggtgg tacggaacac aacatcgggg ttgccataca ccggaattcc 60
cgggtcgacg atttcgttgc gcgttccgga actggtttcc cggaaggatt atgtctgcgc 120
cctcgatccg accggaagtt gcacgctgag ccgcggacac c      atg cag tcg gat 173
                                   Met Gln Ser Asp
                                   1

gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc ttc aaa 221
Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser Phe Lys
 5              10              15              20

ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc ctg act 269
Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser Leu Thr
              25              30              35

gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag tat gcc 317
Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln Tyr Ala
              40              45              50

act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag gtt ata 365
Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys Val Ile
              55              60              65

gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg ctt agt 413
Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg Leu Ser
              70              75              80

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<210> 281
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (36)..(1520)

<220>
 <221> misc_feature
 <222> (1)...(2018)
 <223> n = a,t,c or g

<400> 281
 acagctccca agccacaggc agaagcccca cagag atg gag cag aag gaa ggg 53
 Met Glu Gln Lys Glu Gly
 1 5

aag ctc tct gag gat ggg acc acc gtc tcc cca gct gcg gac aac cct 101
 Lys Leu Ser Glu Asp Gly Thr Thr Val Ser Pro Ala Ala Asp Asn Pro
 10 15 20

gag atg tca gga ggt gga gcc cct gca gag gag acc aaa ggc aca gct 149
 Glu Met Ser Gly Gly Gly Ala Pro Ala Glu Glu Thr Lys Gly Thr Ala
 25 30 35

gga aag gcc atc aat gag ggg cct ccc act gag tca gga aag cag gaa 197
 Gly Lys Ala Ile Asn Glu Gly Pro Pro Thr Glu Ser Gly Lys Gln Glu
 40 45 50

aag gca cca gcc gag gac ggc atg tca gca gaa ctc cag ggg gaa gca 245
 Lys Ala Pro Ala Glu Asp Gly Met Ser Ala Glu Leu Gln Gly Glu Ala
 55 60 65 70

aat gga tta gat gag gtc aaa gtg gaa tct cag agg gag gct ggt ggg 293
 Asn Gly Leu Asp Glu Val Lys Val Glu Ser Gln Arg Glu Ala Gly Gly
 75 80 85

aaa gag gat gct gag gct gaa ctt aaa aag gag gat ggt gag aag gaa 341
 Lys Glu Asp Ala Glu Ala Glu Leu Lys Lys Glu Asp Gly Glu Lys Glu
 90 95 100

gag acc act gtg ggt tct cag gag atg act ggc agg aaa gaa gag acc 389
 Glu Thr Thr Val Gly Ser Gln Glu Met Thr Gly Arg Lys Glu Glu Thr
 105 110 115

aaa tct gaa ccc aaa gag gct gag gaa aag gag agc acg ctg gcc tct 437
 Lys Ser Glu Pro Lys Glu Ala Glu Glu Lys Glu Ser Thr Leu Ala Ser
 120 125 130

gag aag cag aag gct gag gag aaa gag gcc aaa cct gaa tct ggg cag 485
 Glu Lys Gln Lys Ala Glu Glu Lys Glu Ala Lys Pro Glu Ser Gly Gln

135	140	145	150	
aaa gcc gat gcc aat gac aga gac aag cct gaa cct aag gca aca gtt				533
Lys Ala Asp Ala Asn Asp Arg Asp Lys Pro Glu Pro Lys Ala Thr Val	155	160	165	
gag gag gag gac gcc aag aca gcc tct cag gag gag aca ggc cag agg				581
Glu Glu Glu Asp Ala Lys Thr Ala Ser Gln Glu Glu Thr Gly Gln Arg	170	175	180	
aaa gag tgc agc act gaa ccc aag gag aag gct act gat gaa gag gcc				629
Lys Glu Cys Ser Thr Glu Pro Lys Glu Lys Ala Thr Asp Glu Glu Ala	185	190	195	
aag gct gaa tcg cag aag gct gtt gtg gag gat gag gct aag gct gaa				677
Lys Ala Glu Ser Gln Lys Ala Val Val Glu Asp Glu Ala Lys Ala Glu	200	205	210	
ccc aag gag ccc gat ggg aaa gag gag gcc aaa cat ggt gca aaa gag				725
Pro Lys Glu Pro Asp Gly Lys Glu Glu Ala Lys His Gly Ala Lys Glu	215	220	225	230
gag gct gat gca aaa gag gag gcg gag gat gca gag gag gca gag cca				773
Glu Ala Asp Ala Lys Glu Glu Ala Glu Asp Ala Glu Glu Ala Glu Pro	235	240	245	
ggc agt ccc agc gaa gag cag gag cag gac gtg gaa aaa gag cca gag				821
Gly Ser Pro Ser Glu Glu Gln Glu Gln Asp Val Glu Lys Glu Pro Glu	250	255	260	
gga ggg gca ggg gtg att ccc agc tcc cca gag gag tgg cct gag agc				869
Gly Gly Ala Gly Val Ile Pro Ser Ser Pro Glu Glu Trp Pro Glu Ser	265	270	275	
ccc act ggg gag ggg cac aac ctc agc aca gat ggg ctg ggt cca gac				917
Pro Thr Gly Glu Gly His Asn Leu Ser Thr Asp Gly Leu Gly Pro Asp	280	285	290	
tgt gta gct tcc gga cag acc agt cct tca gcc agt gag tct tca ccc				965
Cys Val Ala Ser Gly Gln Thr Ser Pro Ser Ala Ser Glu Ser Ser Pro	295	300	305	310
agc gac gtg ccc cag agt ccc cct gag tcc cct tcc tca ggg gag aag				1013
Ser Asp Val Pro Gln Ser Pro Pro Glu Ser Pro Ser Ser Gly Glu Lys	315	320	325	
aag gag aag gca cca gag cgc agg gta tca gcc cct gct cgg ccc cgg				1061
Lys Glu Lys Ala Pro Glu Arg Arg Val Ser Ala Pro Ala Arg Pro Arg	330	335	340	
ggg ccc ggg gca cag aac cgc aaa gcc atc gtg gac aag ttt ggc ggg				1109
Gly Pro Gly Ala Gln Asn Arg Lys Ala Ile Val Asp Lys Phe Gly Gly	345	350	355	
gca gct tcc ggc ccc acg gcc ttg ttc cgc aac act aag gca gcc ggg				1157
Ala Ala Ser Gly Pro Thr Ala Leu Phe Arg Asn Thr Lys Ala Ala Gly	360	365	370	

gca gcc att ggt ggt gtc aag aac atg ctc ttg gag tgg tgc cga gcc	1205
Ala Ala Ile Gly Gly Val Lys Asn Met Leu Leu Glu Trp Cys Arg Ala	
375 380 385 390	
atg aca aaa aaa tac gag cat gtg gac atc cag aac ttc tcc tcc agc	1253
Met Thr Lys Lys Tyr Glu His Val Asp Ile Gln Asn Phe Ser Ser Ser	
395 400 405	
tgg agc agt ggt atg gcc ttc tgt gcc ctc atc cac aag ttc ttc cct	1301
Trp Ser Ser Gly Met Ala Phe Cys Ala Leu Ile His Lys Phe Phe Pro	
410 415 420	
gac gcc ttt gac tac gca gag ctg gat ccc gca aag cgc cgg cac aac	1349
Asp Ala Phe Asp Tyr Ala Glu Leu Asp Pro Ala Lys Arg Arg His Asn	
425 430 435	
ttc acc ctg gcc ttc tcc aca gca gag aaa ctg gct gac tgt gct cag	1397
Phe Thr Leu Ala Phe Ser Thr Ala Glu Lys Leu Ala Asp Cys Ala Gln	
440 445 450	
ctg ctg gac gtg gat gac atg gtg cgg ttg gct gtg ccc gac tcc aag	1445
Leu Leu Asp Val Asp Asp Met Val Arg Leu Ala Val Pro Asp Ser Lys	
455 460 465 470	
tgc gtc tac aca tac atc cag gaa ctg tac cgc agc ctt gtg cag aaa	1493
Cys Val Tyr Thr Tyr Ile Gln Glu Leu Tyr Arg Ser Leu Val Gln Lys	
475 480 485	
gga ctg gtg aag acc aag aag aag tga ggagg tgactggctc tgtgggcaga	1545
Gly Leu Val Lys Thr Lys Lys Lys *	
490 495	
gatgggcagg gtgcccagct cagcagccac ggcccggggg ttcccttctg ctccatggag	1605
gcaccagagc caggggctta ggcaagggtg tgtggcgttg gttttaactg cattaaggt	1665
acttttgtaa aatcctgtct ggccccctca gtgctctctc ccatacttgg ncccaggaac	1725
ctctgcactc tgggataata aactctggcc cataggggat tcctcacctg ctgaggtctc	1785
aataactgcg caaggtgttt gggaaaggac aatggcctgg tcccaccact aaccagctgt	1845
gtgacacata cagttaacct ctctgggccc cagtttacag tctgaaaggg gataatgaga	1905
gttccaacct tatgaagggtg ttgcaagagt taaacgagat aatgaaatgg gcaaaaagct	1965
ttgcccagtc ctgccactca agtgttcagt aagtggctgc caaaaataaa aaa	2018

<210> 282
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (39) .. (377)

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<400> 282
cgccctccccg ctgaccccg gatctgaggc tgtcagag      atg act ctg gtt ctg      53
                                         Met Thr Leu Val Leu
                                           1              5

tcc atg aat aga ttc tgc gag ccc att gtc tcg gaa gga gct gct gaa      101
Ser Met Asn Arg Phe Cys Glu Pro Ile Val Ser Glu Gly Ala Ala Glu
                10              15              20

att gct ggg tac caa aca cta tgg gag gct gac agc tac gga ggc cca      149
Ile Ala Gly Tyr Gln Thr Leu Trp Glu Ala Asp Ser Tyr Gly Gly Pro
                25              30              35

agc ccc cca ggg cca gca caa gct cct ttg cag gga gac cgg gga gct      197
Ser Pro Pro Gly Pro Ala Gln Ala Pro Leu Gln Gly Asp Arg Gly Ala
                40              45              50

ggt ccc cca ctg gca gct cca ctt ggt gac ttc ctt tct gtg tat cag      245
Gly Pro Pro Leu Ala Ala Pro Leu Gly Asp Phe Leu Ser Val Tyr Gln
                55              60              65

gag cag agc aga gga caa ctt gta gaa gac atg acc att aag aga cat      293
Glu Gln Ser Arg Gly Gln Leu Val Glu Asp Met Thr Ile Lys Arg His
                70              75              80              85

caa ctt cgc aac aaa tat aag aca agg ata caa gga ttc cta tgt gat      341
Gln Leu Arg Asn Lys Tyr Lys Thr Arg Ile Gln Gly Phe Leu Cys Asp
                90              95              100

gca gct agg ttt tta tat cct tct aac aaa tgg tga gcag gagacttttt      391
Ala Ala Arg Phe Leu Tyr Pro Ser Asn Lys Trp *
                105              110

tggaataat tagttgtgaa attccatttt tctgacagcc ccttaaattt gaagttattt      451

catttgtagt taaggttatc acatccctgc caattttact agattttttc agagacaagc      511

attcagcatg gcattagtaa tgatggttta aactaggtgc agaactgtcc catgaagaga      571

agaatgatat cagtatttaa ataataaaag aagagacaat gtatggttta tagtgattca      631

ttttaagatt gctgtatttt gattttgtgg tttaaaataa atgcattaag gatcttttaa      691

gttaaaaaaa aaaaaa                                                    706

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<210> 283
 <211> 758
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (539) .. (697)

<400> 283
 agattatgtg tcatcatttc ttgcttctta gacatagtgc gtataagaac agtggaaatc 60
 aaagtagaaa atttcacact aggatgaaca tactgtattc tctactaggt agcgaagctg 120
 agtagctgac ctgtgatatc attaggagtt gagctgaaac tacttaaaac tgctctagcc 180
 ccaaccacgc tcaactccta atgatatcac aggtcagcta ctcagcttcg ctacctagta 240
 gagaatacag tatgttcatc ctagtgtgaa attttctact ttgatttcca ctgttcttat 300
 acgcattatg tctaagaagc aagaaatgat gacacataat ctaaagaaga aacaatcgat 360
 agaaaaagac cttatggatc acccaagtgt tggaatttag acaaagactt taaaattcca 420
 tgaaaaattht tctttatgtht aaagaaaaac gagaggcaga atgattgaga gaatagaaaa 480
 tttgagcaga gaaaaaaagt aacaaaaatag aaaatctaga actgaaaata tatccgaa 538
 atg aat aaa ttg ttt tat ttg tta ttt att ttt gta gaa aca gga tct 586
 Met Asn Lys Leu Phe Tyr Leu Leu Phe Ile Phe Val Glu Thr Gly Ser
 1 5 10 15
 cat ggt gtt gcc cag gtt ggt ctt gaa ctc ctg agc tca aga gat cct 634
 His Gly Val Ala Gln Val Gly Leu Glu Leu Leu Ser Ser Arg Asp Pro
 20 25 30
 cct gcc tct gcc tcc caa gct gct ggg att aca ggc atg aac cac tgt 682
 Pro Ala Ser Ala Ser Gln Ala Ala Gly Ile Thr Gly Met Asn His Cys
 35 40 45
 gcc cag ctg aaa tga ataaattgga taggcttaac aaaatggata caacaaaatg 737
 Ala Gln Leu Lys *
 50
 gatacaacag aaaaaaaaaa a 758

<210> 284
 <211> 1482
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (939) .. (1475)

<400> 284
 ccagcctgcc ctcttagtcc ctgacagctg cagtgcagc atctgtgatt gcaaagcatg 60
 acaatttata tctctcattt catcacacca tctatcagca gacagtcagg ctttaaaaat 120

caatcccaca ctgactcagt ccccagcaga gatggcctct gacaacagta tccacactgc	180
aggctggaca agggccctat taattttgag actcagccaa atttccttct gaccctaagc	240
tggatgaatcc ctgctccttt gcttttggttg ggggttggtgt gagctaaggc tgtgatccca	300
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	Met Glu Lys Thr Arg
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cat gag act gtg gag aag cca cac cac cag aaa ccc ctg ccc cat gcg	1001
His Glu Thr Val Glu Lys Pro His His Gln Lys Pro Leu Pro His Ala	
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Pro Ser Ser Pro His Leu Trp Met His Gly Gly Leu Gln Ala Gly Leu	
	25 30 35
cca ccg tgg act cag gaa cag gca ggg aag ctg ctg cct cac cag gcg	1097
Pro Pro Trp Thr Gln Glu Gln Ala Gly Lys Leu Leu Pro His Gln Ala	
	40 45 50
aag ggg cca gga ggg gga ggc gga gag gcc cgt cta gcc cct gcg gct	1145
Lys Gly Pro Gly Gly Gly Gly Gly Glu Ala Arg Leu Ala Pro Ala Ala	
	55 60 65
gtc acc gtg gtg cct cct cac tgg cca gtg cgg tcg cgc ctc agc ttc	1193
Val Thr Val Val Pro Pro His Trp Pro Val Arg Ser Arg Leu Ser Phe	
	70 75 80 85
gtt aat agg gga ggg ggc cta aga gtt ttc acg tcc agg ctc ggg cag	1241
Val Asn Arg Gly Gly Gly Leu Arg Val Phe Thr Ser Arg Leu Gly Gln	
	90 95 100
tgg gga ggc agg cag gag tgg ccg ctg gtt ttt cag acc tcc cag gga	1289
Trp Gly Gly Arg Gln Glu Trp Pro Leu Val Phe Gln Thr Ser Gln Gly	
	105 110 115

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 Gly Arg Gly Asn Gly Pro Ser Trp Ser Gly Arg Gly Ser Val Phe Arg
 120 125 130
 tgg atg ctg gag ggt tgg gct gcg tgg gac cct ggg ccc tgc tgc ttc 1385
 Trp Met Leu Glu Gly Trp Ala Ala Trp Asp Pro Gly Pro Cys Cys Phe
 135 140 145
 ccg gag gat gcg ctg tcc ggg gct gca cag gtt ggc tgt gtt ttt tgg 1433
 Pro Glu Asp Ala Leu Ser Gly Ala Ala Gln Val Gly Cys Val Phe Trp
 150 155 160 165
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 <213> Homo sapiens

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 Met Glu Leu Leu Leu Leu Glu
 1 5
 acc ttt cag tgg aac ctc tgc ctt cca aca gcc gcc cat ttc att gag 460
 Thr Phe Gln Trp Asn Leu Cys Leu Pro Thr Ala Ala His Phe Ile Glu
 10 15 20
 tat tat ctc tct gaa gca gta cac gaa aca gat ctt cat gac ggc tgg 508
 Tyr Tyr Leu Ser Glu Ala Val His Glu Thr Asp Leu His Asp Gly Trp
 25 30 35
 cca atg att tgc ttg gaa aag act aaa ctc tac atg gcc aaa tat gca 556
 Pro Met Ile Cys Leu Glu Lys Thr Lys Leu Tyr Met Ala Lys Tyr Ala

40	45	50	55	
gat tac ttc ctg gaa gta tct ttg caa gct gct gca tgt gtg gct tct				604
Asp Tyr Phe Leu Glu Val Ser Leu Gln Ala Ala Cys Val Ala Ser	60	65	70	
tcg agg att ata ctt cgt ctt tct cca acg tgg cct aca aga cta cat				652
Ser Arg Ile Ile Leu Arg Leu Ser Pro Thr Trp Pro Thr Arg Leu His	75	80	85	
cgt ctt act gcc tac tct tgg gat ttc tta gtg cag tgt att gaa cga				700
Arg Leu Thr Ala Tyr Ser Trp Asp Phe Leu Val Gln Cys Ile Glu Arg	90	95	100	
ctg ttg atc gct cat gat aat gat gtg aaa gaa gca aac aaa cag aga				748
Leu Leu Ile Ala His Asp Asn Asp Val Lys Glu Ala Asn Lys Gln Arg	105	110	115	
ggg caa gca gga cct cag tca gcg caa cta agt gta ttc cag aca gcc				796
Gly Gln Ala Gly Pro Gln Ser Ala Gln Leu Ser Val Phe Gln Thr Ala	120	125	130	135
tcc cag cca tca cgg cca gtt cac ttt cag caa cct cag tat ctc cat				844
Ser Gln Pro Ser Arg Pro Val His Phe Gln Gln Pro Gln Tyr Leu His	140	145	150	
cag aca cat cag acc tca ctg cag tat cgc cat cct acg tca gaa caa				892
Gln Thr His Gln Thr Ser Leu Gln Tyr Arg His Pro Thr Ser Glu Gln	155	160	165	
cca agc tgt cag cag att gta tcg acc aca cac acc tca tct tac aca				940
Pro Ser Cys Gln Gln Ile Val Ser Thr Thr His Thr Ser Ser Tyr Thr	170	175	180	
cta cag aca tgt cct gct ggc ttc caa act agt gtt cag ggc ctt ggg				988
Leu Gln Thr Cys Pro Ala Gly Phe Gln Thr Ser Val Gln Gly Leu Gly	185	190	195	
cac atg cag act ggt gtt ggg atg tca ctg gca ata cca gta gaa gtt				1036
His Met Gln Thr Gly Val Gly Met Ser Leu Ala Ile Pro Val Glu Val	200	205	210	215
aag ccc tgt ctg agt gtt tct tac aac cgg agt tat cag ata aat gaa				1084
Lys Pro Cys Leu Ser Val Ser Tyr Asn Arg Ser Tyr Gln Ile Asn Glu	220	225	230	
cat tac cct tgt att act cca tgt ttt gaa agg tga ttat ttgtgaagct				1134
His Tyr Pro Cys Ile Thr Pro Cys Phe Glu Arg *	235	240		
gataaccgac ccagactgct ttgtgacatg aagctatggg taagcgtttt gttaaacttct				
gttcaaaagg aaagggatct aaatgacatc agaactcttc aggtaccagc accaggaaga				
ctgaatatcc tttttaatgc accatgaatc ctgggagact aagcaaatta acagtatgtc				
aaattctgtt acaacaaatc cctgtatgac aaaaatgttc aagtcctggc tgatggtcca				

aatatttcaa	aaatattcag	tacaacagaa	aatttggaca	gacttcaatt	tgccattttg	1434
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gcagatacgt	gactgccaca	atatgcatcg	aagacaaaact	tactataaaag	atgttgtggg	2634
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cccagcaacc tggagtccaa ttttcagtat ttttaactacc tcaataatgc tatgaatgta 3114
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gggtgggatg ggggtggttg agaaccagaa ctatttttaa aacattaggt ttcaatataa 3414
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<210> 286
<211> 650
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (217)..(510)

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<400> 286

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gaagagccca ggtccctgcc ccagttctac cacagctctc atgccacag ccctgtctgt 180
ctggacacat tactaggcac agactgctga cagggg atg tcc tgg gcg gtt gac 234
Met Ser Trp Ala Val Asp
1 5

ctg cct gtg tgt caa agg aca cct cac tgc agg gtc caa gac aga gtg 282
Leu Pro Val Cys Gln Arg Thr Pro His Cys Arg Val Gln Asp Arg Val
10 15 20

ctc cac tgt ggc ttc ctg gga agc ccg ctg gtg gga gct cct ggg agc 330
Leu His Cys Gly Phe Leu Gly Ser Pro Leu Val Gly Ala Pro Gly Ser
25 30 35

agg aga cag ctg tgc tct ccc cac tcc tcc ctc cgg cct cag cac cca 378
Arg Arg Gln Leu Cys Ser Pro His Ser Ser Leu Arg Pro Gln His Pro
40 45 50

cag gtg gcc tct gct ctc ttg gag gcg aag ctg ctc ccc tct cct cca 426
Gln Val Ala Ser Ala Leu Leu Glu Ala Lys Leu Leu Pro Ser Pro Pro
55 60 65 70

acc tca ttc tct gcc tgc ttc atc cgg ccc cac aca cac acc ggt aat 474
Thr Ser Phe Ser Ala Cys Phe Ile Arg Pro His Thr His Thr Gly Asn

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75	80	85	
ctg tgt tcc ttt ctg cca tta atc ctc ctc atg taa atat tcccaatact			524
Leu Cys Ser Phe Leu Pro Leu Ile Leu Leu Met *			
90	95		
ctttcagtc ccaaagccat aggccacat ctgcttgtgg atcagaaaca tgctggcaga			584
gcgcggtggg actgctgccc cctggccctt aggagtgggg tctggggcgc cctcagaaca			644
acgaca			650

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 <211> 1619
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (120)..(1619)

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atg atg gcg gat gcc aag tat gtc ctc tgc cga tgg gaa aag cga tta	167
Met Met Ala Asp Ala Lys Tyr Val Leu Cys Arg Trp Glu Lys Arg Leu	
1 5 10 15	
tggt cct gcg aag gtt ttg gcc cga acc gcg act tca aca aaa aat aag	215
Trp Pro Ala Lys Val Leu Ala Arg Thr Ala Thr Ser Thr Lys Asn Lys	
20 25 30	
aga aga aag gaa tat ttt cta gct gtg caa atc ctc tcc cta gag gaa	263
Arg Arg Lys Glu Tyr Phe Leu Ala Val Gln Ile Leu Ser Leu Glu Glu	
35 40 45	
aaa att aag gtg aaa agc act gaa gtt gag atc cta gag aag tct caa	311
Lys Ile Lys Val Lys Ser Thr Glu Val Glu Ile Leu Glu Lys Ser Gln	
50 55 60	
att gaa gcc att gct tcc tcg tta gcc tca cag aat gag gtt cct gcg	359
Ile Glu Ala Ile Ala Ser Ser Leu Ala Ser Gln Asn Glu Val Pro Ala	
65 70 75 80	
gca ccc ctg gaa gaa ctg gcc tac aga cgg tcg ctt cgc gtg gct ctg	407
Ala Pro Leu Glu Glu Leu Ala Tyr Arg Arg Ser Leu Arg Val Ala Leu	
85 90 95	
gac gtt ctg agc gag ggc tcg att tgg agt caa gaa agc tct gca ggg	455
Asp Val Leu Ser Glu Gly Ser Ile Trp Ser Gln Glu Ser Ser Ala Gly	
100 105 110	
aca ggt aga gct gac cgg tct ctg cga ggg aag ccc atg gag cat gtc	503

Thr	Gly	Arg	Ala	Asp	Arg	Ser	Leu	Arg	Gly	Lys	Pro	Met	Glu	His	Val	
	115						120					125				
tcc	tcg	ccc	tgt	gat	tcg	aac	tcc	tca	tct	ctt	ccc	cgc	gga	gac	gtg	551
Ser	Ser	Pro	Cys	Asp	Ser	Asn	Ser	Ser	Ser	Leu	Pro	Arg	Gly	Asp	Val	
	130						135					140				
ttg	ggc	agt	tcc	aga	cct	cac	agg	agg	agg	cca	tgt	gtg	caa	caa	agc	599
Leu	Gly	Ser	Ser	Arg	Pro	His	Arg	Arg	Arg	Pro	Cys	Val	Gln	Gln	Ser	
	145					150				155					160	
ctg	tca	agt	tcg	ttc	act	tgt	gaa	aag	gac	ccc	gag	tgc	aaa	gtg	gac	647
Leu	Ser	Ser	Ser	Phe	Thr	Cys	Glu	Lys	Asp	Pro	Glu	Cys	Lys	Val	Asp	
				165					170					175		
cac	aag	aag	ggg	ctc	agg	aaa	agt	gaa	aac	cca	aga	ggc	ccg	ttg	gtc	695
His	Lys	Lys	Gly	Leu	Arg	Lys	Ser	Glu	Asn	Pro	Arg	Gly	Pro	Leu	Val	
			180					185					190			
ctc	cca	gct	gga	ggt	ggt	gcc	caa	gat	gag	agt	ggg	tcc	aga	atc	cac	743
Leu	Pro	Ala	Gly	Gly	Gly	Ala	Gln	Asp	Glu	Ser	Gly	Ser	Arg	Ile	His	
			195				200					205				
cac	aaa	aat	tgg	act	ctt	gca	agt	aag	agg	gga	aga	aac	tca	gcg	cag	791
His	Lys	Asn	Trp	Thr	Leu	Ala	Ser	Lys	Arg	Gly	Arg	Asn	Ser	Ala	Gln	
	210					215					220					
aag	gct	agc	ttg	tgc	ctg	aat	gga	tct	tcc	ctt	tca	gag	gac	gac	acg	839
Lys	Ala	Ser	Leu	Cys	Leu	Asn	Gly	Ser	Ser	Leu	Ser	Glu	Asp	Asp	Thr	
	225				230					235					240	
gag	aga	gac	atg	ggg	agc	aaa	gga	ggc	agc	tgg	gca	gcc	ccg	tcc	ttg	887
Glu	Arg	Asp	Met	Gly	Ser	Lys	Gly	Gly	Ser	Trp	Ala	Ala	Pro	Ser	Leu	
				245					250					255		
ccc	tcc	ggg	gtc	agg	gag	gac	gat	ccc	tgt	gcc	aac	gct	gag	gga	cac	935
Pro	Ser	Gly	Val	Arg	Glu	Asp	Asp	Pro	Cys	Ala	Asn	Ala	Glu	Gly	His	
			260					265					270			
gac	ccc	ggt	ctg	ccg	ttg	ggc	agc	ctc	act	gcg	ccc	cca	gcc	cct	gag	983
Asp	Pro	Gly	Leu	Pro	Leu	Gly	Ser	Leu	Thr	Ala	Pro	Pro	Ala	Pro	Glu	
		275					280					285				
ccc	tcg	gcc	tgc	tca	gag	cct	gga	gaa	tgc	cct	gcg	aaa	aag	agg	ccg	1031
Pro	Ser	Ala	Cys	Ser	Glu	Pro	Gly	Glu	Cys	Pro	Ala	Lys	Lys	Arg	Pro	
	290					295					300					
cgc	ctg	gat	ggc	agc	caa	agg	ccg	cct	gcc	gtg	cag	ctg	gag	ccc	atg	1079
Arg	Leu	Asp	Gly	Ser	Gln	Arg	Pro	Pro	Ala	Val	Gln	Leu	Glu	Pro	Met	
	305				310				315						320	
gca	gca	ggg	gcc	gca	cca	tcc	ccc	ggg	ccg	ggg	cca	ggg	ccc	aga	gag	1127
Ala	Ala	Gly	Ala	Ala	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Gly	Pro	Arg	Glu	
				325					330					335		
tct	gtg	acc	ccg	cgc	agc	acc	gcc	agg	ctg	ggc	ccg	cct	ccc	tcc	cac	1175
Ser	Val	Thr	Pro	Arg	Ser	Thr	Ala	Arg	Leu	Gly	Pro	Pro	Pro	Ser	His	

340	345	350	
gcc tct gcg gat gca acc aga tgt ctt cct tgc ccg gat tcc cag aag			1223
Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys			
355	360	365	
ctg gag aaa gag tgc cag tct tcc gaa gag tcc atg ggg tct aat tcc			1271
Leu Glu Lys Glu Cys Gln Ser Ser Glu Glu Ser Met Gly Ser Asn Ser			
370	375	380	
atg cgt tct atc ctg gag gaa gac gag gaa gac gag gag cca cca aga			1319
Met Arg Ser Ile Leu Glu Glu Asp Glu Glu Asp Glu Glu Pro Pro Arg			
385	390	395	400
gtc ctt tta tac cac gaa cca cgt tcg ttt gaa gta gga atg cta gtc			1367
Val Leu Leu Tyr His Glu Pro Arg Ser Phe Glu Val Gly Met Leu Val			
	405	410	415
tgg cat aaa cat aaa aaa tac ccc ttc tgg cca gca gtg gtc aaa agc			1415
Trp His Lys His Lys Lys Tyr Pro Phe Trp Pro Ala Val Val Lys Ser			
	420	425	430
gtc agg cag aga gat aag aaa gca agt gtg cta tac atc gaa gga cac			1463
Val Arg Gln Arg Asp Lys Lys Ala Ser Val Leu Tyr Ile Glu Gly His			
	435	440	445
atg aac ccg aaa atg aaa ggt ttc aca gtg tct ctt aaa agt tta aag			1511
Met Asn Pro Lys Met Lys Gly Phe Thr Val Ser Leu Lys Ser Leu Lys			
	450	455	460
cac ttt gat tgt aaa gag aaa cag acg ctt ctg aat caa gcc agg gag			1559
His Phe Asp Cys Lys Glu Lys Gln Thr Leu Leu Asn Gln Ala Arg Glu			
465	470	475	480
gac ttc aac cag gac atc ggc tgg tgt gct ccc tca tca ccg act aca			1607
Asp Phe Asn Gln Asp Ile Gly Trp Cys Ala Pro Ser Ser Pro Thr Thr			
	485	490	495
ggg tcc ggt tag			1619
Gly Ser Gly *			
500			

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 <213> Homo sapiens

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 <222> (126)..(1091)

<400> 290

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gcacg      atg gcc tcg tct cag ggg aaa aac gag ctg aaa tta gcc gac      167
      Met Ala Ser Ser Gln Gly Lys Asn Glu Leu Lys Leu Ala Asp
            1              5              10

tgg atg gca act ctg ccg gag agc atg cac agc atc ccc ctc acc aat      215
Trp Met Ala Thr Leu Pro Glu Ser Met His Ser Ile Pro Leu Thr Asn
      15              20              25              30

tta gcc att cca ggg tct cat gat tcc ttc agc ttc tac att gat gaa      263
Leu Ala Ile Pro Gly Ser His Asp Ser Phe Ser Phe Tyr Ile Asp Glu
            35              40              45

gcc tct cca gta ggt cct gag cag cca gaa act gtc cag aat ttt gtc      311
Ala Ser Pro Val Gly Pro Glu Gln Pro Glu Thr Val Gln Asn Phe Val
            50              55              60

tct gtg ttt gga act gtg gcc aaa aag ctc atg cgg aaa tgg tta gcc      359
Ser Val Phe Gly Thr Val Ala Lys Lys Leu Met Arg Lys Trp Leu Ala
            65              70              75

act cag aca atg aat ttt act ggc cag cta gga gct gga att cgt tat      407
Thr Gln Thr Met Asn Phe Thr Gly Gln Leu Gly Ala Gly Ile Arg Tyr
            80              85              90

ttt gat ctt cga att tcc acc aag ccc aga gac ccc gac aat gaa ctc      455
Phe Asp Leu Arg Ile Ser Thr Lys Pro Arg Asp Pro Asp Asn Glu Leu
            95              100              105              110

tat ttt gct cat ggt ttg ttc agt gcc aaa gtc aat gaa ggc ctt gag      503
Tyr Phe Ala His Gly Leu Phe Ser Ala Lys Val Asn Glu Gly Leu Glu
            115              120              125

gag atc aat gca ttc ctc aca gat cac cat aag gag gta gtg ttc ttg      551
Glu Ile Asn Ala Phe Leu Thr Asp His His Lys Glu Val Val Phe Leu
            130              135              140

gac ttc aac cac ttc tat ggg atg cag aaa tat cac cat gaa aaa ctg      599
Asp Phe Asn His Phe Tyr Gly Met Gln Lys Tyr His His Glu Lys Leu
            145              150              155

gtc caa atg ctg aaa gac atc tat gga aat aaa atg tgc cca gcg att      647
Val Gln Met Leu Lys Asp Ile Tyr Gly Asn Lys Met Cys Pro Ala Ile
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160	165	170	
ttt gcc cag gaa gtt agt tta aag tac ctg tgg gag aag gac tat caa			695
Phe Ala Gln Glu Val Ser Leu Lys Tyr Leu Trp Glu Lys Asp Tyr Gln			
175	180	185	190
gtg ctg gtc ttc tac cat agt cca gtg gct ctg gaa gtg ccc ttt ctc			743
Val Leu Val Phe Tyr His Ser Pro Val Ala Leu Glu Val Pro Phe Leu			
	195	200	205
tgg cct ggg cag atg atg cca gca ccc tgg gcc aac acc aca gac ccc			791
Trp Pro Gly Gln Met Met Pro Ala Pro Trp Ala Asn Thr Thr Asp Pro			
	210	215	220
gag aaa ctg atc cag ttt ctt caa gca tcc atc act gag aga aga aag			839
Glu Lys Leu Ile Gln Phe Leu Gln Ala Ser Ile Thr Glu Arg Arg Lys			
	225	230	235
aag gga tcg ttt ttt ata tct cag gtg gtg ctg acc ccc aaa gct agc			887
Lys Gly Ser Phe Phe Ile Ser Gln Val Val Leu Thr Pro Lys Ala Ser			
	240	245	250
act gtg gtc aaa ggg gtg gca agt ggc ctc aga gaa aca atc aca gaa			935
Thr Val Val Lys Gly Val Ala Ser Gly Leu Arg Glu Thr Ile Thr Glu			
	255	260	265
aga gct ctt cct gcc atg atg cag tgg gtc cgc acg cag aag cca gga			983
Arg Ala Leu Pro Ala Met Met Gln Trp Val Arg Thr Gln Lys Pro Gly			
	275	280	285
gag agt ggc atc aat att gtc act gcc gat ttt gta gaa ctt ggt gac			1031
Glu Ser Gly Ile Asn Ile Val Thr Ala Asp Phe Val Glu Leu Gly Asp			
	290	295	300
ttt atc agc act gtc ata aag ctc aac tat gtc ttt gat gaa gga gaa			1079
Phe Ile Ser Thr Val Ile Lys Leu Asn Tyr Val Phe Asp Glu Gly Glu			
	305	310	315
gcc aac act tga tag cactacttgg agtttccatg aataagatgg agaaagctca			1134
Ala Asn Thr *			
	320		
ttgtattagg gcatactatc tgtaaact ctgatcttcc tattccactg agtctctgaa			1194
gggaataggg ctggtagtgg gtgggaaaag gggaaaaaact gtttcttcag tgattacaat			1254
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tggttaggaat aaaaaaaaaa aa			1336

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 <212> DNA
 <213> Homo sapiens

	Mean	SD	Median	Mode	Range	Skewness	Kurtosis
1	1.00	0.00	1.00	1.00	1.00	0.00	0.00
2	1.00	0.00	1.00	1.00	1.00	0.00	0.00
3	1.00	0.00	1.00	1.00	1.00	0.00	0.00
4	1.00	0.00	1.00	1.00	1.00	0.00	0.00
5	1.00	0.00	1.00	1.00	1.00	0.00	0.00
6	1.00	0.00	1.00	1.00	1.00	0.00	0.00
7	1.00	0.00	1.00	1.00	1.00	0.00	0.00
8	1.00	0.00	1.00	1.00	1.00	0.00	0.00
9	1.00	0.00	1.00	1.00	1.00	0.00	0.00
10	1.00	0.00	1.00	1.00	1.00	0.00	0.00
11	1.00	0.00	1.00	1.00	1.00	0.00	0.00
12	1.00	0.00	1.00	1.00	1.00	0.00	0.00
13	1.00	0.00	1.00	1.00	1.00	0.00	0.00
14	1.00	0.00	1.00	1.00	1.00	0.00	0.00
15	1.00	0.00	1.00	1.00	1.00	0.00	0.00
16	1.00	0.00	1.00	1.00	1.00	0.00	0.00
17	1.00	0.00	1.00	1.00	1.00	0.00	0.00
18	1.00	0.00	1.00	1.00	1.00	0.00	0.00
19	1.00	0.00	1.00	1.00	1.00	0.00	0.00
20	1.00	0.00	1.00	1.00	1.00	0.00	0.00
21	1.00	0.00	1.00	1.00	1.00	0.00	0.00
22	1.00	0.00	1.00	1.00	1.00	0.00	0.00
23	1.00	0.00	1.00	1.00	1.00	0.00	0.00
24	1.00	0.00	1.00	1.00	1.00	0.00	0.00
25	1.00	0.00	1.00	1.00	1.00	0.00	0.00
26	1.00	0.00	1.00	1.00	1.00	0.00	0.00
27	1.00	0.00	1.00	1.00	1.00	0.00	0.00
28	1.00	0.00	1.00	1.00	1.00	0.00	0.00
29	1.00	0.00	1.00	1.00	1.00	0.00	0.00
30	1.00	0.00	1.00	1.00	1.00	0.00	0.00
31	1.00	0.00	1.00	1.00	1.00	0.00	0.00
32	1.00	0.00	1.00	1.00	1.00	0.00	0.00
33	1.00	0.00	1.00	1.00	1.00	0.00	0.00
34	1.00	0.00	1.00	1.00	1.00	0.00	0.00
35	1.00	0.00	1.00	1.00	1.00	0.00	0.00
36	1.00	0.00	1.00	1.00	1.00	0.00	0.00
37	1.00	0.00	1.00	1.00	1.00	0.00	0.00
38	1.00	0.00	1.00	1.00	1.00	0.00	0.00
39	1.00	0.00	1.00	1.00	1.00	0.00	0.00
40	1.00	0.00	1.00	1.00	1.00	0.00	0.00
41	1.00	0.00	1.00	1.00	1.00	0.00	0.00
42	1.00	0.00	1.00	1.00	1.00	0.00	0.00
43	1.00	0.00	1.00	1.00	1.00	0.00	0.00
44	1.00	0.00	1.00	1.00	1.00	0.00	0.00
45	1.00	0.00	1.00	1.00	1.00	0.00	0.00
46	1.00	0.00	1.00	1.00	1.00	0.00	0.00
47	1.00	0.00	1.00	1.00	1.00	0.00	0.00
48	1.00	0.00					

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.5	0.5	0	1	0.0	3.0	0.99
Marital Status	0.7	0.5	0	1	0.0	3.0	0.99
Education	12.5	2.5	8	16	0.1	3.1	0.98
Income	1500	500	500	3000	0.2	3.3	0.97
Occupation	1.5	1.0	1	5	0.0	3.0	0.99
Health Status	0.8	0.4	0	1	0.0	3.0	0.99
Stress Level	3.5	1.5	1	6	0.1	3.1	0.98
Life Satisfaction	4.2	1.2	1	7	0.1	3.1	0.98
Resilience	5.5	1.5	1	7	0.1	3.1	0.98
Optimism	5.8	1.2	1	7	0.1	3.1	0.98
Emotional Stability	6.0	1.0	1	7	0.1	3.1	0.98
Self-Esteem	6.2	1.0	1	7	0.1	3.1	0.98
Life Purpose	6.5	1.0	1	7	0.1	3.1	0.98
Meaning in Life	6.8	1.0	1	7	0.1	3.1	0.98
Existential Well-being	7.0	1.0	1	7	0.1	3.1	0.98
Overall Well-being	7.2	1.0	1	7	0.1	3.1	0.98

aag ttg aag cta ttg agc ctc agc cag tca ttc tca tcc act gca ccc	747
Lys Leu Lys Leu Leu Ser Leu Ser Gln Ser Phe Ser Ser Thr Ala Pro	
185 190 195 200	
tct gac aca gac ctc ggg gag agc tta ggg gcc aac gtg gcc acc aca	795
Ser Asp Thr Asp Leu Gly Glu Ser Leu Gly Ala Asn Val Ala Thr Thr	
205 210 215	
gac tcg gat gag aga gat gat gca tct gtg tgc agt gga ggt gac tcc	843
Asp Ser Asp Glu Arg Asp Asp Ala Ser Val Cys Ser Gly Gly Asp Ser	
220 225 230	
act gat gac ggt ggc tac agg agc agc atg tgg gac cag ggc gac atc	891
Thr Asp Asp Gly Gly Tyr Arg Ser Ser Met Trp Asp Gln Gly Asp Ile	
235 240 245	
ctg gag tct ggg tca ggc act tcc ttg gag gag gca ttg gag gcc cca	939
Leu Glu Ser Gly Ser Gly Thr Ser Leu Glu Glu Ala Leu Glu Ala Pro	
250 255 260	
gcc aca gac ctg gcc agg cct gag ttc tgt tac gag gct gag agc cct	987
Ala Thr Asp Leu Ala Arg Pro Glu Phe Cys Tyr Glu Ala Glu Ser Pro	
265 270 275 280	
gat gag gcc gcc ctg gtg cac gct gcc cat gcc tac agc ttc aca cta	1035
Asp Glu Ala Ala Leu Val His Ala Ala His Ala Tyr Ser Phe Thr Leu	
285 290 295	
gtg tcc cgg aca cct gag cag gtg act gtg cgc ctg ccc cag ggc acc	1083
Val Ser Arg Thr Pro Glu Gln Val Thr Val Arg Leu Pro Gln Gly Thr	
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tgc ctc acc ttc agc ctc ctc tgc acc ctg ggc ttt gac tct gtc agg	1131
Cys Leu Thr Phe Ser Leu Leu Cys Thr Leu Gly Phe Asp Ser Val Arg	
315 320 325	
aag aga atg tct gtg gtt gtg agg cac cca ctg act ggc gag att gtt	1179
Lys Arg Met Ser Val Val Arg His Pro Leu Thr Gly Glu Ile Val	
330 335 340	
gtc tac acc aag ggt gct gac tcg gtc atc atg gac ctg ctg gaa gac	1227
Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Asp Leu Leu Glu Asp	
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cca gcc tgc gta cct gac att aat atg gaa aag aag ctg aga aaa atc	1275
Pro Ala Cys Val Pro Asp Ile Asn Met Glu Lys Lys Leu Arg Lys Ile	
365 370 375	
cga gcc cgg acc caa aag cat cta gac ttg tat gca aga gat ggc ctg	1323
Arg Ala Arg Thr Gln Lys His Leu Asp Leu Tyr Ala Arg Asp Gly Leu	
380 385 390	
cgc aca cta tgc att gcc aag aag gtt gta agc gaa gag gac ttc cgg	1371
Arg Thr Leu Cys Ile Ala Lys Lys Val Val Ser Glu Glu Asp Phe Arg	
395 400 405	

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Arg Trp Ala Ser Phe Arg Arg Glu Ala Glu Ala Ser Leu Asp Asn Arg	
410 415 420	
gat gag ctt ctc atg gaa act gca cag cat ctg gag aat caa ctc acc	1467
Asp Glu Leu Leu Met Glu Thr Ala Gln His Leu Glu Asn Gln Leu Thr	
425 430 435 440	
tta ctt gga gcc act ggg atc gaa gac cgg ctg cag gaa gga gtt cca	1515
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro	
445 450 455	
gat acg att gcc act ctg cgg gag gct ggg atc cag ctc tgg gtc ctg	1563
Asp Thr Ile Ala Thr Leu Arg Glu Ala Gly Ile Gln Leu Trp Val Leu	
460 465 470	
act gga gat aag cag gag aca gcg gtc aac att gcc cat tcc tgc aga	1611
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala His Ser Cys Arg	
475 480 485	
ctg tta aat cag acc gac act gtt tat acc atc aat aca gag aat cag	1659
Leu Leu Asn Gln Thr Asp Thr Val Tyr Thr Ile Asn Thr Glu Asn Gln	
490 495 500	
gag acc tgt gaa tcc atc ctc aat tgt gca ttg gaa gag cta aag caa	1707
Glu Thr Cys Glu Ser Ile Leu Asn Cys Ala Leu Glu Glu Leu Lys Gln	
505 510 515 520	
ttt cgt gaa cta cag aag cca gac cgc aag ctc ttt gga ttc cgc tta	1755
Phe Arg Glu Leu Gln Lys Pro Asp Arg Lys Leu Phe Gly Phe Arg Leu	
525 530 535	
cct tcc aag aca cca tcc atc acc tca gaa gct gtg gtt cca gaa gct	1803
Pro Ser Lys Thr Pro Ser Ile Thr Ser Glu Ala Val Val Pro Glu Ala	
540 545 550	
gga ttg gtc atc gat ggg aag aca ttg aat gcc atc ttc cag gga aag	1851
Gly Leu Val Ile Asp Gly Lys Thr Leu Asn Ala Ile Phe Gln Gly Lys	
555 560 565	
cta gag aag aag ttt ctg gaa ttg acc cag tat tgt cgg tcc gtc ctg	1899
Leu Glu Lys Lys Phe Leu Glu Leu Thr Gln Tyr Cys Arg Ser Val Leu	
570 575 580	
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Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met Ile Val Lys Leu Val	
585 590 595 600	
cga gac aag ttg cgc gtc atg acc ctt tcc ata ggt gat gga gca aat	1995
Arg Asp Lys Leu Arg Val Met Thr Leu Ser Ile Gly Asp Gly Ala Asn	
605 610 615	
gat gta agc atg att caa gct gct gat att gga att gga ata tct gga	2043
Asp Val Ser Met Ile Gln Ala Ala Asp Ile Gly Ile Gly Ile Ser Gly	
620 625 630	
cag gaa ggc atg cag gct gtc atg tcc agc gac ttt gcc atc acc cgc	2091

Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ser	Ser	Asp	Phe	Ala	Ile	Thr	Arg	
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ttt	aag	cat	ctc	aag	aag	ttg	ctg	ctc	gtg	cat	ggc	cac	tgg	tgt	tac	2139
Phe	Lys	His	Leu	Lys	Lys	Leu	Leu	Leu	Val	His	Gly	His	Trp	Cys	Tyr	
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tcg	cgc	ctg	gcc	agg	atg	gtg	gtg	tac	tac	ctc	tac	aag	aac	gtg	tgc	2187
Ser	Arg	Leu	Ala	Arg	Met	Val	Val	Tyr	Tyr	Leu	Tyr	Lys	Asn	Val	Cys	
	665				670					675					680	
tac	gtc	aac	ctg	ctc	ttc	tgg	tat	cag	ttc	ttc	tgt	ggc	ttc	tcc	agc	2235
Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly	Phe	Ser	Ser	
				685				690						695		
tcc	acc	atg	att	gat	tac	tgg	cag	atg	ata	ttc	ttc	aat	ctc	ttc	ttt	2283
Ser	Thr	Met	Ile	Asp	Tyr	Trp	Gln	Met	Ile	Phe	Phe	Asn	Leu	Phe	Phe	
			700					705					710			
acc	tcc	ttg	cct	cct	ctt	gtc	ttt	gga	gtc	ctt	gac	aaa	gac	atc	tct	2331
Thr	Ser	Leu	Pro	Pro	Leu	Val	Phe	Gly	Val	Leu	Asp	Lys	Asp	Ile	Ser	
		715					720					725				
gca	gaa	aca	ctc	ctg	gca	ttg	cct	gag	cta	tac	aag	agt	ggc	cag	aac	2379
Ala	Glu	Thr	Leu	Leu	Ala	Leu	Pro	Glu	Leu	Tyr	Lys	Ser	Gly	Gln	Asn	
	730					735					740					
tct	gag	tgc	tat	aac	ctg	tcg	act	ttc	tgg	att	tct	atg	gtg	gat	gca	2427
Ser	Glu	Cys	Tyr	Asn	Leu	Ser	Thr	Phe	Trp	Ile	Ser	Met	Val	Asp	Ala	
	745				750					755					760	
ttc	tac	cag	agc	ctc	atc	tgt	ttc	ttt	atc	cct	tac	ctg	gcc	tat	aag	2475
Phe	Tyr	Gln	Ser	Leu	Ile	Cys	Phe	Phe	Ile	Pro	Tyr	Leu	Ala	Tyr	Lys	
				765					770					775		
ggc	tct	gat	ata	gat	gtc	ttt	acc	ttt	ggg	aca	cca	atc	aac	acc	atc	2523
Gly	Ser	Asp	Ile	Asp	Val	Phe	Thr	Phe	Gly	Thr	Pro	Ile	Asn	Thr	Ile	
			780					785					790			
tcc	ctc	acc	aca	atc	ctt	ttg	cac	cag	gca	atg	gaa	atg	aag	aca	tgg	2571
Ser	Leu	Thr	Thr	Ile	Leu	Leu	His	Gln	Ala	Met	Glu	Met	Lys	Thr	Trp	
		795					800					805				
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Thr	Ile	Phe	His	Gly	Val	Val	Leu	Leu	Gly	Ser	Phe	Leu	Met	Tyr	Phe	
	810					815					820					
ctg	gta	tcc	ctc	ctg	tac	aat	gcc	acc	tgc	gtc	atc	tgc	aac	agc	ccc	2667
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Ala	Thr	Cys	Val	Ile	Cys	Asn	Ser	Pro	
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acc	aat	ccc	tat	tgg	gtg	atg	gaa	ggc	cag	ctc	tca	aac	ccc	act	ttc	2715
Thr	Asn	Pro	Tyr	Trp	Val	Met	Glu	Gly	Gln	Leu	Ser	Asn	Pro	Thr	Phe	
				845					850					855		
tac	ctc	gtc	tgc	ttt	ctc	aca	cca	gtt	gtt	gct	ctt	ctc	cca	aga	tac	2763
Tyr	Leu	Val	Cys	Phe	Leu	Thr	Pro	Val	Val	Ala	Leu	Leu	Pro	Arg	Tyr	

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Phe Phe Leu Ser Leu Gln Gly Thr Cys Gly Lys Ser Leu Ile Ser Lys			
875	880	885	
gct cag aaa att gac aaa ctc ccc cca gac aaa aga aac ctg gaa atc			2859
Ala Gln Lys Ile Asp Lys Leu Pro Pro Asp Lys Arg Asn Leu Glu Ile			
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cag agt tgg aga agc aga cag agg cct gcc cct gtc ccc gaa gtg gct			2907
Gln Ser Trp Arg Ser Arg Gln Arg Pro Ala Pro Val Pro Glu Val Ala			
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cga cca act cac cac cca gtg tca tct atc aca gga cag gac ttc agt			2955
Arg Pro Thr His His Pro Val Ser Ser Ile Thr Gly Gln Asp Phe Ser			
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gcc agc acc cca aag agc tct aac cct ccc aag agg aag cat gtg gaa			3003
Ala Ser Thr Pro Lys Ser Ser Asn Pro Pro Lys Arg Lys His Val Glu			
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gag tca gta ctc cac gaa cag aga tgt ggc acg gag tgc atg agg gat			3051
Glu Ser Val Leu His Glu Gln Arg Cys Gly Thr Glu Cys Met Arg Asp			
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gac tca tgc tca ggg gac tcc tca gct caa ctc tca tcc ggg gag cac			3099
Asp Ser Cys Ser Gly Asp Ser Ser Ala Gln Leu Ser Ser Gly Glu His			
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ctg ctg gga cct aac agg ata atg gcc tac tca aga gga cag act gat			3147
Leu Leu Gly Pro Asn Arg Ile Met Ala Tyr Ser Arg Gly Gln Thr Asp			
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Met Cys Arg Cys Ser Lys Arg Ser Ser His Arg Arg Ser Gln Ser Ser			
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ctg acc ata tga gga gctgcagaaa tctgtacaaa ctcaacagag gccacctagt			3250
Leu Thr Ile *			
1020			
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3764

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<400> 292

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gtccaatggc aatttgttca cctctaattt ttataatcat agtttagggg tgtgggctaaa	180
agcacaaact ctggaactag actgctagat atataatctt gggtatgctg tttgattgct	240
ctggtactct gtacctcaat tttcaccagt taaatgcaga ttaggggtgg gtagttgtga	300
ggattaaaat gtatgggtat accttagaaa ggtgccaaat atggctgggt gtggtggctc	360
atg tct gta atc cca acc cct tgg aag gcc gag gcg ggt ggc tca caa	408
Met Ser Val Ile Pro Thr Pro Trp Lys Ala Glu Ala Gly Gly Ser Gln	
1 5 10 15	
ggt cag gag atc aag acc act ctg gcc aac acg gtg aaa cac cgt ctc	456
Gly Gln Glu Ile Lys Thr Thr Leu Ala Asn Thr Val Lys His Arg Leu	
20 25 30	
cac taa aaatacaaaa tacaataaat tacaataata caaagtacaa aaaatacaaa	512
His *	
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ccagctactt gggaatctgc ggacgcgtgg gtcgacccgg gt	614

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ccgatcatgg cggatggggc ccggtgcaag aggcgcaaac aagccaatcc caggaggaaa      180
aacgccttgg agtcagaaat gagcactcgg agcggggag      atg ccc tgc tgc tgc      233
                               Met Pro Cys Cys Cys
                               1                               5

ttg cca ccg gtg cgg ccc gtt tgt aac ttg caa agt ttg ttg ctt ttg      281
Leu Pro Pro Val Arg Pro Val Cys Asn Leu Gln Ser Leu Leu Leu Leu
                               10                               15                               20

ccc ctg att cgg gca gcg ggt cct ggg atg ctc ctg ctt ccc tcc tgc      329
Pro Leu Ile Arg Ala Ala Gly Pro Gly Met Leu Leu Leu Pro Ser Cys
                               25                               30                               35

ctc cca cgg agc ccg gga aga ggg tct gcc tcc cca tcc cgc cac ctt      377
Leu Pro Arg Ser Pro Gly Arg Gly Ser Ala Ser Pro Ser Arg His Leu
                               40                               45                               50

cca gca tca gcc tct gaa aaa tct cac aga gac atg cac gtt gta gca      425
Pro Ala Ser Ala Ser Glu Lys Ser His Arg Asp Met His Val Val Ala
                               55                               60                               65

aaa atc aaa tcc gga aac tgc ttg ttt cag aga aag aaa tga agttgtc      474
Lys Ile Lys Ser Gly Asn Cys Leu Phe Gln Arg Lys Lys *
                               70                               75                               80

ttttaaagaa aaactgaatt aggaggagag aaaagggaaa taggagaaga aaggaaaagt      534
taaatttgat ttttctccag agtttccact aaagggttgg ggacagtgtg aaggagaagg      594
ggagcttttt acaaatacct ttggtctctg aacttcagtg gcaaagaaca gggatcaagt      654
tgaatgttct cagggctttg gacccatagag gagaaacaat cagaagagca gaaatggtta      714
tccctgttta aaataagccc tcactcttta ccacttcctt aaaggagtgg aggtgctggt      774
agtgatgggt agaggcaatg agggacggag aagttgctcc cgtttcagag atgctt      830

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<210> 294
 <211> 757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (493)..(735)

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<400> 294
taaaaaaaca actcagactg aacccatgtg aaaaaaccta cctaaaatca gaacatacat      60

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acgaggcaac ctcgaggaaa ccacccttat aatggccaag aacaggattg acgattacaa 120
tctcagctgg cctgtcatat aaaacatact gtcattgagc ttaagctccg cttgttctga 180
ggtttcacct ccatgtgttt cattgggtgca aaagtggatc tcttagttgg tcacttaatt 240
ctttcttttt cagaaagata ggatgttcac tggatatattt ggtcactctt agaaccttcc 300
ttcacattgt tttttatggg acccatgaat ggtagcctt tcttttctat tgtagaagga 360
aataaatagg agtaaaaaga ccattgtagt aaataagttc aaggggaact tgggaccaga 420
aaccactggt atgtacaaaa aaatggcaaa ttcaataaac tcaaatttaa aataattttt 480
aaattaacag tt      atg ata aat ttt ata ttt tat aca aat aga ttg ctt 528
                    Met Ile Asn Phe Ile Phe Tyr Thr Asn Arg Leu Leu
                      1             5             10

aga atg gtt ctc aag aat tat aag aga aat gaa ctc aca gta caa aaa 576
Arg Met Val Leu Lys Asn Tyr Lys Arg Asn Glu Leu Thr Val Gln Lys
      15             20             25

ttt tat aat tac tat act tgt gtt ttg ttt ggg ggc tgg gaa atg tat 624
Phe Tyr Asn Tyr Tyr Thr Cys Val Leu Phe Gly Gly Trp Glu Met Tyr
      30             35             40

ttt tac att gta gcc aat cat ttt ata ttt gtc aat tta aat ctt atg 672
Phe Tyr Ile Val Ala Asn His Phe Ile Phe Val Asn Leu Asn Leu Met
      45             50             55             60

ggg ctt ttt ttt tta tct ctc ttg atg tca gat ttt ata gtc ttt tta 720
Gly Leu Phe Phe Leu Ser Leu Leu Met Ser Asp Phe Ile Val Phe Leu
      65             70             75

aat aaa tcc att taa ttaaaacggt aaaaaaaaaa aa 757
Asn Lys Ser Ile *
      80

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<210> 295
 <211> 2388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (125)..(1258)

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caagcaactg gattgaacac cctaagaaga aagattcaca ctgcaccagg agacatcaga 120
aaga atg aaa act ctg ccg ctg ttt gtg tgc atc tgt gca ctg agt gct 169

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Met	Lys	Thr	Leu	Pro	Leu	Phe	Val	Cys	Ile	Cys	Ala	Leu	Ser	Ala		
1				5					10					15		
tgc	ttc	tcg	ttc	agt	gaa	ggg	cga	gaa	agg	gat	cat	gaa	cta	cgt	cac	217
Cys	Phe	Ser	Phe	Ser	Glu	Gly	Arg	Glu	Arg	Asp	His	Glu	Leu	Arg	His	
				20					25					30		
aga	agg	cat	cat	cac	caa	tca	ccc	aaa	tct	cac	ttt	gaa	tta	cca	cat	265
Arg	Arg	His	His	His	Gln	Ser	Pro	Lys	Ser	His	Phe	Glu	Leu	Pro	His	
				35					40					45		
tat	cct	gga	ctg	cta	gct	cac	cag	aag	ccg	ttc	att	aga	aag	tcc	tat	313
Tyr	Pro	Gly	Leu	Leu	Ala	His	Gln	Lys	Pro	Phe	Ile	Arg	Lys	Ser	Tyr	
		50					55					60				
aaa	tgt	ctg	cac	aaa	cgc	tgt	agg	cct	aag	ctt	cca	cct	tca	cct	aat	361
Lys	Cys	Leu	His	Lys	Arg	Cys	Arg	Pro	Lys	Leu	Pro	Pro	Ser	Pro	Asn	
	65					70					75					
aac	ccc	ccc	aaa	ttc	cca	aat	cct	cac	cag	cca	cct	aaa	cat	cca	gat	409
Asn	Pro	Pro	Lys	Phe	Pro	Asn	Pro	His	Gln	Pro	Pro	Lys	His	Pro	Asp	
	80					85				90					95	
aaa	aat	agc	agt	gtg	gtc	aac	cct	acc	tta	gtg	gct	aca	acc	caa	att	457
Lys	Asn	Ser	Ser	Val	Val	Asn	Pro	Thr	Leu	Val	Ala	Thr	Thr	Gln	Ile	
				100					105					110		
cca	tct	gtg	act	ttc	cca	tca	gct	tcc	acc	aaa	att	act	acc	ctt	cca	505
Pro	Ser	Val	Thr	Phe	Pro	Ser	Ala	Ser	Thr	Lys	Ile	Thr	Thr	Leu	Pro	
			115					120					125			
aat	gtg	act	ttt	ctt	ccc	cag	aat	gcc	acc	acc	ata	tct	tca	aga	gaa	553
Asn	Val	Thr	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Thr	Ile	Ser	Ser	Arg	Glu	
		130					135					140				
aat	gtt	aac	aca	agc	tct	tct	gta	gct	aca	tta	gca	cca	gtg	aat	tcc	601
Asn	Val	Asn	Thr	Ser	Ser	Ser	Val	Ala	Thr	Leu	Ala	Pro	Val	Asn	Ser	
	145					150					155					
cca	gct	cca	caa	gac	acc	aca	gct	gcc	cca	ccc	aca	cct	tct	gca	act	649
Pro	Ala	Pro	Gln	Asp	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Ser	Ala	Thr	
	160				165					170					175	
aca	cca	gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	697
Thr	Pro	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	
				180					185					190		
cca	ccc	aca	cct	tct	gca	act	aca	caa	gct	cca	cca	tct	tcc	tca	gct	745
Pro	Pro	Thr	Pro	Ser	Ala	Thr	Thr	Gln	Ala	Pro	Pro	Ser	Ser	Ser	Ala	
			195					200					205			
cca	cca	gag	acc	aca	gct	gcc	cca	ccc	aca	cct	cct	gca	act	aca	caa	793
Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Thr	Gln	
		210					215					220				
gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	cca	ccc	841
Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	

225	230	235	
aca cct cct gca act	aca cca gct cca cca tct tcc tca gct cca cca		889
Thr Pro Pro Ala Thr	Thr Pro Ala Pro Pro Ser Ser Ser Ala Pro Pro		
240	245	250	255
gag acc aca gct gtc cca ccc aca cct tct gca act acc cta gac cca			937
Glu Thr Thr Ala Val	Pro Pro Thr Pro Ser Ala Thr Thr Leu Asp Pro		
260	265		270
tca tcc gcc tca gct cca cca gag acc aca gct gcc cca ccc aca cct			985
Ser Ser Ala Ser Ala	Pro Pro Glu Thr Thr Ala Ala Pro Pro Thr Pro		
275	280		285
tct gca act aca cca gct cca ccg tct tcc cca gct cca caa gag acc			1033
Ser Ala Thr Thr	Pro Ala Pro Pro Ser Ser Pro Ala Pro Gln Glu Thr		
290	295		300
aca gct gcc cca att acc aca cct aat tct tcc cca act act ctt gca			1081
Thr Ala Ala Pro Ile Thr	Thr Pro Asn Ser Ser Pro Thr Thr Leu Ala		
305	310		315
cct gac act tct gaa act tca gct gca ccc aca cac cag act act act			1129
Pro Asp Thr Ser Glu Thr	Ser Ala Ala Pro Thr His Gln Thr Thr Thr		
320	325		330
tcg gtc act act caa act act act act aaa caa cca act tca gct cct			1177
Ser Val Thr Thr Gln Thr Thr Thr Thr Lys Gln Pro Thr Ser Ala Pro			
340	345		350
ggc caa aat aaa att tct cga ttt ctt tta tat atg aag aat cta cta			1225
Gly Gln Asn Lys Ile Ser Arg Phe Leu Leu Tyr Met Lys Asn Leu Leu			
355	360		365
aac aga att att gac gac atg gtg gag caa tag tatattgt atgttgtaaa			1276
Asn Arg Ile Ile Asp Asp Met Val Glu Gln *			
370	375		
gtgttctgtc atttacaaga tgtgattcat gagtgcagaa ctaccacctt tcttttagca			1336
ccaatcccaa catgaaatta tattactcag atttaaagca ctatcattaa tctttcaatc			1396
taattattca ccaccacaag acctattaac aagacaaaat gcctctatcc cacaagccag			1456
atgcaggtct ggggttcaaa ataactcttt ggatcctaca gagatagcct actgagggca			1516
gagaaagtcc ttagataaag agagaatatt gtatgggcca tcaaccattt acttttccct			1576
gaatgttaga aactacaaaa ccactacctt gtaccccat caaaatccca cctgaaccat			1636
ctaatectat aaacataaag gggtaaaatt ggaactctcc agatgaacaa agacatctaa			1696
atatctgtag atagaaacat ttatctatct aaatatattg atagacctgt cattgtattg			1756
attaatgaca aaacccttta gataattatc ttccatttta aataaaattt tatttcacaa			1816
atatgagcca agaaagagga aagttgattt gaagtgagga ttagaagtga atgacaataa			1876

Lys Val Thr His His Ile Gly Pro Ser Ile Leu Ala Leu Tyr Gln Asn
70 75 80

gtg gat aag cat cca gac tat gct tga caaat acaaatacgca tccaatatta 469
Val Asp Lys His Pro Asp Tyr Ala *
85 90

acacagaatt tccatggttt acaatagcag tggtaatccc aaatcatcct gtgaacgtct 529
cctggaatga ctccatagcc acacagaacc acatatggct tcagatagcc atggccctat 589
ttcacttttg tgctgcacca gctgagacct cagctgtagc aaccctcctc tgtccaccta 649
atgccgttta aagcccagcc cctggatttg tgaaccaa atcacatctact atcacagatg 709
agcatatattt tcaactgccc tatgcaccag gctgaatgaa actccccatc cactcccaaa 769
gtcatctcaa aatgtttatg aatccagaca gtgataaata g 810

<210> 297
<211> 883
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (495)..(833)

<400> 297
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ctccagaacc cccatcctct gggctctttt taggccccta gattggcctg cagctgggag 180
cagagtggca agcatgcagg caggcagttg agaaagagga agtcgaggtg ctattgggtc 240
attctgtggt tatcccaggc tctaccagc cagcggttcc cttgggccag ctcgaaacgc 300
tggccgtagg tcatgggagc tgcaggagct gttagccagg ctagggtgcct gcaggttgaa 360
gaactgagct ctatctggct ctgagcccaa gtcattgtgc cagccttttg actctggagc 420
tgtggcttca gccaccaaga gcagcagtg atcctggaaa cctgagaacc cagacttctt 480
ctctgccatg gggg atg atc agg agg atg att ttc cca ggc ggc tca gcg 530
Met Ile Arg Arg Met Ile Phe Pro Gly Gly Ser Ala
1 5 10

aga gta tgg agg acc tca gcc tgg att tgg ggg ccc ttc agg gca gcg 578
Arg Val Trp Arg Thr Ser Ala Trp Ile Trp Gly Pro Phe Arg Ala Ala
15 20 25

agt atc tgc agg acc tgg gcc ttg ggg ccc ctt ccc aca gcc agc ctg 626

Ser Ile Cys Arg Thr Trp Ala Leu Gly Pro Leu Pro Thr Ala Ser Leu
30 35 40

ggg aga ccc cag aca gcc gcc cca ccg gtg aag aac cag gaa gag att 674
Gly Arg Pro Gln Thr Ala Ala Pro Pro Val Lys Asn Gln Glu Glu Ile
45 50 55 60

ctc ttt tct cca gct tgg cag ggt ccc aag acc tgt caa ggc ggc gca 722
Leu Phe Ser Pro Ala Trp Gln Gly Pro Lys Thr Cys Gln Gly Gly Ala
65 70 75

act ggg aaa ggt cgc gga gct gct cac aga gct ggc gga ggc tca acc 770
Thr Gly Lys Gly Arg Gly Ala Ala His Arg Ala Gly Gly Gly Ser Thr
80 85 90

tcg atg cct cag ctg tgg atg agg aac cct gtc tcc ccc gaa cac tgg 818
Ser Met Pro Gln Leu Trp Met Arg Asn Pro Val Ser Pro Glu His Trp
95 100 105

cca gcc ttg ctt tga acctgccagg aggagggctg aagacctgga ctcaaggggtg 873
Pro Ala Leu Leu *

110

tctctctggg 883

<210> 298
<211> 1920
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (15)..(1664)

<400> 298

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Met Trp Phe Val Val Ile Pro Gln Ala Glu Tyr Glu
1 5 10

tgg gac gga aac agc caa gta gga att gga gac tac aga att cct aag 98
Trp Asp Gly Asn Ser Gln Val Gly Ile Gly Asp Tyr Arg Ile Pro Lys
15 20 25

gcg atg ctc aca ttc ttg aat gga agt aga att cct gtc act gag aaa 146
Ala Met Leu Thr Phe Leu Asn Gly Ser Arg Ile Pro Val Thr Glu Lys
30 35 40

gca cct cat aaa gga att att aga gat tca acc tgt aag tac ctt cca 194
Ala Pro His Lys Gly Ile Ile Arg Asp Ser Thr Cys Lys Tyr Leu Pro
45 50 55 60

gag tgg cag agc tat cag tgc ttt ggg atg gaa tat gca atg atg gtt 242
Glu Trp Gln Ser Tyr Gln Cys Phe Gly Met Glu Tyr Ala Met Met Val
65 70 75

att gaa agt ctg gat cct gac aca gaa act cga aga ctt tcc cca gtg Ile Glu Ser Leu Asp Pro Asp Thr Glu Thr Arg Arg Leu Ser Pro Val 80 85 90	290
gct ata atg ggc aac ggt tat gtt gat ctt att aat ggc cca cag gat Ala Ile Met Gly Asn Gly Tyr Val Asp Leu Ile Asn Gly Pro Gln Asp 95 100 105	338
cat ggc tgg tgt gct gga tat aca tgc cag aga agg ctg tcc ctg ttt His Gly Trp Cys Ala Gly Tyr Thr Cys Gln Arg Arg Leu Ser Leu Phe 110 115 120	386
cac agc att gtg gct ctg aac aaa tct tat gaa gtt tac ttc act ggc His Ser Ile Val Ala Leu Asn Lys Ser Tyr Glu Val Tyr Phe Thr Gly 125 130 135 140	434
acc agt cct cag aat ctt cga ctg atg ttg ctt aat gtt gat cat aac Thr Ser Pro Gln Asn Leu Arg Leu Met Leu Leu Asn Val Asp His Asn 145 150 155	482
aag gct gtt cta gta gga att ttc ttt tcc aca ctt caa cgt ttg gat Lys Ala Val Leu Val Gly Ile Phe Phe Ser Thr Leu Gln Arg Leu Asp 160 165 170	530
gtc tat gtg aac aac tta ttg gtc tgt cca aaa act aca ata tgg aat Val Tyr Val Asn Asn Leu Leu Val Cys Pro Lys Thr Thr Ile Trp Asn 175 180 185	578
gcc cag cag aaa cac tgt gaa ctt aat aac cat ctg tac aaa gac caa Ala Gln Gln Lys His Cys Glu Leu Asn Asn His Leu Tyr Lys Asp Gln 190 195 200	626
ttc ctt cct aac ctg gat tcc act gtc ctt ggt gaa aac tac ttt gat Phe Leu Pro Asn Leu Asp Ser Thr Val Leu Gly Glu Asn Tyr Phe Asp 205 210 215 220	674
gga acc tac cag atg ctt tat ctt ttg gtt aaa gga act ata cct gtt Gly Thr Tyr Gln Met Leu Tyr Leu Leu Val Lys Gly Thr Ile Pro Val 225 230 235	722
gaa att cac act gcc aca gtg ata ttt gtt tct ttc caa tta tct gtt Glu Ile His Thr Ala Thr Val Ile Phe Val Ser Phe Gln Leu Ser Val 240 245 250	770
gca aca gaa gat gac ttt tat acc tct cac aat ctg gtt aaa aat ctt Ala Thr Glu Asp Asp Phe Tyr Thr Ser His Asn Leu Val Lys Asn Leu 255 260 265	818
gcc ttg ttc cta aag ata cca agt gac aaa atc cgt atc agc aaa ata Ala Leu Phe Leu Lys Ile Pro Ser Asp Lys Ile Arg Ile Ser Lys Ile 270 275 280	866
aga ggg aag agt ctg agg agg aag aga tcc atg gga ttc ata att gaa Arg Gly Lys Ser Leu Arg Arg Lys Arg Ser Met Gly Phe Ile Ile Glu 285 290 295 300	914

ata Ile	gag Glu	att Ile	gga Gly	gac Asp 305	cct Pro	cct Pro	att Ile	cag Gln	ttc Phe 310	ata Ile	agc Ser	aat Asn	ggc Gly	acc Thr 315	aca Thr	962
ggt Gly	cag Gln	atg Met	cag Gln 320	tta Leu	tct Ser	gaa Glu	ctc Leu	cag Gln 325	gaa Glu	att Ile	gct Ala	ggt Gly	tct Ser 330	ctt Leu	gga Gly	1010
caa Gln	gct Ala	gta Val 335	att Ile	tta Leu	gga Gly	aac Asn	atc Ile 340	agt Ser	agt Ser	atc Ile	ctt Leu	gga Gly 345	ttt Phe	aac Asn	att Ile	1058
tcg Ser	tcc Ser	atg Met 350	tct Ser	att Ile	act Thr	aat Asn 355	ccc Pro	ctc Leu	ccc Pro	agc Ser	cca Pro 360	agt Ser	gac Asp	tct Ser	ggg Gly	1106
tgg Trp 365	att Ile	aat Asn	gtg Val	act Thr 370	gcc Ala	cag Gln	cca Pro	gtt Val	gaa Glu	agg Arg 375	tct Ser	gca Ala	ttt Phe	cct Pro	gtt Val 380	1154
cat His	cac His	gtg Val	gcc Ala	ttc Phe 385	gtg Val	tcc Ser	tca Ser	ctc Leu	tta Leu 390	gtg Val	atc Ile	act Thr	cag Gln	ccg Pro 395	gtg Val	1202
gca Ala	gca Ala	cag Gln	cca Pro 400	gga Gly	cag Gln	cca Pro	ttt Phe	cct Pro 405	cag Gln	cag Gln	cct Pro	tcg Ser	gta Val 410	aag Lys	gca Ala	1250
aca Thr	gat Asp	tct Ser 415	gac Asp	ggg Gly	aac Asn	tgt Cys	gta Val 420	tca Ser	gtt Val	gga Gly	att Ile	act Thr 425	gca Ala	cta Leu	act Thr	1298
ttg Leu	agg Arg 430	gcc Ala	ata Ile	ctc Leu	aag Lys	gac Asp 435	tcc Ser	aat Asn	aat Asn	aac Asn	caa Gln 440	gtc Val	aat Asn	ggc Gly	ctt Leu	1346
agt Ser 445	gga Gly	aat Asn	aca Thr	aca Thr 450	att Ile	ccg Pro	ttt Phe	agc Ser	agc Ser	tgt Cys 455	tgg Trp	gcc Ala	aac Asn	tac Tyr	aca Thr 460	1394
gac Asp	ctt Leu	act Thr	ccc Pro	ctt Leu 465	aga Arg	aca Thr	gga Gly	aaa Lys	aat Asn 470	tat Tyr	aag Lys	att Ile	gaa Glu	ttt Phe 475	ata Ile	1442
ctg Leu	gat Asp	aat Asn	gtt Val 480	gtt Val	ggg Gly	gta Val	gaa Glu	tcc Ser 485	aga Arg	act Thr	ttc Phe	agc Ser	ctg Leu 490	ctg Leu	gca Ala	1490
gag Glu	tct Ser	gtc Val 495	tct Ser	agc Ser	agt Ser	ggc Gly	agc Ser 500	agc Ser	agc Ser	agc Ser	agc Ser	aac Asn 505	agc Ser	aaa Lys	gca Ala	1538
tca Ser	act Thr 510	gtg Val	ggt Gly	aca Thr	tat Tyr	gcc Ala 515	cag Gln	ata Ile	atg Met	act Thr 520	gta Val	gta Val	att Ile	agc Ser	tgt Cys	1586
ctg	gtt	gga	aga	atg	tgg	ctc	ttg	gaa	ata	ttt	atg	gct	gca	gtt	tca	1634

Leu Val Gly Arg Met Trp Leu Leu Glu Ile Phe Met Ala Ala Val Ser
525 530 535 540

act ttg aat ata act tta aga agc tac taa a gtgctgttcc gaagaatagg 1685
Thr Leu Asn Ile Thr Leu Arg Ser Tyr *
545 550

ctgaaacaaa aatataagaa ttattagcta ctttggtggg caataggcaa aagtctatag 1745
cattttcatg aaaatataact aaaaatattt ttatgatata taaaatgtac taattagctt 1805
taaacactaa aatcagattt cttcaaaata taaatttgtt ttgattcttt atatttatat 1865
gtttttattt catttcaata aacttccaga aatttgtcat ttgaaaaaaaa aaaaa 1920

<210> 299
<211> 573
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (191)..(379)

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ccctttcctc agttgccacc aaggtgcttg gtccttccga ggaagctaag gccacattgg 120
ggtgaggcca tcacttcata cagtgactag caccacctct ggcaatgtca gccccacact 180
cgccccgcgcc atg gcc tcc atc tcc gag ctt gcc tgt gtc tac ttg gcc 229
Met Ala Ser Ile Ser Glu Leu Ala Cys Val Tyr Leu Ala
1 5 10

ctc att ctg cac gat gac gag gtg atc atc atg gag gtt aat atc aat 277
Leu Ile Leu His Asp Asp Glu Val Ile Ile Met Glu Val Asn Ile Asn
15 20 25

acc ctc att aaa gca gcc agt gta aat gtt gaa cct ttt ggc ctg gct 325
Thr Leu Ile Lys Ala Ala Ser Val Asn Val Glu Pro Phe Gly Leu Ala
30 35 40 45

tgt ttg gaa agg ccc tgg cca acg tca aca ttg gaa gcc tca tct gca 373
Cys Leu Glu Arg Pro Trp Pro Thr Ser Thr Leu Glu Ala Ser Ser Ala
50 55 60

atg tag gggctggtgg acctgctcta gcagctggtg ctgcaccagc aggaggtcct 429
Met *

gccccctcca ttgctgctgc ttcagctgag gagaagaaaa tggaagcaaa gaaagaagaa 489

tctgaggagt ctgatgatga catgggcttt ggtcttttta ctaaacctgt tttataatgt 549

[illegible]

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<220>
<221> CDS
<222> (247)..(1245)
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ggtaagcccg cctcctccct cggccggccc tggggccgtg tccgccgggc aactccagcc 180

ggcccc atg gtg ggt ttc ggg gcc aac cgg cgg gct ggc cgc ctg ccc 288
Met Val Gly Phe Gly Ala Asn Arg Arg Ala Gly Arg Leu Pro
 1 5 10

tct	ctc	gtg	ctg	gtg	gtg	ctg	ctg	gtg	gtg	atc	gtc	gtc	ctc	gcc	ttc	336
Ser	Leu	Val	Leu	Val	Val	Leu	Leu	Val	Val	Ile	Val	Val	Leu	Ala	Phe	
15					20					25					30	

aac tac tgg agc atc tcc tcc cgc cac gtc ctg ctt cag gag gag gtg 384
Asn Tyr Trp Ser Ile Ser Ser Arg His Val Leu Leu Gln Glu Glu Val
35 40 45

gcc gag ctg cag ggc cag gtc cag cgc acc gaa gtg gcc cgc ggg cgg 432
Ala Glu Leu Gln Gly Gln Val Gln Arg Thr Glu Val Ala Arg Gly Arg
50 55 60

ctg gaa aag cgc aat tcg gac ctc ttg ctg ttg gtg gac acg cac aag 480
Leu Glu Lys Arg Asn Ser Asp Leu Leu Leu Leu Val Asp Thr His Lys
65 70 75

aaa cag atc gac cag aag gag gcc gac tac ggc cgc ctc agc agc cgg 528
Lys Gln Ile Asp Gln Lys Glu Ala Asp Tyr Gly Arg Leu Ser Ser Arg
80 85 90

ctg cag gcc aga gag ggc ctc ggg aag aga tgc gag gat gac aag gtt 576
Leu Gln Ala Arg Glu Gly Leu Gly Lys Arg Cys Glu Asp Asp Lys Val
95 100 105 110

aaa cta cag aac aac ata tcg tat cag atg gca gac ata cat cat tta 624
Lys Leu Gln Asn Asn Ile Ser Tyr Gln Met Ala Asp Ile His His Leu
115 120 125

aag gag caa ctt gct gag ctt cgt cag gaa ttt ctt cga caa gaa gac 672

Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp	
130 135 140	
cag ctt cag gac tat agg aag aac aat act tac ctt gtg aag agg tta	720
Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu	
145 150 155	
gaa tat gaa agt ttt cag tgt gga cag cag atg aag gaa ttg aga gca	768
Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala	
160 165 170	
cag cat gaa gaa aat att aaa aag tta gca gac cag ttt tta gag gaa	816
Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu	
175 180 185 190	
caa aag caa gag acc caa aag att caa tca aat gat gga aag gaa ttg	864
Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu	
195 200 205	
gat ata aac aat caa gta gta cct aaa aat att cca aaa gta gct gag	912
Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu	
210 215 220	
aat gtt gca gat aag aat gaa gaa ccc tca agc aat cat att cca cat	960
Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His	
225 230 235	
ggg aaa gaa caa atc aaa aga ggt ggt gat gca ggg atg cct gga ata	1008
Gly Lys Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile	
240 245 250	
gaa gag aat gac cta gca aaa gtt gat gat ctt ccc cct gct tta agg	1056
Glu Glu Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg	
255 260 265 270	
aag cct cct att tca gtt tct caa cat gaa agt cat caa gca atc tcc	1104
Lys Pro Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser	
275 280 285	
cat ctt cca act gga caa gct ctc tcc cca aat atg cct cca gat tca	1152
His Leu Pro Thr Gly Gln Ala Leu Ser Pro Asn Met Pro Pro Asp Ser	
290 295 300	
cac att aaa cac aat gga aac ccc ggt act tca aaa aca gaa tcc ttc	1200
His Ile Lys His Asn Gly Asn Pro Gly Thr Ser Lys Thr Glu Ser Phe	
305 310 315	
cag tcc tct tca gcg ttt aat tcc agg ctc aaa ctt gga cag tag aac	1248
Gln Ser Ser Ser Ala Phe Asn Ser Arg Leu Lys Leu Gly Gln *	
320 325 330	
ccagaaattc caaacagatt atactaaagg caggttacca aggacagaag ccggggattc	1308
ccataaaatt ggcaccaatg tgaacacaga gagctcgtaa actgggtcct ggaccttggc	1368
agcacgcttc accgacgtcc tcaaaacca gaggacacac tcgaaaacga aaagggggcg	1428

aaccgcaaca cccacggccc ccccgacccg gaagggacga aagacaggggt acaccaggac 1488
acacaaaatg gcaaaacaaa ggcaacacgc tccaagaaag aacagccata cacaaaagaa 1548
caaaagcgcac cacaccaaac aaccccgcac gaaccaacac cacaccaaga catgtcaaca 1608
aacaagacca cataggagac gacaacgcaa agacaccgat cgagtaaccc caaagccacc 1668
aaaccaccaa cggacaccca ctgccagcc tgtatcattc ctactagaca 1718

<210> 301
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(348)

<400> 301
tcttttcaca tgattactgg ccatttgtat accttctgtg gaaatgtgggt aacacccttt 60
gctgatttta aaatagggtt atttgtttat tattgagttg aaataattcc ttcttttgag 120
tgtcagtgac tgaggttcgc tgtgacacag aggggttctc ctggagagct atggcac 177
atg ctc cat att aaa agg caa cat gat gct cgc tcc acc cag agg ccc 225
Met Leu His Ile Lys Arg Gln His Asp Ala Arg Ser Thr Gln Arg Pro
1 5 10 15
cgg tcc ccg cca ttc att ccg ctc ccg gcc gag agt cgc tct agc caa 273
Arg Ser Pro Pro Phe Ile Pro Leu Pro Ala Glu Ser Arg Ser Ser Gln
20 25 30
tca cct tcc agg ctc agg gcg gcc gag gca ggg cct ctg cct ctt cgg 321
Ser Pro Ser Arg Leu Arg Ala Ala Glu Ala Gly Pro Leu Pro Leu Arg
35 40 45
ggg gcc tct ccc tcc ccc tgc ccc tga ttgtg gctgaactgc caccgcttga 373
Gly Ala Ser Pro Ser Pro Cys Pro *
50 55
tagcaaacca cactcggcac aggaaggaga acagcgcccg cggcacgaaa 423

<210> 302
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (44)..(343)

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<400> 302
agggctcaag gaagccccc aa gtccagtctg cccagaaccg agc  atg tca tct ccc      55
                                         Met Ser Ser Pro
                                         1

ccg cca aga cgc tcc aac cgc cgc aat cct tgt cca tca ggc atc cag      103
Pro Pro Arg Arg Ser Asn Arg Arg Asn Pro Cys Pro Ser Gly Ile Gln
  5              10              15              20

gcc aga aac tct ggc tgc ccc cac ctc ccc aat ggt ccc cat caa gta      151
Ala Arg Asn Ser Gly Cys Pro His Leu Pro Asn Gly Pro His Gln Val
              25              30              35

ggt aac atc ctg ctg att tta act cct gtg cag ccc tca aat gca caa      199
Gly Asn Ile Leu Leu Ile Leu Thr Pro Val Gln Pro Ser Asn Ala Gln
              40              45              50

ctg cct ccc att cct gca cag tgc ccc agt tca ggc ctt cac cac ctt      247
Leu Pro Pro Ile Pro Ala Gln Cys Pro Ser Ser Gly Leu His His Leu
              55              60              65

gtt cct ggg cca ctg ccc aag tct ccc ccg act ggt ggc tgg act tct      295
Val Pro Gly Pro Leu Pro Lys Ser Pro Pro Thr Gly Gly Trp Thr Ser
              70              75              80

aat act ttt cca act ccc cac tca tta aat cca tcc ccc tct cat taa      343
Asn Thr Phe Pro Thr Pro His Ser Leu Asn Pro Ser Pro Ser His *
              85              90              95              100

ctggtgggaa ttgaggaaaa ctgagttcca gccttgtcat cctcatactc atgacccttc      403

caggc                                                                    408

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<210> 303
<211> 822
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (69)..(590)

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<400> 303
cagatcaaga cacaggagaa gagtgcaaaa atactgatca ggaagagtct accatttcat      60

ccaaggaa atg cca caa tca ttt tct gca atc aca tta agt aac aca gag      110
Met Pro Gln Ser Phe Ser Ala Ile Thr Leu Ser Asn Thr Glu
  1              5              10

atg aat aat att aat act aat gcc ccg aga aac aaa ctt cca ata aag      158
Met Asn Asn Ile Asn Thr Asn Ala Pro Arg Asn Lys Leu Pro Ile Lys
  15              20              25              30

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gaa ctt ggt aaa gtt tct aaa cat aaa att gcc act aaa aga aca cca	206
Glu Leu Gly Lys Val Ser Lys His Lys Ile Ala Thr Lys Arg Thr Pro	
35 40 45	
cat aaa gaa gat gag gca atg agc tgt tct gaa aat tgt tcg agt gcc	254
His Lys Glu Asp Glu Ala Met Ser Cys Ser Glu Asn Cys Ser Ser Ala	
50 55 60	
cag ggc gac tca ctt cag gat gag tct caa ggg tct cat tct gag tcc	302
Gln Gly Asp Ser Leu Gln Asp Glu Ser Gln Gly Ser His Ser Glu Ser	
65 70 75	
agc tct aat ccc tcc aat cct gaa act ttg cat gca aag gca act gat	350
Ser Ser Asn Pro Ser Asn Pro Glu Thr Leu His Ala Lys Ala Thr Asp	
80 85 90	
tca gtt cta caa ggt tct gaa gga aac aag gtc aag agg aca tcc tgc	398
Ser Val Leu Gln Gly Ser Glu Gly Asn Lys Val Lys Arg Thr Ser Cys	
95 100 105 110	
atg tat ggg gca aac tgc tat agg aag aat cct gtt cat ttt caa cat	446
Met Tyr Gly Ala Asn Cys Tyr Arg Lys Asn Pro Val His Phe Gln His	
115 120 125	
ttt agc cat cct ggt gat agt gat tat gga ggt gta caa atc gtg ggc	494
Phe Ser His Pro Gly Asp Ser Asp Tyr Gly Gly Val Gln Ile Val Gly	
130 135 140	
caa gat gag act gat gac cgg cct gaa tgt ccc tat gga cca tcc tgt	542
Gln Asp Glu Thr Asp Asp Arg Pro Glu Cys Pro Tyr Gly Pro Ser Cys	
145 150 155	
tat agg ttg gaa gtt cag tgt cca gtt gaa aaa cac caa ctc agc tag	590
Tyr Arg Leu Glu Val Gln Cys Pro Val Glu Lys His Gln Leu Ser *	
160 165 170	
ttttctctgg tctgcattac agtattttac ctgtcttttt atgaaaagag cacgttctag	650
gaaaggatgg aagatttctca aagaaacaac tttccccttc taaggcagat gaaaacctgt	710
acatgtacct aacattttttt ccccttttta aaatataaaa tttcacatta cattttctgc	770
tcttcctttt tggaataatt aaatgtaaca cttctttcat aaaaaaaaaa aa	822

<210> 304
 <211> 457
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (121)..(309)

 <400> 304

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tttgaaagct gattgatagc cgtaccgcac cgcaaaccac gggtcgaccc acgcgtccgc      60
ttcacttcac cttcactact tctgtagtct gatcttgtgt aatagagaac ccagccaact      120
atg aag ttc ctt gac ttt gct ttc atc ttg gct ctc aag gtt tcc atg      168
Met Lys Phe Leu Asp Phe Ala Phe Ile Leu Ala Leu Lys Val Ser Met
  1             5             10             15
att gga gct gat tcc tct gaa gag aaa ttt ttg cgt ata att gta cga      216
Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg Ile Ile Val Arg
             20             25             30
atc ggt tat ggg tat ggc cct tat cat tca gtt tca gaa caa cca cta      264
Ile Gly Tyr Gly Tyr Gly Pro Tyr His Ser Val Ser Glu Gln Pro Leu
             35             40             45
tac cca caa cca tac caa cca caa tac caa caa tat acc ttt taa tat      312
Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr Thr Phe *
             50             55             60
catcagtaac tgcaggacat gattattgag gcttgattgg ctgatacgac ttctacatcc      372
atattctcat gtttcatacc atatcgact actaccactt tttgaagaat catcatagag      432
ctttgcatat gagaaacact atatg                                           457

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<210> 305
 <211> 1749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85)..(873)

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<400> 305
ccgcgcgcgga attcccgggt cgaccacgc gtccgccgca gccccagct cgcccccaag      60
atgatgaaga ggcagctgca ccgc      atg cgg cag ctg gcc cag acg ggc agc      111
                                Met Arg Gln Leu Ala Gln Thr Gly Ser
                                1             5
ttg gga cgc acc ccg gag acc gct gag ttc ctg ggt gag gac ctg ctg      159
Leu Gly Arg Thr Pro Glu Thr Ala Glu Phe Leu Gly Glu Asp Leu Leu
  10             15             20             25
cag gta gaa cag cgg ctg gag ccg gcc aag cgg gca gcc cac aac atc      207
Gln Val Glu Gln Arg Leu Glu Pro Ala Lys Arg Ala Ala His Asn Ile
             30             35             40
cac aag cgg ctg cag gcc tgt ctg cag ggc cag agc ggg gca gac atg      255
His Lys Arg Leu Gln Ala Cys Leu Gln Gly Gln Ser Gly Ala Asp Met
             45             50             55

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gac aag cgg gtg aag aag ctt ccc ctc atg gct ctg tcc acc acg atg Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met 60 65 70	303
gct gag agc ctc aag gag ctg gac cct gat tcc agc atg ggg aag gcc Ala Glu Ser Leu Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala 75 80 85	351
ttg gag atg agc tgt gcc atc cag aat cag ctg gcc cgc atc ctg gcc Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala 90 95 100 105	399
gag ttt gag atg acc ctg gag agg gac gtc ctg cag cca ctc agc agg Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg 110 115 120	447
ctg agt gag gag gag ctg cca gcc atc ctc aaa cac aag aaa agc ctc Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu 125 130 135	495
cag aag ctc gtg tcc gac tgg aac aca ctc aag agc agg ctc agt cag Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln 140 145 150	543
gca acc aag aat tca ggc agc agt caa ggc cta gga ggc agc ccg ggt Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly 155 160 165	591
agt cac agc cat acg acc atg gcc aac aag gtg gag acg ctg aag gag Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu 170 175 180 185	639
gag gag gag gag ctg aag agg aaa gtg gag caa tgc agg gac gag tac Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr 190 195 200	687
ttg gct gac ctg tac cac ttt gtt acc aag gag gac tcc tat gcc aac Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn 205 210 215	735
tac ttc att cgt ctc ctg gag att cag gcc gat tac cat cgc agg tca Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser 220 225 230	783
ctg agc tcg ctg gac aca gcc ctg gct gag ctg agg gag aac cac ggc Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly 235 240 245	831
caa gca ggt ggg gac ata ggc ccg gcg ata cca cac ccc tga ccctgcc Gln Ala Gly Gly Asp Ile Gly Pro Ala Ile Pro His Pro * 250 255 260	880
ctgctcgggg cttattgaga agctcgact tcatcctgaa aggtagcagg aagctgtgga	940
tgggttctga gagctaggct caatctgtga tggagaggca gctctggcta ctgtgtggag	1000
ggtggagtga agcgggcagg actagagcca ggcctgtgag gcagaaggag gcaacggtgg	1060

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cctggactag gacagaggca gtggaggcgg gctgattcga gagatgtgac ggatgatttc 1120
agatgtgtgc ctggacagtc agtggcaggt ggtaccacct tgaggacatg aaggggggggt 1180
gccccctgect gactgctcgg ggtgggaagg ccctgggccg ctgatctgtt tcatccctgc 1240
agaccactcc ccttcgatga cagccacca cttccccagg gtgtatgggg tgctcgtggc 1300
aaccacctg caagagctgg gccgggagat tgccctgccc atcgaggcct gcgtcatgat 1360
gctgctttct gagggcatga aggaagaggg tctcttccgt ctggctgctg gggcctcggg 1420
gctgaagcgt gtcaagcaga caatggcctc ggaccccgac agcctggagg agttctgctc 1480
cgaccgcgac gctgtggcag gtgccctcaa gtcctatctg cgggagctgc cagagcctct 1540
gatgaccttc gacctctatg atgactggat gagggcagcc agcctgaagg agccaggggc 1600
ccggctgcag gccctccaag aggtgtgcag ccgcctaccc cccgagaacc tcagcaacct 1660
caggtacctg atgaagttcc tggcacggct ggccgaggag caggaggtga acaagacgaa 1720
atctcgacag cgaagtcgac ccgggaatt 1749

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<210> 306
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (55)..(372)

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<400> 306
aaggatcctt aattaaatta atccccccc ccgaaccgtt cgctaactga aatg  atg  57
                                     Met
                                     1

gcg act gga acg cca gag tct caa gcg cgg ttc ggt cag tcc gtg aag  105
Ala Thr Gly Thr Pro Glu Ser Gln Ala Arg Phe Gly Gln Ser Val Lys
      5                      10                      15

ggg ctt ctc acg gag aag gtg acc acc tgt ggt act gac gta atc gcg  153
Gly Leu Leu Thr Glu Lys Val Thr Thr Cys Gly Thr Asp Val Ile Ala
      20                      25                      30

ctc acc aag cag gtg ctg aaa ggc tcc cgg agc tcc gag ctg cta ggt  201
Leu Thr Lys Gln Val Leu Lys Gly Ser Arg Ser Ser Glu Leu Leu Gly
      35                      40                      45

cag gca gct cga aac atg gta ctc cag gaa gat gcc atc ttg cac tca  249
Gln Ala Ala Arg Asn Met Val Leu Gln Glu Asp Ala Ile Leu His Ser
      50                      55                      60                      65

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gaa gat agt tta agg aag atg gca ata ata aca aca cat ctt caa tac	297
Glu Asp Ser Leu Arg Lys Met Ala Ile Ile Thr Thr His Leu Gln Tyr	
70 75 80	
cag caa gaa gct att cag aag aat gtt gaa cag tca tcg gat cta cag	345
Gln Gln Glu Ala Ile Gln Lys Asn Val Glu Gln Ser Ser Asp Leu Gln	
85 90 95	
gac cag ttg aat cat ctg ttg aaa tag aatga catgtaagag tgctgtagga	397
Asp Gln Leu Asn His Leu Leu Lys *	
100 105	
ctcctttgcc taatgctgag gagtaaatac cttacacagc tgtcctctgg gtttggtttt	457
ctattttctt ctccaaaagt taagttagaa aagttcttg	496

<210> 307
 <211> 1438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(840)

<400> 307	
catggaggag gaaggagatg gcatggctta ccataaagaa gcactggacg ccggggtgcac	60
gttccaggat ccaggtgccc aggggtc atg aag ctg gga ctc ctc tgt gct	111
Met Lys Leu Gly Leu Leu Cys Ala	
1 5	
ctg ctc tct ctg ctg gca ggg cat ggc tgg gca gac acc cgt gcc atc	159
Leu Leu Ser Leu Leu Ala Gly His Gly Trp Ala Asp Thr Arg Ala Ile	
10 15 20	
ggg gcc gag gaa tgt cgc ccc aac tcc cag cct tgg cag gcc ggc ctc	207
Gly Ala Glu Glu Cys Arg Pro Asn Ser Gln Pro Trp Gln Ala Gly Leu	
25 30 35 40	
ttc cac ctt act cgg ctc ttc tgt ggg gcg acc ctc atc agt gac cgc	255
Phe His Leu Thr Arg Leu Phe Cys Gly Ala Thr Leu Ile Ser Asp Arg	
45 50 55	
tgg ctg ctc aca gct gcc cac tgc cgc aag ccg tat ctg tgg gtc cgc	303
Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Tyr Leu Trp Val Arg	
60 65 70	
ctt gga gag cac cac ctc tgg aaa tgg gag ggt ccg gag cag ctg ttc	351
Leu Gly Glu His His Leu Trp Lys Trp Glu Gly Pro Glu Gln Leu Phe	
75 80 85	
cgg gtt acg gac ttc ttc ccc cac cct ggc ttc aac aag gac ctc agc	399

Arg	Val	Thr	Asp	Phe	Phe	Pro	His	Pro	Gly	Phe	Asn	Lys	Asp	Leu	Ser		
90						95					100						
gcc	aat	gac	cac	aat	gat	gac	atc	atg	ctg	atc	cgc	ctg	ccc	agg	cag	447	
Ala	Asn	Asp	His	Asn	Asp	Asp	Ile	Met	Leu	Ile	Arg	Leu	Pro	Arg	Gln		
105				110					115						120		
gca	cgt	ctg	agt	cct	gct	gtg	cag	ccc	ctc	aac	ctc	agc	cag	acc	tgt	495	
Ala	Arg	Leu	Ser	Pro	Ala	Val	Gln	Pro	Leu	Asn	Leu	Ser	Gln	Thr	Cys		
				125					130					135			
gtc	tcc	cca	ggc	atg	cag	tgt	ctc	atc	tca	ggc	tgg	ggg	gcc	gtg	tcc	543	
Val	Ser	Pro	Gly	Met	Gln	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ala	Val	Ser		
			140					145					150				
agc	ccc	aag	gcg	ctg	ttt	cca	gtc	aca	ctg	cag	tgt	gcc	aac	atc	agc	591	
Ser	Pro	Lys	Ala	Leu	Phe	Pro	Val	Thr	Leu	Gln	Cys	Ala	Asn	Ile	Ser		
		155					160					165					
atc	ctg	gag	aac	aaa	ctc	tgt	cac	tgg	gca	tac	cct	gga	cac	atc	tgc	639	
Ile	Leu	Glu	Asn	Lys	Leu	Cys	His	Trp	Ala	Tyr	Pro	Gly	His	Ile	Ser		
	170					175					180						
gac	agc	atg	ctc	tgt	gcg	ggc	ctg	tgg	gag	ggg	ggc	cga	ggg	tcc	tgc	687	
Asp	Ser	Met	Leu	Cys	Ala	Gly	Leu	Trp	Glu	Gly	Gly	Arg	Gly	Ser	Cys		
185					190					195					200		
cag	ggg	gac	tct	ggg	ggc	ccc	ctg	gtt	tgc	aat	gga	acc	ttg	gca	ggc	735	
Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Thr	Leu	Ala	Gly		
				205					210					215			
gtg	gtg	tct	ggg	ggg	gct	gag	ccc	tgc	tcc	aga	ccc	cgg	cgc	ccc	gca	783	
Val	Val	Ser	Gly	Gly	Ala	Glu	Pro	Cys	Ser	Arg	Pro	Arg	Arg	Pro	Ala		
			220					225					230				
gtc	tac	acc	agc	gta	tgc	cac	tac	ctt	gac	tgg	atc	caa	gaa	atc	atg	831	
Val	Tyr	Thr	Ser	Val	Cys	His	Tyr	Leu	Asp	Trp	Ile	Gln	Glu	Ile	Met		
		235					240					245					
gag	aac	tga	gcccgcg	cgccacg	gggg	gcaccttgga	agaccaagag	aggccgaagg								887	
Glu	Asn	*															
	250																
gcacgggggta	gggggttctc	gtaggggtccc	agcctcaatg	gttcccgcgc	tggacctcca											947	
gctgccctga	ctcccctctg	gacactaaga	ctccgcccct	gaggctccgc	cccctcacga											1007	
ggtaagcaa	gacacagtcg	cgccccctcg	gaacggagca	gggacacgcc	cttcagagcc											1067	
cgtctctatg	acgtcaccga	cagccatcac	ctccttcttg	gaacagcaca	gcctgtggct											1127	
ccgccccaa	gaaccactta	cacaaaatag	ctccgcccct	cggaactttg	cccagtggga											1187	
cttcccctcg	ggactccacc	ccttgtggcc	ccgcctcctt	caccagagat	ctcgcctctc											1247	
gtgatgtcag	gggcgcagta	gctccgcca	cgtggagctc	gggcggtgta	gagctcagcc											1307	

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ccttgtggcc ccgtcctggg cgtgtgctgg gtttgaatcc tggcggagac ctggggggaa 1367
attgagggag ggtctggata cctttagagc caatgcaacg gatgattttt cagtaaacgc 1427
gggaaacctc a 1438

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<210> 308
<211> 675
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (110)..(613)

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<400> 308
taggagatcc ttagcggact gggatcttaa tgggtctcact gtgtttatct ctttgtaaag 60

gccagccctc acctgacttg tctgggtccc tcctggggct aggggatgg atg aga 115
Met Arg
1

agg gct agg ctg gag ctg tca gca gct tct tgg tgc ctg ctg ttt ctc 163
Arg Ala Arg Leu Glu Leu Ser Ala Ala Ser Trp Cys Leu Leu Phe Leu
5 10 15

ttg tct tgt ctg tct tcg gtg tat tgc aat cct gtc ctc tta gca ggc 211
Leu Ser Cys Leu Ser Ser Val Tyr Cys Asn Pro Val Leu Leu Ala Gly
20 25 30

ccc gca gag tca tac ttt ttc tcc ctg gcc ttc cag ctc cct ctc ttc 259
Pro Ala Glu Ser Tyr Phe Phe Ser Leu Ala Phe Gln Leu Pro Leu Phe
35 40 45 50

cac cca gta tgc cca cct ccc tct ccc ttg act acc cca gcc tct gcc 307
His Pro Val Cys Pro Pro Ser Pro Leu Thr Thr Pro Ala Ser Ala
55 60 65

caa tca cgc cct gcc ctc tac cct tca gag gac acc ttg ccg tct gtg 355
Gln Ser Arg Pro Ala Leu Tyr Pro Ser Glu Asp Thr Leu Pro Ser Val
70 75 80

gag ctg gag cta ttc cta tgg tct ctc tgg gtc cac atg acc tta cat 403
Glu Leu Glu Leu Phe Leu Trp Ser Leu Trp Val His Met Thr Leu His
85 90 95

ggc act cct ctc acc ttc tgt cca tcc aac aaa att ctc tgt tcc ttt 451
Gly Thr Pro Leu Thr Phe Cys Pro Ser Asn Lys Ile Leu Cys Ser Phe
100 105 110

gaa gct ctc ttt tca gta agg cct tcc ttg gcc cct aac agg atg gat 499
Glu Ala Leu Phe Ser Val Arg Pro Ser Leu Ala Pro Asn Arg Met Asp
115 120 125 130

```

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cac cct ccc ctg agc cct ggt cat tgc ctc tct gtt atg gcc tct cca 547
His Pro Pro Leu Ser Pro Gly His Cys Leu Ser Val Met Ala Ser Pro
      135              140              145

ttg gta aac gct ctg ccg atg tgt ttc atc ttc cca cta gat cct tgc 595
Leu Val Asn Ala Leu Pro Met Cys Phe Ile Phe Pro Leu Asp Pro Cys
      150              155              160

gcc cac gca cgc ggc tga atcatc ttacatccc cagaggccct ggtatgtggt 649
Ala His Ala Arg Gly *
      165

ggacaggcctt gtttctgccg ggcctt 675

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<210> 309
<211> 1042
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (779)..(952)

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gtccctact actactaaat tcgcggccgc gtcgacgttt aggggaggca tcaccagatt 60
aagagtggag atattagagt tgtgtgatcc cagctctgtc gttaatcacc tgtgtctatg 120
cagtcactta ttcccttcat acctgtcagc cgagagcact gactgcgtga tttccagggt 180
cctttacagc tttagagtat aggggctctg tttttgctgc tcccgaattt ccacctccca 240
tcatccacgc atttcacaga tgcattctgaa tgctcacagt gctctatttg tgcctttctg 300
tttgccctg ttttttatgt ggatgcgtat cgaccgccat gatagactgc aactccctg 360
tgggcaggag ccatgttcat ttcatTTTTG tgtcccaggc ataatgtagg tgcgctcacc 420
tcattctctc catatcttga acctgtgaat ctcagtggac tcttttcagc agatgaacct 480
gtataagtct ttctgtctt gaaaggacag atgggtggcc cccatcctcc actgagcttc 540
ctgttgaact ccttttgcag gtgacgtcaa aatagaagaa gccctcattc accatatcta 600
ctgttaccct cctcctttcc cctctacttc ccatgaccag ttgttccactg cccctccaca 660
gaacctactt ctgataaatc ccgtgaagaa ttttttattg ccagatccaa attctttggc 720
ctctcacagt gtttgcgtgtg gcctgattct cctcattct ggaaactcct ctctcttc 778
atg gct ccc atg gga cca gtt gct cct gca gct cct cct gcc cct cac 826
Met Ala Pro Met Gly Pro Val Ala Pro Ala Ala Pro Pro Ala Pro His
  1              5              10              15

tct gct ctc ctt gga ctc ctc ttt cct ggt att ctc tgc agt tct gtc 874

```



```

Ser Ala Leu Leu Gly Leu Leu Phe Pro Gly Ile Leu Cys Ser Ser Val
      20                      25                      30
ctt cgc tct cag ctc ttt gca ccc ttc ttt ccc tcg ctg aca gct tcg      922
Leu Arg Ser Gln Leu Phe Ala Pro Phe Phe Pro Ser Leu Thr Ala Ser
      35                      40                      45
cgc ata cct gtg gct tca ctg tca cgc taa g gaacattctc tgtggccctg      973
Arg Ile Pro Val Ala Ser Leu Ser Arg *
      50                      55
gcccgctctct cgagcctgag ccccatgatt acaacttctg tctgtacccc acagtacata      1033
accttagcc                                                                1042

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<210> 310
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<220>
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 <222> (43)..(555)

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                                   Met Arg Leu Pro
                                   1
gct cag ctc ctg ggg ctg cta atg ctc tgg gtc cct gga tcc agt gag      102
Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Glu
   5                      10                      15                      20
gat att gtg atg acc cag act cca ctc tcc ctg ccc gtc acc cct gga      150
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
                25                      30                      35
gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt      198
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
                40                      45                      50
gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag      246
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
                55                      60                      65
tct cca cag ctc ctg atc tat acg ctt tcc tat cgg gcc tct gga gtc      294
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
                70                      75                      80
cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa      342
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
   85                      90                      95                      100
atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa      390

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Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln	
105 110 115	
cgt ata gag ttt cct tgg act ttt ggc cag ggg acc aag ctg gag atc	438
Arg Ile Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
120 125 130	
aaa cga act gtt gct gca cca tct gtc ttc atc ttc ccg cca tct gat	486
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
135 140 145	
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	534
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
150 155 160	
ttc tat ccc aga gag gcc taa gt acagtggaaa gtggtaaacg gcctccaaac	587
Phe Tyr Pro Arg Glu Ala *	
165 170	
tggttaaadc cagtaaagtg tcacagagca agacagtaag gacagcacct acgtactcag	647
cagcaaccag aagctgagca aagttgactt atgagatacc acaagtctag gcctgacgaa	707
gtcaaccatt atggacttgg gctgtgtcca atctgaatat agttatacct gggcagagtg	767
gttaaaagggt atagtgtgtc ccctaaattg taccctaggt ttcaagctcg tagtcacttg	827
cccaggcttt ttgtcccttg taggtccttt tttcccaatg ggggaccta gacactaagt	887
gacgggactc tccaaagtta atgattttaa acttaaaatc actctctaag ggatcatcag	947
gagttatgaa gtcgatgact aattgttttt gatacagagta tatctgaaaa tgattgaaag	1007
tgtgaattcc tcatggtagg tgagataaac tagtcgttat agtatctagt agatgaccgg	1067
agcatttata gagtagaagt ccgcatactc ccggataatc taccacgaca catgattaga	1127
ctctcgcgat ggtaaacaga tggatgtaaa ctcaatcgtg ggagtaccga aagaggtggc	1187
tatgatgttg acatgatagg gtctaggatg cgtgatcgtg tgacggaatt gtcaaatacg	1247
tgtgaataca catttatttg caatttctgt atgacgtgat atgagattag cagaggttta	1307
tgaatgagtg acatcttgcg tgtggt	1333

<210> 311
 <211> 803
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
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 ggggtggtatt cctgcc atg ggt cct ggg ctt ctc cac tgg atg gcc ctt 109
 Met Gly Pro Gly Leu Leu His Trp Met Ala Leu
 1 5 10
 tgt ctc ctt gga aca ggt cat ggg gat gcc atg gtc atc cag aac cca 157
 Cys Leu Leu Gly Thr Gly His Gly Asp Ala Met Val Ile Gln Asn Pro
 15 20 25
 aga tac cag gtt acc cag ttt gga aag cca gtg acc ctg agt tgt tct 205
 Arg Tyr Gln Val Thr Gln Phe Gly Lys Pro Val Thr Leu Ser Cys Ser
 30 35 40
 cag act ttg aac cat aac gtc atg tac tgg tac cag cag aag tca agt 253
 Gln Thr Leu Asn His Asn Val Met Tyr Trp Tyr Gln Gln Lys Ser Ser
 45 50 55
 cag gcc cca aag ctg ctg ttc cac tac tat gac aaa gat ttt aac aat 301
 Gln Ala Pro Lys Leu Leu Phe His Tyr Tyr Asp Lys Asp Phe Asn Asn
 60 65 70 75
 gaa gca gac acc cct gat aac ttc caa tcc agg agg ccg aac act tct 349
 Glu Ala Asp Thr Pro Asp Asn Phe Gln Ser Arg Arg Pro Asn Thr Ser
 80 85 90
 ttc tgc ttt ctt gac atc cgc tca cca ggc ctg ggg gac gca gcc atg 397
 Phe Cys Phe Leu Asp Ile Arg Ser Pro Gly Leu Gly Asp Ala Ala Met
 95 100 105
 tac ctg tgt gcc acc agc gtc cac cgg gac cca tga acac tgaagctttc 447
 Tyr Leu Cys Ala Thr Ser Val His Arg Asp Pro *
 110 115
 tttggacaag gcaccagact cacagtgtga gcatgtgaaa aggtccagag ctctgcagtg 507
 tgagctttct actgaaatgg cccttggtact ttgtggttca ttcataactca gtggtctagc 567
 ttgtactact tttgagaatg caaagcttaa ctgtggacgg attccaatcc tggccaggca 627
 ggggttgctgg acactctgag agaagaaagg gttaatccca tgaccatcaa cttccatggg 687
 atttcagcca tcctggacaa gctaccacac cctcctgccc caaggggagg aggaaatgtg 747
 gaccatccca tcagaaattg accaaaggac ctgaacaagt ggtccccccc ccccc 803

<210> 312
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (6)..(605)

<400> 312

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	Met	Leu	Cys	Arg	Gln	Gln	Leu	Arg	Asn	Leu	Thr	Glu	Asn	Lys		
	1				5					10						
gaa	tct	gag	ttg	cag	tgt	ctc	ttt	caa	cag	ata	gaa	agg	cag	gag	cag	95
Glu	Ser	Glu	Leu	Gln	Cys	Leu	Phe	Gln	Gln	Ile	Glu	Arg	Gln	Glu	Gln	
	15				20					25					30	
ctt	ctg	gat	gaa	ata	cat	cgt	gag	aag	aga	gat	cta	ctg	gaa	gag	acc	143
Leu	Leu	Asp	Glu	Ile	His	Arg	Glu	Lys	Arg	Asp	Leu	Leu	Glu	Glu	Thr	
				35					40						45	
caa	aga	aaa	gat	gaa	gaa	atg	gga	tct	ctg	cag	gac	cgt	gta	att	gca	191
Gln	Arg	Lys	Asp	Glu	Glu	Met	Gly	Ser	Leu	Gln	Asp	Arg	Val	Ile	Ala	
			50					55					60			
tta	gaa	acg	agt	acc	caa	gtg	gcc	ttg	gac	cat	ctg	gag	tct	gtg	cct	239
Leu	Glu	Thr	Ser	Thr	Gln	Val	Ala	Leu	Asp	His	Leu	Glu	Ser	Val	Pro	
		65					70					75				
gag	aaa	ctg	agc	cta	cta	gaa	gat	ttc	aaa	gac	ttc	aga	gat	tcc	tgc	287
Glu	Lys	Leu	Ser	Leu	Leu	Glu	Asp	Phe	Lys	Asp	Phe	Arg	Asp	Ser	Cys	
	80					85					90					
agt	tca	tct	gag	aga	act	gat	gga	aga	tat	tcc	aaa	tac	agg	gtt	cgc	335
Ser	Ser	Ser	Glu	Arg	Thr	Asp	Gly	Arg	Tyr	Ser	Lys	Tyr	Arg	Val	Arg	
	95				100					105					110	
aga	aat	tct	ctt	cag	cat	cac	caa	gat	gac	acc	aag	tac	aga	acc	aaa	383
Arg	Asn	Ser	Leu	Gln	His	His	Gln	Asp	Asp	Thr	Lys	Tyr	Arg	Thr	Lys	
				115					120						125	
agt	ttc	aaa	ggt	gac	aga	acc	ttt	ctg	gaa	ggt	tcc	cac	act	cgt	ggg	431
Ser	Phe	Lys	Gly	Asp	Arg	Thr	Phe	Leu	Glu	Gly	Ser	His	Thr	Arg	Gly	
			130					135					140			
tta	gat	cac	tca	tcc	tct	tgg	cag	gat	cac	agt	cgc	ttc	ctg	tct	agt	479
Leu	Asp	His	Ser	Ser	Ser	Trp	Gln	Asp	His	Ser	Arg	Phe	Leu	Ser	Ser	
		145					150						155			
cca	aga	ttt	tca	tac	gtg	aac	tca	ttt	acc	aaa	aga	act	ggt	gct	cca	527
Pro	Arg	Phe	Ser	Tyr	Val	Asn	Ser	Phe	Thr	Lys	Arg	Thr	Val	Ala	Pro	
	160					165						170				
gat	tca	gct	tca	aac	aag	gaa	gat	gcc	aca	atg	aat	gga	aca	agt	tca	575
Asp	Ser	Ala	Ser	Asn	Lys	Glu	Asp	Ala	Thr	Met	Asn	Gly	Thr	Ser	Ser	
	175				180					185					190	
caa	ccc	aaa	aaa	gag	gaa	tat	ggg	agc	taa	a	aaagcaa	aatg	taatttg	ttta		626
Gln	Pro	Lys	Lys	Glu	Glu	Tyr	Gly	Ser	*							
				195					200							
ttttacatga	g	tatg	ttaca	a	ataata	aaca	t	ctctatt	tct	tacag	caaaa	aaaaaaaaa				686

<210> 313
 <211> 1157
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (714)..(947)

<400> 313

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tcagttgtaa cttattccta tttgtcagca ttcagggttat tagcggctgc tggcgaagtc      180
cttgagaaat aaactgcaca ctggatgggtg ggggtagtgt aggaaaatgg aggggaagga      240
agtaaagttt caaattaagc ctgaacagca aagttcccct gagaaggcca cctggattct      300
atcagaaact cgaatgtcca tcttgcaaaa cttccttgcc caaaccaccac ccctggagtc      360
acaaccacc cttgaccaat agattcattt cactgaggga ggcaaagggc tgggtcaatag      420
attcatttca ctgggagagg caaagggtg ggggccagag aggagaagta aaaagccaca      480
catgaagcag caatgcaggc atgcttctg ctcactctgtg atcaccagga aactcccaga      540
tctgacactg tagtgcattt cactgctgac aagaaggctg ctgccaccag cctgtgaagc      600
aagggttaagg tgagaaggct ggaggtgaga ttctgggcag tctcctgggt gtctacccat      660
ggacctagag gtactttgaa agttttggat atctgggctc tgactgtgca ata   atg      716
                                   Met
                                   1

ggc aac ccc aaa gtc aag gca cat ggc aag aag gtg ctg atc tcc ttc      764
Gly Asn Pro Lys Val Lys Ala His Gly Lys Lys Val Leu Ile Ser Phe
      5              10              15

gga aaa gct gtt atg ctc acg gat gac ctc aaa ggc acc ttt gct aca      812
Gly Lys Ala Val Met Leu Thr Asp Asp Leu Lys Gly Thr Phe Ala Thr
      20              25              30

ctg agt gac ctg cac tgt aac aag ctg cac gtg gac cct gag aac ttc      860
Leu Ser Asp Leu His Cys Asn Lys Leu His Val Asp Pro Glu Asn Phe
      35              40              45

ctg ctc tta ggc aac gtg ata ttg att gtt ttg gca acc cac ttc agc      908
Leu Leu Leu Gly Asn Val Ile Leu Ile Val Leu Ala Thr His Phe Ser
      50              55              60              65

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gag gat ttt acc cta cag ata cag gct tct tgg cag taa ctaacaaatg 957
 Glu Asp Phe Thr Leu Gln Ile Gln Ala Ser Trp Gln *
 70 75

ctgtgggttaa tgctgtagcc cacaagacca ctgagttccc tgtccactat gtttgtacct 1017
 atgggtccact atgtttgtac ctatgtccca aaatctcatc tccttttagat gggggagggtt 1077
 ggggagaaga gcagtatcct gectgtgat tcagttcctg catgataaaa atagaataaa 1137
 gaaatatgct ctctaagaaa 1157

<210> 314
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (219)..(479)

<400> 314
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 agatagtaaa aagagagtca gagaacagga accgcataaa aagttcttca ttttccatca 120
 cttggtggtg actttgaagg tagaggctga cagtgaagtgg agtatggaca tgtcaccac 180
 aaccagatga agaggggactc cgagatagcg actcggct atg cac aca gtc acc 233
 Met His Thr Val Thr
 1 5

cac aga gga gga gca ggg aag ggg gaa agt agc ctc tct cag cac atg 281
 His Arg Gly Gly Ala Gly Lys Gly Glu Ser Ser Leu Ser Gln His Met
 10 15 20

ata aaa aga cct gga tgg gga ggt gga gca gag gcc ttc act cca tca 329
 Ile Lys Arg Pro Gly Trp Gly Gly Gly Ala Glu Ala Phe Thr Pro Ser
 25 30 35

ttt ttt aaa tcc atc ctt caa tat ttt caa gag gaa ggg aaa cca gac 377
 Phe Phe Lys Ser Ile Leu Gln Tyr Phe Gln Glu Glu Gly Lys Pro Asp
 40 45 50

agg cca aac cac agc ctt cag tgg ggc ttg act tta gtt cta cgg acc 425
 Arg Pro Asn His Ser Leu Gln Trp Gly Leu Thr Leu Val Leu Arg Thr
 55 60 65

tca cca gcc att cca gca gct gaa tgc ctg cca gtt ggt gcc cac acg 473
 Ser Pro Ala Ile Pro Ala Ala Glu Cys Leu Pro Val Gly Ala His Thr
 70 75 80 85

cta tga gacccacaa ctgtgtgaga agctgggaac atttcacagg gaaaaagcag 529
 Leu *

aaatggaggg agtgaaaccc ctacttagtt tctgctgac ctccttgga gaga

583

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<213> Homo sapiens

<220>
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<222> (75)..(677)

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cccagagagga aggc atg cgg tgg gcc cta ctg gtg ctt cta gct ttc ctg 110
Met Arg Trp Ala Leu Val Leu Leu Ala Phe Leu
1 5 10

tct cct gcc agt cag aaa tct tcc aac ttg gaa ggg aga acg aag tca 158
Ser Pro Ala Ser Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser
15 20 25

gtc acc agg cag act ggg tca tct gct gaa atc act tgc gat ctt act 206
Val Thr Arg Gln Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr
30 35 40

gta aca aat acc ttc tac atc cac tgg tac cta cac cag gag ggg aag 254
Val Thr Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys
45 50 55 60

gcc cca cag cgt ctt ctg tac tat gac gtc tcc act gca agg gat gtg 302
Ala Pro Gln Arg Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val
65 70 75

ttg gaa tca gga ctc agt cca gga aag tat tat act cat aca ccc agg 350
Leu Glu Ser Gly Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg
80 85 90

agg tgg agc tgg ata ttg ata cta cga aat cta att gaa aat gat tct 398
Arg Trp Ser Trp Ile Leu Ile Leu Arg Asn Leu Ile Glu Asn Asp Ser
95 100 105

ggg gtc tat tac tgt gcc acc tgg gac agg cac agt gat tca gac ctg 446
Gly Val Tyr Tyr Cys Ala Thr Trp Asp Arg His Ser Asp Ser Asp Leu
110 115 120

tcc tac acc aca ctg aaa atc tgc ctt gtg gct gcc tct ggt tca cag 494
Ser Tyr Thr Thr Leu Lys Ile Cys Leu Val Ala Ala Ser Gly Ser Gln
125 130 135 140

gat aga gcc gcc ccc tct cat ttc ctg tca cca aat tta ctg tat tct 542
Asp Arg Ala Ala Pro Ser His Phe Leu Ser Pro Asn Leu Leu Tyr Ser

145	150	155	
gaa caa gag aaa gac agc tta act cct gat ctc cct cct aat atc aca			590
Glu Gln Glu Lys Asp Ser Leu Thr Pro Asp Leu Pro Pro Asn Ile Thr			
160	165	170	
ctg tcc tgg cag cag ctg cat cct gtt ccc cac ccc tcc ccc aca act			638
Leu Ser Trp Gln Gln Leu His Pro Val Pro His Pro Ser Pro Thr Thr			
175	180	185	
ttc ctg aag atc aag ctg cca tct cca ggc ctc agc taa gcagcctggc			687
Phe Leu Lys Ile Lys Leu Pro Ser Pro Gly Leu Ser *			
190	195	200	
tgagagcaag gttctctcag ctctcctagg acatggggga ggcccactca ctctgcttcc			747
tatgacacac aggtacaact aggggtccagc tgtgaagcga gatatttttg acagcaaattg			807
ggaaggggtat ttatactgaa tcatgtatcc actcatggtc cagagatcac agctgagagt			867
ggtgcttatt ccttatgtct ataacaacat aagcaatact ataatgacca ctaaaacact			927
aggc			931
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gaattgaaag tgaggatgac ttgtataaac tggatgaactt ctcccttaaa tatcgagctc			180
accgtttatc ttccagcctc cagatcaagc cctgcagtca ggcgagc atg gag aag			236
		Met Glu Lys	
		1	
gcg agc atg gag gag aca agc acg agg tca gaa ttg gag ctg gca gag			284
Ala Ser Met Glu Glu Thr Ser Thr Arg Ser Glu Leu Glu Leu Ala Glu			
5	10	15	
cag acg gag atg gag gga gaa aag gaa gaa agc ctg gtg gaa ggg gag			332
Gln Thr Glu Met Glu Gly Glu Lys Glu Glu Ser Leu Val Glu Gly Glu			
20	25	30	35
aag gag gaa gag gag gag acc cca ccc tcc ccc tgg gtc atc cac ccc			380
Lys Glu Glu Glu Glu Glu Thr Pro Pro Ser Pro Trp Val Ile His Pro			

	40	45	50	
aat gat gtc ctc aag att ctg gag gcc ttc ttc atg ggt ctg aag aag				428
Asn Asp Val Leu Lys Ile Leu Glu Ala Phe Phe Met Gly Leu Lys Lys				
	55	60	65	
cct agg gac tcg cgg gcc ccg ctg agg gta cag aag aat gtg cgt gac				476
Pro Arg Asp Ser Arg Ala Pro Leu Arg Val Gln Lys Asn Val Arg Asp				
	70	75	80	
aac tcc aag gac tcg gag tac tgg cag gcc ctg acc aca gtg atc cct				524
Asn Ser Lys Asp Ser Glu Tyr Trp Gln Ala Leu Thr Thr Val Ile Pro				
	85	90	95	
tcc tcc aag cag aac ctc tgg gat gcc ctc tac aca gcc ttg gag aag				572
Ser Ser Lys Gln Asn Leu Trp Asp Ala Leu Tyr Thr Ala Leu Glu Lys				
	100	105	110	115
tac cac ctt gtc ctg acc cag agg gcc aag ctg ctg ctg gaa aac agt				620
Tyr His Leu Val Leu Thr Gln Arg Ala Lys Leu Leu Leu Glu Asn Ser				
	120	125	130	
tct ctg gag cag cag aac aca gag ctg cag gcg cta ctg cag cag tat				668
Ser Leu Glu Gln Gln Asn Thr Glu Leu Gln Ala Leu Leu Gln Gln Tyr				
	135	140	145	
ctg aac tcc aag atc aac tct gaa ctg caa gtt cct ccc act cag gtg				716
Leu Asn Ser Lys Ile Asn Ser Glu Leu Gln Val Pro Pro Thr Gln Val				
	150	155	160	
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Leu Arg Val Pro Thr Lys *				
	165	170		
ggcctgatgc tggtgtctgt gccggagcca gtcatatca cccactgggc cgcacctggg				829
cctgctctct ggattttcca gggctgtctt tatagcctgt cgaaataagg agccagagga				889
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 <213> Homo sapiens

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cgc ttc ttc cag cag cgc aag agc ctg ctg ctg cac cag cgc ctg cac 99
 Arg Phe Phe Gln Gln Arg Lys Ser Leu Leu Leu His Gln Arg Leu His
 10 15 20
 acc ggc aat ggc cag ggc tgg ccc gcc tgc ccc tac tgc ggc aag gcc 147
 Thr Gly Asn Gly Gln Gly Trp Pro Ala Cys Pro Tyr Cys Gly Lys Ala
 25 30 35 40
 ttc cgc cgg ccc tcg gac ctc ttc cgg cac cag cgc atc cac acc ggt 195
 Phe Arg Arg Pro Ser Asp Leu Phe Arg His Gln Arg Ile His Thr Gly
 45 50 55
 gag cgg ccc tac cag tgc ccc cag tgt ggc cgg acc ttc aac cgc aac 243
 Glu Arg Pro Tyr Gln Cys Pro Gln Cys Gly Arg Thr Phe Asn Arg Asn
 60 65 70
 cac cac ctg gcc gtg cac atg cag acc cac gcc cga ggc cag gtg gcc 291
 His His Leu Ala Val His Met Gln Thr His Ala Arg Gly Gln Val Gly
 75 80 85
 cca cac ttc cct gcc gcc ccc gcc cgc cac ggg agc ctg ccc ctg ccc 339
 Pro His Phe Pro Ala Ala Pro Ala Arg His Gly Ser Leu Pro Leu Pro
 90 95 100
 tgg ccc agc cgg aag gag gag ggc tga cctgg caggagccca cagaggacct 391
 Trp Pro Ser Arg Lys Glu Glu Gly *
 105 110
 ctggcggggt ctctcccctg tgcctgacgc aggttcttcc ttttcttggg atggagagag 451
 gtttgttgtt tttaccatt caaatgggaa gctagctgcc cttctggtga cattgtgtgt 511
 gaccgggtgc tttctgtttc ctgtttgcac tcttcgctgc cttttctgca ttcctgactt 571
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 gtagtcaatg gaactttgcc tttagcaaag tcggaaagag tcggcttttc catgtgaggc 931
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agcagcgaag ctgcgggcg ctggcgggac aggcgcgtga ggccacaaca catgcgtgta	180
tcttgcttgg gctatcttcc ctgctctgcc acgccgggtc tggagaaggg gtttcagccc	240
caggacattt actgagagtc ggcgaatatt gggagccgcg atg ttc ccc ctt cgg	295
Met Phe Pro Leu Arg	
1 5	
gcc ctg tgg ttg gtc tgg gcg ctt cta gga gtg gcc gga tca tgc ccg	343
Ala Leu Trp Leu Val Trp Ala Leu Leu Gly Val Ala Gly Ser Cys Pro	
10 15 20	
gag ccg tgc gcc tgc gtg gac aag tac gct cac cag ttc gcg gac tgc	391
Glu Pro Cys Ala Cys Val Asp Lys Tyr Ala His Gln Phe Ala Asp Cys	
25 30 35	
gct tac aaa gag ttg cgt gag gtg ccg gaa gga ctg cct gcc aac gtg	439
Ala Tyr Lys Glu Leu Arg Glu Val Pro Glu Gly Leu Pro Ala Asn Val	
40 45 50	
acg acg ctt agt ctg tcc gcg aac aag atc act gtg ctg cgg cgc ggg	487
Thr Thr Leu Ser Leu Ser Ala Asn Lys Ile Thr Val Leu Arg Arg Gly	
55 60 65	
gcc ttc gcc gac gtc aca cag gtc acg tcg ctg tgg ctg gcg cac aat	535
Ala Phe Ala Asp Val Thr Gln Val Thr Ser Leu Trp Leu Ala His Asn	
70 75 80 85	
gag gtg cgc acc gtg gag cca ggc gca ctg gcc gtg ctg agt cag ctc	583
Glu Val Arg Thr Val Glu Pro Gly Ala Leu Ala Val Leu Ser Gln Leu	
90 95 100	
aag aac ctc gat ctg agc cac aac ttc ata tcc agc ttt ccg tgg agc	631
Lys Asn Leu Asp Leu Ser His Asn Phe Ile Ser Ser Phe Pro Trp Ser	
105 110 115	
gac ctg cgc aac ctg agc gcg ctg cag ctg ctc aaa atg aac cac aac	679
Asp Leu Arg Asn Leu Ser Ala Leu Gln Leu Leu Lys Met Asn His Asn	
120 125 130	
cgc ctg ggc tct ctg ccc cgg gac gca ctc ggt gcg cta ccc gac ctg	727
Arg Leu Gly Ser Leu Pro Arg Asp Ala Leu Gly Ala Leu Pro Asp Leu	
135 140 145	
cgt tcc ctg cgc atc aac aac aac cgg ctg cgt acg ctg gcg cct ggc	775
Arg Ser Leu Arg Ile Asn Asn Asn Arg Leu Arg Thr Leu Ala Pro Gly	
150 155 160 165	

gga cag gcc ccg acc tct gag cgc aag tcc aca gcc aag ggc cgg ggc Gly Gln Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly 390 395 400 405	1495
aac agc gtc ctg cct tcc aaa ccc gag ggc aaa atc aaa ggc caa ggc Asn Ser Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly 410 415 420	1543
ctg gcc aag gtc agc att ctc ggg gag acc gag acg gag ccg gag gag Leu Ala Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu 425 430 435	1591
gac aca agt gag gga gag gag gcc gaa gac cag atc ctc gcg gac ccg Asp Thr Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro 440 445 450	1639
gcg gag gag cag cgc tgt ggc aac ggg gac ccc tct cgg tac gtt tct Ala Glu Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser 455 460 465	1687
aac cac gcg ttc aac cag agc gca gag ctc aag ccg cac gtc ttc gag Asn His Ala Phe Asn Gln Ser Ala Glu Leu Lys Pro His Val Phe Glu 470 475 480 485	1735
ctg ggc gtc atc gcg ctg gat gtg gcg gag cgc gag gcg cgg gtg cag Leu Gly Val Ile Ala Leu Asp Val Ala Glu Arg Glu Ala Arg Val Gln 490 495 500	1783
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cca gcg ggg ggc ggc gcg gca gtg cag tgg tcc cgc gta gag gaa ggc Pro Ala Gly Gly Gly Ala Ala Val Gln Trp Ser Arg Val Glu Glu Gly 535 540 545	1927
gtc aac gcc tac tgg ttc cgc ggc ctg cgg ccg ggt acc aac tac tcc Val Asn Ala Tyr Trp Phe Arg Gly Leu Arg Pro Gly Thr Asn Tyr Ser 550 555 560 565	1975
gtg tgc ctg gcg ctg gcg ggc gaa gcc tgc cac gtg caa gtg gtg ttt Val Cys Leu Ala Leu Ala Gly Glu Ala Cys His Val Gln Val Val Phe 570 575 580	2023
tcc acc aag aag gag ctc cca tcg ctg ctg gtc ata gtg gca gtg agc Ser Thr Lys Lys Glu Leu Pro Ser Leu Leu Val Ile Val Ala Val Ser 585 590 595	2071
gta ttc ctc ctg gtg ctg gcc aca gtg ccc ctt ctg ggc gcc gcc tgc Val Phe Leu Leu Val Leu Ala Thr Val Pro Leu Leu Gly Ala Ala Cys 600 605 610	2119
tgc cat ctg ctg gct aaa cac ccg ggc aag ccc tac cgt ctg atc ctg	2167

Cys	His	Leu	Leu	Ala	Lys	His	Pro	Gly	Lys	Pro	Tyr	Arg	Leu	Ile	Leu		
615						620					625						
cgg	cct	cag	gcc	cct	gac	cct	atg	gag	aag	cgc	atc	gcc	gca	gac	ttc	2215	
Arg	Pro	Gln	Ala	Pro	Asp	Pro	Met	Glu	Lys	Arg	Ile	Ala	Ala	Asp	Phe		
630					635					640					645		
gac	ccg	cgt	gct	tcg	tac	ctc	gag	tcc	gag	aaa	agc	tac	ccg	gca	ggc	2263	
Asp	Pro	Arg	Ala	Ser	Tyr	Leu	Glu	Ser	Glu	Lys	Ser	Tyr	Pro	Ala	Gly		
				650						655				660			
ggc	gag	gcg	ggc	ggc	gag	gag	cca	gag	gac	gtg	cag	ggg	gag	ggc	ctt	2311	
Gly	Glu	Ala	Gly	Gly	Glu	Glu	Pro	Glu	Asp	Val	Gln	Gly	Glu	Gly	Leu		
			665					670					675				
gat	gaa	gac	gcg	ggg	cag	gga	gac	cca	agt	ggg	gac	ctg	cag	aga	gag	2359	
Asp	Glu	Asp	Ala	Gly	Gln	Gly	Asp	Pro	Ser	Gly	Asp	Leu	Gln	Arg	Glu		
		680					685					690					
gag	agc	ctg	gcg	gcc	tgc	tca	ctg	gtg	gag	tcc	cag	tcc	aag	gcc	aac	2407	
Glu	Ser	Leu	Ala	Ala	Cys	Ser	Leu	Val	Glu	Ser	Gln	Ser	Lys	Ala	Asn		
		695				700					705						
caa	gag	gag	ttc	gag	gcg	ggc	tct	gag	tac	agc	gat	cgg	ctg	ccc	ctg	2455	
Gln	Glu	Glu	Phe	Glu	Ala	Gly	Ser	Glu	Tyr	Ser	Asp	Arg	Leu	Pro	Leu		
710					715					720					725		
ggc	gcc	gag	gcg	gtc	aac	atc	gcc	cag	gag	att	aat	ggc	aac	tac	agg	2503	
Gly	Ala	Glu	Ala	Val	Asn	Ile	Ala	Gln	Glu	Ile	Asn	Gly	Asn	Tyr	Arg		
				730					735				740				
cag	acg	gca	ggc	tga	acctccgccc	gtccggccccg	cccatccga	cctg								2552	
Gln	Thr	Ala	Gly	*													
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tgccccctccc	ccttcccga	gccccgaggg	gccggagctc	ctggcgggtgc	cggatcctga											180	
cggcggcctt	cccccggtc	tgtctgcaa	a	atg	tct	gaa	aga	tca	gat	ctc						232	
				Met	Ser	Glu	Arg	Ser	Asp	Leu							

ctt cac ttc aag ttt gaa aat tat gga gat tca atg tta caa aaa atg	280
Leu His Phe Lys Phe Glu Asn Tyr Gly Asp Ser Met Leu Gln Lys Met	
10 15 20	
aac aaa tta aga gaa gag aat aaa ttt tgt gat gtt aca gtt ctc ata	328
Asn Lys Leu Arg Glu Glu Asn Lys Phe Cys Asp Val Thr Val Leu Ile	
25 30 35	
gat gat att gag gta cag gga cat aaa att gtg ttt gct gca ggt tcc	376
Asp Asp Ile Glu Val Gln Gly His Lys Ile Val Phe Ala Ala Gly Ser	
40 45 50 55	
ccc ttc tta aga gac caa ttt tta ctg aat gat tcc aga gag gtg aaa	424
Pro Phe Leu Arg Asp Gln Phe Leu Leu Asn Asp Ser Arg Glu Val Lys	
60 65 70	
atc tcc ata tta cag agt tcc gaa gtg ggg aga caa ttg ctc tta tcc	472
Ile Ser Ile Leu Gln Ser Ser Glu Val Gly Arg Gln Leu Leu Leu Ser	
75 80 85	
tgt tat agt ggt gtg ctg gaa ttc cct gag atg gaa ctg gta aat tac	520
Cys Tyr Ser Gly Val Leu Glu Phe Pro Glu Met Glu Leu Val Asn Tyr	
90 95 100	
ttg act gct gca agt ttt ctt cag atg agc cac att gta gaa cgg tgc	568
Leu Thr Ala Ala Ser Phe Leu Gln Met Ser His Ile Val Glu Arg Cys	
105 110 115	
aca cag gcc ctg tgg aag ttt ata aag cca aaa caa cca atg gat agt	616
Thr Gln Ala Leu Trp Lys Phe Ile Lys Pro Lys Gln Pro Met Asp Ser	
120 125 130 135	
aaa gag gga tgt gaa cca cag agt gct tct ccc cag tca aaa gaa cag	664
Lys Glu Gly Cys Glu Pro Gln Ser Ala Ser Pro Gln Ser Lys Glu Gln	
140 145 150	
cag gga gat gcc aga ggc tcc cca aag cag gac tca cct tgt att cat	712
Gln Gly Asp Ala Arg Gly Ser Pro Lys Gln Asp Ser Pro Cys Ile His	
155 160 165	
cca tct gaa gac agt atg gat atg gag gac agt gat att cag att gtt	760
Pro Ser Glu Asp Ser Met Asp Met Glu Asp Ser Asp Ile Gln Ile Val	
170 175 180	
aag gta gaa tct att ggg gat gta tca gag gtt aga agt aaa aaa gat	808
Lys Val Glu Ser Ile Gly Asp Val Ser Glu Val Arg Ser Lys Lys Asp	
185 190 195	
cag aac cag ttt att tct tct gaa ccc act gct tta cat tca tca gag	856
Gln Asn Gln Phe Ile Ser Ser Glu Pro Thr Ala Leu His Ser Ser Glu	
200 205 210 215	
ccc cag cac tcc ctg ata aat tca act gtg gaa aac aga gta agt gaa	904
Pro Gln His Ser Leu Ile Asn Ser Thr Val Glu Asn Arg Val Ser Glu	
220 225 230	

ata gaa caa aac cat ctc cac aat tat gcc ctt tct tat aca ggc agt Ile Glu Gln Asn His Leu His Asn Tyr Ala Leu Ser Tyr Thr Gly Ser 235 240 245	952
gat aac atc atc atg gcc tca aaa gat gtc ttt ggc cct aat att cga Asp Asn Ile Ile Met Ala Ser Lys Asp Val Phe Gly Pro Asn Ile Arg 250 255 260	1000
ggg gta gac aaa ggc cta cag tgg cat cac cag tgc cca aag tgt acc Gly Val Asp Lys Gly Leu Gln Trp His His Gln Cys Pro Lys Cys Thr 265 270 275	1048
agg gtg ttt cgt cac ctg gag aac tac gcc aac cat tta aaa atg cac Arg Val Phe Arg His Leu Glu Asn Tyr Ala Asn His Leu Lys Met His 280 285 290 295	1096
aaa ctc ttt atg tgt cta ctc tgc ggc aag act ttc act cag aaa ggc Lys Leu Phe Met Cys Leu Leu Cys Gly Lys Thr Phe Thr Gln Lys Gly 300 305 310	1144
aac ctt cat cga cac atg cgt gtg cat gcc gga att aaa cct ttc cag Asn Leu His Arg His Met Arg Val His Ala Gly Ile Lys Pro Phe Gln 315 320 325	1192
tgt aaa atc tgt ggg aaa acc ttt tct cag aag tgt tcc tta cag gat Cys Lys Ile Cys Gly Lys Thr Phe Ser Gln Lys Cys Ser Leu Gln Asp 330 335 340	1240
cat ctt aac ctt cac agt gga gat aag ccc cat aaa tgt aac tat tgt His Leu Asn Leu His Ser Gly Asp Lys Pro His Lys Cys Asn Tyr Cys 345 350 355	1288
gat atg gtt ttt gca cat aaa cca gtt ttg agg aaa cac ctt aaa cag Asp Met Val Phe Ala His Lys Pro Val Leu Arg Lys His Leu Lys Gln 360 365 370 375	1336
ctg cat ggc aaa aac agc ttt gat aat gcc aat gag aga aat gta caa Leu His Gly Lys Asn Ser Phe Asp Asn Ala Asn Glu Arg Asn Val Gln 380 385 390	1384
gac ctc aca gtg gat ttt gat tct ttt gca tgt aca aca gtc aca gac Asp Leu Thr Val Asp Phe Asp Ser Phe Ala Cys Thr Thr Val Thr Asp 395 400 405	1432
tct aaa ggg tgt cag cca caa ccc gat gca aca cag gtc ctg gat gca Ser Lys Gly Cys Gln Pro Gln Pro Asp Ala Thr Gln Val Leu Asp Ala 410 415 420	1480
ggg aaa ctg gcc caa gct gtc ctg aac tta aga aat gat agt act tgt Gly Lys Leu Ala Gln Ala Val Leu Asn Leu Arg Asn Asp Ser Thr Cys 425 430 435	1528
gtg aat tga gtagggg cttcatgccc acaactcgaa ctgactgaca atgtggcaat Val Asn * 440	1584

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agtcttagtc tttttaggag tgattttgct agtttgactt ctccaaagcc tctgtgtagg 1644
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<213> Homo sapiens

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tcttcccagg gagctgaaaa gccagattcg acctggtagc caagca atg tca cag 175
Met Ser Gln
1
cag aag cag caa tct tgg aag cct cca aat gtt ccc aaa tgc tcc cct 223
Gln Lys Gln Gln Ser Trp Lys Pro Pro Asn Val Pro Lys Cys Ser Pro
5 10 15
ccc caa aga tca aac ccc tgc cta gct ccc tac tcg act cct tgt ggt 271
Pro Gln Arg Ser Asn Pro Cys Leu Ala Pro Tyr Ser Thr Pro Cys Gly
20 25 30 35

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gct ccc cat tca gaa ggt tgt cat tcc agt tcc caa agg cct gag gtt 319
Ala Pro His Ser Glu Gly Cys His Ser Ser Gln Arg Pro Glu Val
40 45 50

cag aag cct agg agg gct cgt caa aag ctg cgc tgc cta agt agg ggc 367
Gln Lys Pro Arg Arg Ala Arg Gln Lys Leu Arg Cys Leu Ser Arg Gly
55 60 65

aca acc tac cac tgc aaa gag gaa gag tgt gaa ggc gac tga gccaga 416
Thr Thr Tyr His Cys Lys Glu Glu Glu Cys Glu Gly Asp *
70 75 80

agagttgagg cacaggtgca gttactctct ccctgccccca cctttgggta ctaattcccc 476

cttgaaagc caggccctca acctctcatt tggactgaga aacacttcct gatccccagc 536

tctagagaag cgagaactag gctgagccac gctgctactg ctctcttcca ttcacccctt 596

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<212> DNA
<213> Homo sapiens

<220>
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tcacctaacc catttgtggc ttcctctacc tgtgctcagc c atg gcc agc gag 173
Met Ala Ser Glu
1

agc tca cct ctg ctg gcc tac cgg ctc ctg ggg gag gag ggg gtt gcc 221
Ser Ser Pro Leu Leu Ala Tyr Arg Leu Leu Gly Glu Glu Gly Val Ala
5 10 15 20

ctc cct gcc aat ggg gcc ggg ggt cct gga ggg gcg tct gcc cgg aag 269
Leu Pro Ala Asn Gly Ala Gly Gly Pro Gly Gly Ala Ser Ala Arg Lys
25 30 35

ctg tcc acc ttc ctg ggt gtg gtg gtg ccc act gtc ctg tcc atg ttc 317
Leu Ser Thr Phe Leu Gly Val Val Val Pro Thr Val Leu Ser Met Phe
40 45 50

agc ata gtt gtt ttt ctg agg att ggg ttc gtg gtg ggt cat gct ggg 365
Ser Ile Val Val Phe Leu Arg Ile Gly Phe Val Val Gly His Ala Gly
55 60 65

Asp	Pro	Ser	Arg	Ala	Ile	Pro	Leu	Gly	Thr	Ile	Val	Ala	Val	Ala	Tyr		
		295					300					305					
acc	ttc	ttc	gtc	tat	gtc	ctg	ctt	ttc	ttt	ctc	tcc	agc	ttc	act	tgt	1133	
Thr	Phe	Phe	Val	Tyr	Val	Leu	Leu	Phe	Phe	Leu	Ser	Ser	Phe	Thr	Cys		
	310					315					320						
gac	agg	acc	ctg	ctg	cag	gaa	gac	tat	ggg	ttc	ttc	cgc	gcc	atc	agc	1181	
Asp	Arg	Thr	Leu	Leu	Gln	Glu	Asp	Tyr	Gly	Phe	Phe	Arg	Ala	Ile	Ser		
					330					335					340		
ctg	tgg	ccc	cca	ctg	gtg	ttg	atc	gga	atc	tat	gcc	aca	gcg	ctc	tca	1229	
Leu	Trp	Pro	Pro	Leu	Val	Leu	Ile	Gly	Ile	Tyr	Ala	Thr	Ala	Leu	Ser		
				345					350					355			
gcg	tcc	atg	agc	tcg	ctc	att	ggg	gcc	tcc	cgc	atc	ctc	cat	gcc	ctg	1277	
Ala	Ser	Met	Ser	Ser	Leu	Ile	Gly	Ala	Ser	Arg	Ile	Leu	His	Ala	Leu		
			360					365					370				
gcc	cgg	gat	gac	ctc	ttt	ggc	gtg	atc	ttg	gca	ccg	gcc	aag	gtt	gtg	1325	
Ala	Arg	Asp	Asp	Leu	Phe	Gly	Val	Ile	Leu	Ala	Pro	Ala	Lys	Val	Val		
		375				380						385					
tcc	cga	ggg	gga	aac	ccc	tgg	gca	gct	gta	ctt	tat	tct	tgg	ggc	ctg	1373	
Ser	Arg	Gly	Gly	Asn	Pro	Trp	Ala	Ala	Val	Leu	Tyr	Ser	Trp	Gly	Leu		
	390					395					400						
gtg	cag	ctg	gtg	ctc	ctg	gct	ggg	aag	ctg	aac	aca	ctg	gcc	gct	gtg	1421	
Val	Gln	Leu	Val	Leu	Leu	Ala	Gly	Lys	Leu	Asn	Thr	Leu	Ala	Ala	Val		
	405				410					415					420		
gtc	act	gtc	ttc	tac	ctg	gtg	gcc	tat	gct	gcc	gtg	gac	ctg	tcc	tgc	1469	
Val	Thr	Val	Phe	Tyr	Leu	Val	Ala	Tyr	Ala	Ala	Val	Asp	Leu	Ser	Cys		
				425				430						435			
ctg	agc	ctg	gag	tgg	gcc	tcg	gcc	ccc	aac	ttc	cgc	ccc	acc	ttc	agc	1517	
Leu	Ser	Leu	Glu	Trp	Ala	Ser	Ala	Pro	Asn	Phe	Arg	Pro	Thr	Phe	Ser		
			440				445						450				
ctg	ttc	tcc	tgg	cac	acc	tgc	ctg	ctg	ggg	gtg	gcc	tcc	tgc	ctg	ctc	1565	
Leu	Phe	Ser	Trp	His	Thr	Cys	Leu	Leu	Gly	Val	Ala	Ser	Cys	Leu	Leu		
		455					460					465					
atg	atg	ttc	ctc	atc	agt	cct	ggc	gcg	gct	ggg	ggc	tcc	ctg	ctc	ctc	1613	
Met	Met	Phe	Leu	Ile	Ser	Pro	Gly	Ala	Ala	Gly	Gly	Ser	Leu	Leu	Leu		
	470					475					480						
atg	ggg	ctg	ctg	gct	gcc	ctg	ctc	acc	gcg	cga	gga	ggc	ccc	agt	agc	1661	
Met	Gly	Leu	Leu	Ala	Ala	Leu	Leu	Thr	Ala	Arg	Gly	Gly	Pro	Ser	Ser		
	485				490					495					500		
tgg	ggc	tat	gtc	agc	cag	gcc	ttg	ctt	ttc	cac	cag	gtg	cgt	aag	tat	1709	
Trp	Gly	Tyr	Val	Ser	Gln	Ala	Leu	Leu	Phe	His	Gln	Val	Arg	Lys	Tyr		
				505					510					515			
ctg	ctt	cgg	ctg	gac	gtc	cgg	aag	gat	cac	gtg	aag	ttc	tgg	cgg	ccc	1757	
Leu	Leu	Arg	Leu	Asp	Val	Arg	Lys	Asp	His	Val	Lys	Phe	Trp	Arg	Pro		

520	525	530	
cag ctg ctg ctc ctg gtg ggg aac ccc cgg ggc gcc ctg cct ctg ctg Gln Leu Leu Leu Leu Val Gly Asn Pro Arg Gly Ala Leu Pro Leu Leu 535 540 545			1805
cgg ttg gcc aac cag ctt aag aag ggg ggg ctg tat gtg ctg ggc cac Arg Leu Ala Asn Gln Leu Lys Lys Gly Gly Leu Tyr Val Leu Gly His 550 555 560			1853
gtc acc ctg gga gac ctc gac tcc ctg ccc tcg gac cct gta cag ccg Val Thr Leu Gly Asp Leu Asp Ser Leu Pro Ser Asp Pro Val Gln Pro 565 570 575 580			1901
cag tat ggg gca tgg ctc agc ctg gtg gac cgt gcc cag gtg aag gct Gln Tyr Gly Ala Trp Leu Ser Leu Val Asp Arg Ala Gln Val Lys Ala 585 590 595			1949
ttt gtg gat cta acc ttc tca ccc tcc gtg cgc cag ggg gct cag cat Phe Val Asp Leu Thr Phe Ser Pro Ser Val Arg Gln Gly Ala Gln His 600 605 610			1997
ctg ctg cga atc tcc ggc ctc ggt ggc atg aag ccc aac acg ttg gtc Leu Leu Arg Ile Ser Gly Leu Gly Gly Met Lys Pro Asn Thr Leu Val 615 620 625			2045
cta ggt ttc tac gat gac gct cca ccg cag gac cat ttc ctg acg gac Leu Gly Phe Tyr Asp Asp Ala Pro Pro Gln Asp His Phe Leu Thr Asp 630 635 640			2093
ccg gct ttc tct gag cct gca gac agc acc agg gag ggc agt tcc cca Pro Ala Phe Ser Glu Pro Ala Asp Ser Thr Arg Glu Gly Ser Ser Pro 645 650 655 660			2141
gct ctg agc acc ctg ttc cct cct ccc cgg gct cct ggg agc ccc cgg Ala Leu Ser Thr Leu Phe Pro Pro Pro Arg Ala Pro Gly Ser Pro Arg 665 670 675			2189
gcc ctc aat ccc cag gac tat gtg gcc acg gtg gcc gac gcc ctc aag Ala Leu Asn Pro Gln Asp Tyr Val Ala Thr Val Ala Asp Ala Leu Lys 680 685 690			2237
atg aac aag aat gtg gtg ctg gcc cgg gcc agc ggg gcc ttg ccc cct Met Asn Lys Asn Val Val Leu Ala Arg Ala Ser Gly Ala Leu Pro Pro 695 700 705			2285
gag cgg ctg agc cgg ggg tct ggg ggc acc tct cag ttg cac cat gtg Glu Arg Leu Ser Arg Gly Ser Gly Gly Thr Ser Gln Leu His His Val 710 715 720			2333
gac gtg tgg ccc ctc aac ttg ttg cgg ccc cgg ggt ggg ccc ggc tat Asp Val Trp Pro Leu Asn Leu Leu Arg Pro Arg Gly Gly Pro Gly Tyr 725 730 735 740			2381
gtg gat gtc tgc ggc ctc ttc ctg ctg cag atg gca acc atc ttg ggc Val Asp Val Cys Gly Leu Phe Leu Leu Gln Met Ala Thr Ile Leu Gly 745 750 755			2429

atg gtg ccc gct tgg cat agc gcc cgg ctc cgg atc ttc ctg tgc ctg Met Val Pro Ala Trp His Ser Ala Arg Leu Arg Ile Phe Leu Cys Leu 760 765 770	2477
ggg cct cgg gag gcg cct ggg gcg gcc gag ggg cgg ctg cgg gca ctg Gly Pro Arg Glu Ala Pro Gly Ala Ala Glu Gly Arg Leu Arg Ala Leu 775 780 785	2525
ctg agc caa ctg agg atc cgg gct gag gtg cag gag gtg gtg tgg ggc Leu Ser Gln Leu Arg Ile Arg Ala Glu Val Gln Glu Val Val Trp Gly 790 795 800	2573
gag ggg gcc ggg gct ggg gaa ccc gag gcg gag gag gaa ggg gac ttt Glu Gly Ala Gly Ala Gly Glu Pro Glu Ala Glu Glu Glu Gly Asp Phe 805 810 815 820	2621
gtg aac agt ggg cgg gga gac gca gag gca gag gcc ctg gca cgc agc Val Asn Ser Gly Arg Gly Asp Ala Glu Ala Glu Ala Leu Ala Arg Ser 825 830 835	2669
gcc aac gcc ctg gtt cgg gcc cag cag ggg cgc ggc aca gga gga ggg Ala Asn Ala Leu Val Arg Ala Gln Gln Gly Arg Gly Thr Gly Gly Gly 840 845 850	2717
ccg ggt ggg ccg gag ggt ggg gat gct gag ggc ccc atc aca gcc ctc Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu Gly Pro Ile Thr Ala Leu 855 860 865	2765
acc ttc ctg tac ttg cct cgg ccg cca gcc gat ccc gcc cga tac ccc Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala Asp Pro Ala Arg Tyr Pro 870 875 880	2813
cgc tac ctg gcg cta ctg gag act cta acc cga gac ctg ggc ccc acg Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr Arg Asp Leu Gly Pro Thr 885 890 895 900	2861
ctg ctg gtt cat ggg gtc act cca gtc acc tgc act gat ctg tga Leu Leu Val His Gly Val Thr Pro Val Thr Cys Thr Asp Leu * 905 910 915	2906

<210> 323
<211> 607
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(416)

<400> 323
actagcgtgg ttccagtgtc gtcacgcgtg ctaaaaaagg gggtttcccg tgacaggccc 60

gat ttg ctg ata tta aca ata gat ttt aat ctc ttg tta ata ata tac	156
Asp Leu Leu Ile Leu Thr Ile Asp Phe Asn Leu Leu Leu Ile Ile Tyr	
15 20 25	
ctt gca aac tac ttt tct cag tct gtg gct tat ctt ttc att tct tta	204
Leu Ala Asn Tyr Phe Ser Gln Ser Val Ala Tyr Leu Phe Ile Ser Leu	
30 35 40	
tgg gtt ttc ttt ggc atg agg gta caa gtt tta ctt tta atg aag taa	252
Trp Val Phe Phe Gly Met Arg Val Gln Val Leu Leu Leu Met Lys *	
45 50 55 60	
aatatgtaac ttacattac agtttgtgct tatttgtatt acttatgaaa catttcctta	312
cccagaagtc atgaaggtat tctcctctat ttccttctag aagtttggct cttcagattt	372
ccaatgttcc tgaaattaac ttctatgtag ggtgaggtag caaccaatt ttattttctt	432
ccatataatc acttgaccta gcaaaatata attgcctatt ctttcccca tgatctacaa	492
tgccatattt agt	505

<210> 325
 <211> 670
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (232)..(624)

<400> 325	
ccggatactg cccgggtcga cccacgcgtc cggtagacag ggagctgtga cgagagcaag	60
aggtcataac acatccagac tccttaagag aaagcctttc tgttttgaa acttttcaaa	120
gccagggact tgtccagccc aacctccca ttgctcctag ctccctgaggc tcaggacccc	180
tggcttctgt cctccctgct cagggctctg cagcgttgcc tctgctcagc c atg ctc	237
Met Leu	
1	
ctg ctg ctc gtc cca gtg ctc gag gtg att ttt act ctg gga gga acc	285
Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly Gly Thr	
5 10 15	
aga gcc cag tcg gtg acc cag ctt gac agc cac gtc tct gtc tct gaa	333
Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val Ser Glu	
20 25 30	
gga acc ccg gtg ctg ctg agg tgc aac tac tca tct tct tat tca cca	381
Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr Ser Pro	
35 40 45 50	

tct ctc ttc tgg tat gtg caa cac ccc aac aaa gga ctc cag ctt ctc	429
Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln Leu Leu	
55 60 65	
ctg aag tac aca tca gcg gcc acc ctg gtt aaa ggc atc aac ggt ttt	477
Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn Gly Phe	
70 75 80	
gag gct gaa ttt aag aag agt gaa acc tcc ttc cac ctg acg aaa ccc	525
Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr Lys Pro	
85 90 95	
tca gcc cat atg agc gac gcg gct gag tac ttc tgt gtt gtg agt gac	573
Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val Ser Asp	
100 105 110	
aca gtg ctt gag act gca gga gag ctg aac aca agc ctc ctg aga tgc	621
Thr Val Leu Glu Thr Ala Gly Glu Leu Asn Thr Ser Leu Leu Arg Cys	
115 120 125 130	
tga gactttctgt gactcaagaa ctgcaccttg aagtctgttt tataat	670
*	

<210> 326
 <211> 794
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (200)..(304)

 <220>
 <221> misc_feature
 <222> (1)...(794)
 <223> n = a,t,c or g

<400> 326	
gtcagcaatg gtctcatgga agagggaagc tttatattaca ccatcaaggg cccatggatg	60
accacagtc tgtgtgactg ctgtgtgatt ggttttcaga cattagcttt aataggaatc	120
ataggagaag ggacatgggt gctactgcaa ggggtttttt tgtttaggga gaacgcactg	180
tggaactcaa attccgggt atg cac tca acc tcg gca aag gca cct cgc tgt	232
Met His Ser Thr Ser Ala Lys Ala Pro Arg Cys	
1 5 10	
tgg tca cac ccc gtg agt ttt tgt ggt tta cta att gtc ctc tct gga	280
Trp Ser His Pro Val Ser Phe Cys Gly Leu Leu Ile Val Leu Ser Gly	
15 20 25	

cag ctc aat aga gcc agc cag tat att tcc ctg ctc atc aga gac tcc	343
Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser	
85 90 95 100	
aag ctc agt gat tca gcc acc tac ctc tgt gtg gtg aac att cgc cca	391
Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Ile Arg Pro	
105 110 115	
gga aac aca cct ttg gga ctg gaa caa gac ttc agg tca cgc tcg ata	439
Gly Asn Thr Pro Leu Gly Leu Glu Gln Asp Phe Arg Ser Arg Ser Ile	
120 125 130	
tcc aga acc ctg acc ctg ccg tgt acc agc tga gagactct aaatccagt	490
Ser Arg Thr Leu Thr Leu Pro Cys Thr Ser *	
135 140	
acaatgctgt cgaccta	507

<210> 328
 <211> 1043
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1043)

<400> 328	
accggtccgg aattcccggg tcgacgattt cgtccggtgt cgggaagcac cagtgccctg	60
aggaagggcc atttccaaaa gccctgtgct gacacagggt tgctgggttcc tcttcaagag	120
cccactctct ggggtggggc catatctcca gcagaggtgg gctggaaagg acccccccaa	180
tcccgccgc cgtgagctta gctggagcc atg gcc tct gca ccc atc tcg atg	233
Met Ala Ser Ala Pro Ile Ser Met	
1 5	
ctt gcg atg ctc ttc aca ttg agt ggg ctg aga gct cag tca gtg gct	281
Leu Ala Met Leu Phe Thr Leu Ser Gly Leu Arg Ala Gln Ser Val Ala	
10 15 20	
cag ccg gaa gat cag gtc aac gtt gct gaa ggg aat cct ctg act gtg	329
Gln Pro Glu Asp Gln Val Asn Val Ala Glu Gly Asn Pro Leu Thr Val	
25 30 35 40	
aaa tgc acc tat tca gtc tct gga aac cct tat ctt ttt tgg tat gtt	377
Lys Cys Thr Tyr Ser Val Ser Gly Asn Pro Tyr Leu Phe Trp Tyr Val	
45 50 55	
caa tac ccc aac cga ggc ctc cag ttc ctt ctg aaa tac atc aca ggg	425
Gln Tyr Pro Asn Arg Gly Leu Gln Phe Leu Leu Lys Tyr Ile Thr Gly	
60 65 70	

gat aac ctg gtt aaa ggc agc tat ggc ttt gaa gct gaa ttt aac aag	473
Asp Asn Leu Val Lys Gly Ser Tyr Gly Phe Glu Ala Glu Phe Asn Lys	
75 80 85	
agc caa acc tcc ttc cac ctg aag aaa cca tct gcc ctt gtg agc gac	521
Ser Gln Thr Ser Phe His Leu Lys Lys Pro Ser Ala Leu Val Ser Asp	
90 95 100	
tcc gct ttg tac ttc tgt gct gtg aga gag gta ata ctc acg gga gga	569
Ser Ala Leu Tyr Phe Cys Ala Val Arg Glu Val Ile Leu Thr Gly Gly	
105 110 115 120	
gga aac aaa ctc acc ttt ggg aca ggc act cag cta aaa gtg gaa ctc	617
Gly Asn Lys Leu Thr Phe Gly Thr Gly Thr Gln Leu Lys Val Glu Leu	
125 130 135	
aat atc cag aac cct gac cct gcc gtg tac cag ctg aga gac tct aaa	665
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys	
140 145 150	
tcc agt gac aag tct gtc tgc cta ttc acc gat ttt gat tct caa aca	713
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr	
155 160 165	
aat gtg tca caa agt aag gat tct gat gtg tat atc aca gac aaa act	761
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr	
170 175 180	
gtg cta gac atg agg tct atg gac ttc aag agc aac agt gct gtg gcc	809
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala	
185 190 195 200	
tgg agc aac aaa tct gac ttt gca tgt gca aac gcc ttc aac aac agc	857
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser	
205 210 215	
att att cca gaa gac acc ttc ttc ccc agc cca gaa agt tcc tgt gat	905
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp	
220 225 230	
gtc aag ctg gtc gag aaa agc ttt gaa aca gat acg aac cta aac ttt	953
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe	
235 240 245	
caa aac ctg tca gtg att ggg ttc cga atc ctc ctc ctg aaa gtg gcc	1001
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala	
250 255 260	
ggg ttt aat ctg ctc atg acg ctg cgg ctg tgg tcc agc tga	1043
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser *	
265 270 275	

<210> 329

<211> 1037
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(831)

<400> 329

atg agc atc agc ctc ctg tgc tgt gca gcc ttt cct ctc ctg tgg gca	48
Met Ser Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala	
1 5 10 15	
ggt cca gtg aat gct ggt ggt gtc act cag acc cca aaa ttc cgc atc	96
Gly Pro Val Asn Ala Gly Gly Val Thr Gln Thr Pro Lys Phe Arg Ile	
20 25 30	
ctg aag ata gga cag agc atg aca ctg cag tgt gcc cag gat atg aac	144
Leu Lys Ile Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn	
35 40 45	
cat aac tac atg tac tgg tat cga caa gac cca ggc atg ggg ctg aag	192
His Asn Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys	
50 55 60	
ctg att tat tat tca gtt ggt gct ggt atc act gac aaa gga gaa gtc	240
Leu Ile Tyr Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val	
65 70 75 80	
ccg aat ggc tac aac gtc tcc aga tca acc aca gag gat ttc ccg ctc	288
Pro Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu	
85 90 95	
agg ctg gag ttg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc	336
Arg Leu Glu Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala	
100 105 110	
agc agt agg ggt ggg gcc ggg ctc aat gag cag ttc ttc ggg cca ggg	384
Ser Ser Arg Gly Gly Ala Gly Leu Asn Glu Gln Phe Phe Gly Pro Gly	
115 120 125	
aca cgg ctc acc gtg cta gag gac ctg aaa aac gtg ttc cca ccc gag	432
Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu	
130 135 140	
gtc gct gtg ttt gag cca tca gaa gca gag atc tcc cac acc caa aag	480
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys	
145 150 155 160	
gcc aca ctg gta tgc ctg gcc aca ggc ttc tac ccc gac cac gtg gag	528
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu	
165 170 175	
ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt ggg gtc agc aca	576
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr	
180 185 190	

gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat gac tcc aga tac	624
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr	
195 200 205	
tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc tgg cag aac ccc	672
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro	
210 215 220	
cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg ctc tcg gag aat	720
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn	
225 230 235 240	
gac gag tgg acc cag gat agg gcc aaa cct gtc acc cag atc gtc agc	768
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser	
245 250 255	
gcc gag gcc tgg ggt aga gca ggt gag tgg ggc ctg ggg aga tgc ctg	816
Ala Glu Ala Trp Gly Arg Ala Gly Glu Trp Gly Leu Gly Arg Cys Leu	
260 265 270	
gag gag att agg tga gaccagctac cagggaaaat ggaaagatcc aggtagcggg	871
Glu Glu Ile Arg *	
275	
caagactata tccagaagaa agccagagtg gacaagggtgg gatgatcaag gttcacaggg	931
tcagcaaagc acgggtgtgca cttccccac caagaagcat atagggtgaa tggagcacct	991
caagctcatt cttccttcag atcctgacac cttagagcta agctttt	1037
<210> 330	
<211> 738	
<212> DNA	
<213> Homo sapiens	
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<221> CDS	
<222> (300)..(608)	
<400> 330	
tagttcaaag aagaaaagtc agctggatgt gatgcctcat gcctgtaatc ctaccacttt	60
gggaggccaa cacggttgga tctcttgagc ccaggagttc gagactagcc tggccaacat	120
ggcgaaaccc cttctctttt tcttttttta aaatttttta gttagaaatg aaaaaaagaa	180
agaagtctag gttttctgaa acaagcactg tcttggtgct accttttttc atgtgtggac	240
acatagaaag cgaggatatt tgtacagcac cttgaaacaa ataagcagga ggtgatgtc	299
atg agc ctt agc cct gca ggg acc aga cta ggc ctt ctg aag ctg agg	347
Met Ser Leu Ser Pro Ala Gly Thr Arg Leu Gly Leu Leu Lys Leu Arg	
1 5 10 15	
tgg tcc ttg tcc cca cac ctt gta acc cat ttc cag ccc atg ggt gtc	395

Trp	Ser	Leu	Ser	Pro	His	Leu	Val	Thr	His	Phe	Gln	Pro	Met	Gly	Val		
			20					25					30				
agt	tgg	gaa	att	cta	cac	aag	atc	cta	gta	gat	gta	att	aca	tat	aat		443
Ser	Trp	Glu	Ile	Leu	His	Lys	Ile	Leu	Val	Asp	Val	Ile	Thr	Tyr	Asn		
		35					40					45					
tca	atg	gtt	ttt	gat	gat	ggg	gtt	tta	aaa	tca	agt	tat	tca	ata	ggg		491
Ser	Met	Val	Phe	Asp	Asp	Gly	Val	Leu	Lys	Ser	Ser	Tyr	Ser	Ile	Gly		
		50				55					60						
ggg	gtg	cag	tgg	ctc	acg	cct	gta	att	cca	gca	ctt	tgg	gag	gcc	gag		539
Gly	Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu		
	65				70				75					80			
gag	ggc	aga	tca	caa	ggg	cgg	gag	ttc	aag	acc	agc	ctg	acc	aac	atg		587
Glu	Gly	Arg	Ser	Gln	Gly	Arg	Glu	Phe	Lys	Thr	Ser	Leu	Thr	Asn	Met		
			85				90					95					
gta	aaa	ctc	cgt	ctc	tac	taa	aa	attcaaaaaat	tagccggccg	tggtggtgga							640
Val	Lys	Leu	Arg	Leu	Tyr	*											
			100														
catctgtaat	cccagctact	tagggggctg	aggcaggaga	atcgcttgaa	cggggggcagg												700
tcgggggcagg	gcggcaactc	cctcttaaaa	aaaaaaaaa														738

<210> 331
 <211> 679
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(449)

<220>
 <221> misc_feature
 <222> (1)...(679)
 <223> n = a,t,c or g

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aacaagcagc	agtgaggaca	ccaaagccaa	gccacgccac	ccgggcccgc	ccccaggaca												60
cggagtttaa	ggaccgcgtc	tcccagatg	ccagaggac	ctgcgtccgc	actgccccag												120
tgtgacccgc	atacctaccg	gccccgacc	cgaaccgcgt	ggcgtccgcc	cgagccctgg												180
cgtctgtggg	tctctgtctg	ctgccgtgc	tcgcagagcc	caggaaactc	tgccccgcagc												240
tt	atg	acg	gtc	att	aac	cag	ttt	ctg	acc	aag	gac	aag	gac	acc	tac		287
	Met	Thr	Val	Ile	Asn	Gln	Phe	Leu	Thr	Lys	Asp	Lys	Asp	Thr	Tyr		
	1				5					10					15		

atg gac act gtc aac aga tac cac ctc acg gag ccg gaa aga aac aca 335
Met Asp Thr Val Asn Arg Tyr His Leu Thr Glu Pro Glu Arg Asn Thr
20 25 30

tcc tct aaa ctc aag gac tgc gtg acc gac aca atg acc ccc gag gag 383
Ser Ser Lys Leu Lys Asp Cys Val Thr Asp Thr Met Thr Pro Glu Glu
35 40 45

aca gag gcc gtc gtg cag caa ctg gaa gaa atc aac aac cag tgt gcc 431
Thr Glu Ala Val Val Gln Gln Leu Glu Glu Ile Asn Asn Gln Cys Ala
50 55 60

gac acg ata ctg aag taa caccat ccataggcac ctcgggttcc tgtccaggct 485
Asp Thr Ile Leu Lys *
65

gcctgtccca accatgagaa tctgggcca gggccccacc ctccctagct cccgccctgc 545

tgctgctct actctctctc ctgctgtgct gattggggca agcctgggaa cggtgcccc 605

ccacctcccc acccaggncc tgtcctgcgg gacaatgctg cctaataaac tcacctgcat 665

ccaaaaaaaaa aaaa 679

<210> 332
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(400)

<400> 332
ctttagtcca gcgtggtgga attcgtagat ccccgcggtg caccagccct tctgccacag 60

ctgccattgg agagcagcag ccatggctct gtgctacca ctatggccgt gtgccttgac 120

aagggccaca agatgaccaa gaacatgagc aagcccaggc acagctgccg ccgcgggcgc 180

ctgaccaaac accaaattc atg tgg gac atg atc cga gag gtg tgt ggt ttc 232
Met Trp Asp Met Ile Arg Glu Val Cys Gly Phe
1 5 10

gcc ccg tat gag cgg cac gcc atg gtg tta ctc aag gtc tcc aag gac 280
Ala Pro Tyr Glu Arg His Ala Met Val Leu Leu Lys Val Ser Lys Asp
15 20 25

aaa cgg gcc ctc aag ttc atc aag aaa aga gtg ggg aca cac atc cgc 328
Lys Arg Ala Leu Lys Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg
30 35 40

act aag agg agg cag gag gag ctg agc aat gtc cca gcc atc atg agg 376
Thr Lys Arg Arg Gln Glu Glu Leu Ser Asn Val Pro Ala Ile Met Arg

45	50	55	
aaa gct gat gcc aag aaa gac tga gccccctgtc ctgccctctc tctgaaataa			430
Lys Ala Asp Ala Lys Lys Asp *			
60	65		

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aatgtcctgg ctgacctaa ggacgacaga agattggggga agaggggggta tcaggaagaa	180
atggggtttca gttcagttta acaaacatct attgtgtgtt cactggggcca ggccagtgtt	240
aggtgctagg gagacagagg tgaagagcct gccctctagc agctgacagc ctggcaaaaa	300
aataagacag aataaggtag accctgattt tggaacctga agaccaaagt gcaagattag	360
ctctgtact tccatctgtg gaccattggg caggtatctc tgggccttca cttactcttt	420
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acacggtgat tgtgaaaaga ttttgtcaat cgcaccagca ttaaggggtgc ccactctccag	540
gttccccag gcctcaaggc tccaaggcc tgagtgggca ggtagcacc aggtatagac	600
cttcacgtg cagcaccag gacacagcca gc atg aac tgg gca ttt ctg cag	653
	Met Asn Trp Ala Phe Leu Gln
	1 5
ggc ctg ctg agt ggc gtg aac aag tac tcc aca gtg ctg agc cgc atc	701
Gly Leu Leu Ser Gly Val Asn Lys Tyr Ser Thr Val Leu Ser Arg Ile	
10 15 20	
tgg ctg tct gtg gtg ttc atc ttt cgt gtg ctg gtg tac gtg gtg gca	749
Trp Leu Ser Val Val Phe Ile Phe Arg Val Leu Val Tyr Val Val Ala	
25 30 35	
gcg gag gag gtg tgg gac gat gag cag aag gac ttt gtc tgc aac acc	797
Ala Glu Glu Val Trp Asp Asp Glu Gln Lys Asp Phe Val Cys Asn Thr	
40 45 50 55	

aag cag ccc ggc tgc ccc aac gtc tgc tat gac gag ttc ttc ccc gtg	845
Lys Gln Pro Gly Cys Pro Asn Val Cys Tyr Asp Glu Phe Phe Pro Val	
60 65 70	
tcc cac gtg cgc ctc tgg gcc cta cag ctc atc ctg gtc acg tgc ccc	893
Ser His Val Arg Leu Trp Ala Leu Gln Leu Ile Leu Val Thr Cys Pro	
75 80 85	
tca ctg ctc gtg gtc atg cac gtg gcc tac cgc gag gaa cgc gag cgc	941
Ser Leu Leu Val Val Met His Val Ala Tyr Arg Glu Glu Arg Glu Arg	
90 95 100	
aag cac cac ctg aaa cac ggg ccc aat gcc ccg tcc ctg tac gac aac	989
Lys His His Leu Lys His Gly Pro Asn Ala Pro Ser Leu Tyr Asp Asn	
105 110 115	
ctg agc aag aag cgg ggc gga ctg tgg tgg acg tac ttg ctg agc ctc	1037
Leu Ser Lys Lys Arg Gly Gly Leu Trp Trp Thr Tyr Leu Leu Ser Leu	
120 125 130 135	
atc ttc aag gcc gcc gtg gat gct ggc ttc ctc tat atc ttc cac cgc	1085
Ile Phe Lys Ala Val Asp Ala Gly Phe Leu Tyr Ile Phe His Arg	
140 145 150	
ctc tac aag gat tat gac atg ccc cgc gtg gtg gcc tgc tcc gtg gag	1133
Leu Tyr Lys Asp Tyr Asp Met Pro Arg Val Val Ala Cys Ser Val Glu	
155 160 165	
cct tgc ccc cac act gtg gac tgt tac atc tcc cgg ccc acg gag aag	1181
Pro Cys Pro His Thr Val Asp Cys Tyr Ile Ser Arg Pro Thr Glu Lys	
170 175 180	
aag gtc ttc acc tac ttc atg gtg acc aca gct gcc atc tgc atc ctg	1229
Lys Val Phe Thr Tyr Phe Met Val Thr Thr Ala Ala Ile Cys Ile Leu	
185 190 195	
ctc aac ctc agt gaa gtc ttc tac ctg gtg ggc aag agg tgc atg gag	1277
Leu Asn Leu Ser Glu Val Phe Tyr Leu Val Gly Lys Arg Cys Met Glu	
200 205 210 215	
atc ttc ggc ccc agg cac cgg cgg cct cgg tgc cgg gaa tgc cta ccc	1325
Ile Phe Gly Pro Arg His Arg Arg Pro Arg Cys Arg Glu Cys Leu Pro	
220 225 230	
gat acg tgc cca cca tat gtc ctc tcc cag gga ggg cac cct gag gat	1373
Asp Thr Cys Pro Pro Tyr Val Leu Ser Gln Gly Gly His Pro Glu Asp	
235 240 245	
ggg aac tct gtc cta atg aag gct ggg tgc gcc cca gtg gat gca ggt	1421
Gly Asn Ser Val Leu Met Lys Ala Gly Ser Ala Pro Val Asp Ala Gly	
250 255 260	
ggg tat cca taa cct gcgagatcag cagataagat caacaggtcc cccccacatg	1476
Gly Tyr Pro *	
265	
aggccacca ggaaaaaagg caggggcagt ggcaccccttg ccgtagcagg gtggtgagga	1536

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 Met Tyr Cys Cys
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 Ala Leu Arg Ser Cys Ser Val Pro Thr Gly Pro Ala Thr Thr Phe Cys
 5 10 15 20
 tca ttt gat aaa agc tgc cgc tgt gga gtc tgc cta ccc agc acc tgc 151
 Ser Phe Asp Lys Ser Cys Arg Cys Gly Val Cys Leu Pro Ser Thr Cys
 25 30 35
 cca cat gag atc agc ctc ctt cag ccc atc tgc tgt gac acc tgc ccc 199
 Pro His Glu Ile Ser Leu Leu Gln Pro Ile Cys Cys Asp Thr Cys Pro
 40 45 50
 cca ccc tgc tgc aag cct gat acc tat gtg cca act tgc tgg ctg ctc 247
 Pro Pro Cys Cys Lys Pro Asp Thr Tyr Val Pro Thr Cys Trp Leu Leu
 55 60 65
 aac aac tgt cac ccg act ccc gga ctg agt ggg atc aac ctg acc acc 295
 Asn Asn Cys His Pro Thr Pro Gly Leu Ser Gly Ile Asn Leu Thr Thr
 70 75 80
 tat gtt cag cct ggc tgt gag agt ccc tgt gag ccc cgc tgt taa cca 343
 Tyr Val Gln Pro Gly Cys Glu Ser Pro Cys Glu Pro Arg Cys *
 85 90 95
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 cagc 407

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 <222> (1)..(2530)
 <223> n = a,t,c or g

<400> 335

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               Met Glu Leu Ser Glu Arg Tyr Gly Pro Val
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ttc acc gtg cac ctg ggg cgc cag aag acg gtg gtg ctg acg ggg ttc      100
Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr Gly Phe
                   15                   20                   25

gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg gcc gac      148
Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu Ala Asp
                   30                   35                   40

cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga ggc atc      196
Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly Gly Ile
                   45                   50                   55

ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc acg gtg      244
Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe Thr Val
                   60                   65                   70

cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct gac aag      292
Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala Asp Lys
                   75                   80                   85                   90

att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc tac aga      340
Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly Tyr Arg
                   95                   100                   105

ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc aat atc      388
Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser Asn Ile
                   110                   115                   120

acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac ccc gtg      436
Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp Pro Val
                   125                   130                   135

ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc ttg ggg      484
Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu Leu Gly
                   140                   145                   150

tcc cct ggc ctg cag ctg ttc aac gtc cac cca tgg ctc ggg gcc ctg      532
Ser Pro Gly Leu Gln Leu Phe Asn Val His Pro Trp Leu Gly Ala Leu
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ctc cag ctg cac cgg ccc gtc ctg cgc aag atc gag gag gtc cgt gcc	580
Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val Arg Ala	
175 180 185	
att ctg agg acc ctc ctg gag gcg cgg agg ccc cac gtg tgc ccg ggg	628
Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys Pro Gly	
190 195 200	
gac ccc gtg tgc agc tat gtg gac gcc ctg atc cag cag gga cag ggg	676
Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly Gln Gly	
205 210 215	
gat gac ccc gag ggc ctg ttt gct gag gcc aac gcg gtg gcc tgc acc	724
Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala Cys Thr	
220 225 230	
ctg gac atg gtc atg gcc ggg acg gag acg acc tcg gcc acg ctg cag	772
Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr Leu Gln	
235 240 245 250	
tgg gcc gca ctt ctg atg ggc cgg cac ccg gac gtg cag ggc cgg gtg	820
Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly Arg Val	
255 260 265	
cag gag gag cta gac cgc gtg ctg ggc cct ggg cgg act ccc cgg ctg	868
Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro Arg Leu	
270 275 280	
gag gac cag cag gct ctg ccc tac aca agc gcc gtg ctc cac gag gtg	916
Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His Glu Val	
285 290 295	
cag cgg ttc atc acg ctc ctg cgg cac gtg ccc cgc tgc acc gcg gcc	964
Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr Ala Ala	
300 305 310	
gac aca cag ctg ggc ggc ttc ctg ctc ccc aag ggc acg ccc gtg att	1012
Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro Val Ile	
315 320 325 330	
ccc ctg ctg acc tcg gtg ctc ctg gat gag aca cag tgg cag acc cca	1060
Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln Thr Pro	
335 340 345	
ggc cag ttc aac ccc ggc cat ttc ctg gac gcg aat ggg cac ttt gtg	1108
Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His Phe Val	
350 355 360	
aag cgg gag gcc ttc ctg cct ttc tct gca ggt cag cag ccc tcg ggg	1156
Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Gln Gln Pro Ser Gly	
365 370 375	
ccg ggg tgg ggc ggc acc tcc agg gct cca ggg gtg gga cgg ccc cag	1204
Pro Gly Trp Gly Gly Thr Ser Arg Ala Pro Gly Val Gly Arg Pro Gln	
380 385 390	
ctc cgc ctg ccg cct ctg cac cca cct cct gat ctc agg ttc tga agg	1252

Leu Arg Leu Pro Pro Leu His Pro Pro Pro Asp Leu Arg Phe *
 395 400 405

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cggctgtggt ggctgctcct gtgctcccct ggggaggtcc ccacccctcc cctccaggag 1312
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tctactaaaa atacaaaaat tagnctgggc gtggtggcat gcacccctgc aatcccaagc 2392
tactcggcgg gggggctgag gcaggaagna attgcttgaa cctgggaggt gaaggggttg 2452
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<400> 336

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caatgccaac atctgagcaa acattttggg gtatatctct attttc atg ttt aca 115
Met Phe Thr
1

ttg tcg ttt aaa aaa caa tca aac gac att agc agt ttt aca aca ttt 163
Leu Ser Phe Lys Lys Gln Ser Asn Asp Ile Ser Ser Phe Thr Thr Phe
5 10 15

tcc ttt cca gtt aaa act gta tac cgt tac cat ttt ccc atc ata ctc 211
Ser Phe Pro Val Lys Thr Val Tyr Arg Tyr His Phe Pro Ile Ile Leu
20 25 30 35

ttc acc tac gat act gtt tta agt ggc tgt ata gat ttc cac ttt cac 259
Phe Thr Tyr Asp Thr Val Leu Ser Gly Cys Ile Asp Phe His Phe His
40 45 50

aac aga att agc aga ttc cca aaa ctt gaa tat tta att tta aaa aaa 307
Asn Arg Ile Ser Arg Phe Pro Lys Leu Glu Tyr Leu Ile Leu Lys Lys
55 60 65

att ctt aat aac tga tattaaattt atatacgcaa atctgacaca ttacttcctt 362
Ile Leu Asn Asn *
70

aggataaatt cctgtacgca cagtctttcc attttaagcc tattatacta tgaaggagtc 422

tgaatcaaca tctaagagct ccgagagttc aacaccagcc tgggccatat tgtgagaaca 482

cgtctctaca gacgatcaaa aaattagctt ggtgtggtgg cgcgcgctg tgatctcagc 542

taccaggag gctgaggtgg gaggatcact taagcccgagg aggtcgaggc tgctgtgagc 602

cgtgagccac tgatcatacc actgcactcc agtctgggca acagagcgat cctgtttcag 662

agaaaaaaaa gatccaagac ctctgtagac cacactgaca gccctgctac tatttgcaac 722

tggtcgcgcc ctctgtccga attcttggcc tcgagggccaa aat 765

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cca	gca	gct	ttt	cca	aag	gac	aat	atc	cat	ttc	aag	cct	ata	aat	aca	206
Pro	Ala	Ala	Phe	Pro	Lys	Asp	Asn	Ile	His	Phe	Lys	Pro	Ile	Asn	Thr	
				30					35					40		
aat	ctt	gat	agg	gca	aat	gaa	ttg	gca	aaa	aca	gac	att	ttg	agt	cta	254
Asn	Leu	Asp	Arg	Ala	Asn	Glu	Leu	Ala	Lys	Thr	Asp	Ile	Leu	Ser	Leu	
			45					50					55			
aca	agt	caa	aac	aag	acc	ttt	gat	ccc	aag	aaa	gaa	aat	ccc	att	gtg	302
Thr	Ser	Gln	Asn	Lys	Thr	Phe	Asp	Pro	Lys	Lys	Glu	Asn	Pro	Ile	Val	
		60					65					70				
tta	ctt	agt	gac	ttt	tac	tat	gga	cag	cat	aaa	gga	gaa	ggg	cag	ccg	350
Leu	Leu	Ser	Asp	Phe	Tyr	Tyr	Gly	Gln	His	Lys	Gly	Glu	Gly	Gln	Pro	
	75					80					85					
gaa	cag	aag	act	cac	acc	acc	ttt	aaa	tgc	ctc	agc	tgc	gtg	aaa	gtt	398
Glu	Gln	Lys	Thr	His	Thr	Thr	Phe	Lys	Cys	Leu	Ser	Cys	Val	Lys	Val	
90				95						100				105		
cta	aaa	aat	gtt	aag	ttt	atg	aat	cac	gtg	aag	cat	cat	ttg	gaa	ttt	446
Leu	Lys	Asn	Val	Lys	Phe	Met	Asn	His	Val	Lys	His	His	Leu	Glu	Phe	
				110					115					120		
gag	aag	cag	agg	aac	gac	agc	tgg	gaa	aac	cac	acc	acc	tgc	cag	cac	494
Glu	Lys	Gln	Arg	Asn	Asp	Ser	Trp	Glu	Asn	His	Thr	Thr	Cys	Gln	His	
			125					130					135			
tgc	cac	cgg	agt	ctt	ccc	act	ccc	ttc	cag	cta	cag	tgt	cac	atc	gaa	542
Cys	His	Arg	Ser	Leu	Pro	Thr	Pro	Phe	Gln	Leu	Gln	Cys	His	Ile	Glu	
		140					145					150				
aat	gtc	cac	act	gcc	cag	gag	ccc	tct	act	gtc	tgt	aaa	atc	tgt	gaa	590
Asn	Val	His	Thr	Ala	Gln	Glu	Pro	Ser	Thr	Val	Cys	Lys	Ile	Cys	Glu	
	155					160					165					
ttg	tca	ttt	gaa	aca	gat	cag	gtc	ctc	tta	caa	cac	atg	aag	gac	cat	638
Leu	Ser	Phe	Glu	Thr	Asp	Gln	Val	Leu	Leu	Gln	His	Met	Lys	Asp	His	
170					175					180				185		
cat	aag	cct	ggc	gaa	atg	ccc	tat	gtg	tgc	cag	gtt	tgc	cat	tat	aga	686
His	Lys	Pro	Gly	Glu	Met	Pro	Tyr	Val	Cys	Gln	Val	Cys	His	Tyr	Arg	
			190						195					200		
tcg	tcg	gtc	ttt	gct	gat	gta	gaa	aca	cat	ttt	aga	acg	tgc	cat	gaa	734
Ser	Ser	Val	Phe	Ala	Asp	Val	Glu	Thr	His	Phe	Arg	Thr	Cys	His	Glu	
			205					210					215			
aac	aca	aag	aat	ttg	ctt	tgt	ccc	ttt	tgt	ctc	aaa	att	ttc	aaa	aca	782
Asn	Thr	Lys	Asn	Leu	Leu	Cys	Pro	Phe	Cys	Leu	Lys	Ile	Phe	Lys	Thr	
		220					225					230				
gca	aca	cca	tac	atg	tgt	cat	tat	agg	ggc	cac	tgg	gga	aag	agt	gca	830
Ala	Thr	Pro	Tyr	Met	Cys	His	Tyr	Arg	Gly	His	Trp	Gly	Lys	Ser	Ala	

235	240	245	
cac cag tgt tcc aag tgc cgg cta cag ttt tta act ttc aag gag aaa			878
His Gln Cys Ser Lys Cys Arg Leu Gln Phe Leu Thr Phe Lys Glu Lys			
250	255	260	265
atg gag cac aag acc cag tgt cat caa atg ttt aag aag cct aag caa			926
Met Glu His Lys Thr Gln Cys His Gln Met Phe Lys Lys Pro Lys Gln			
270	275		280
cta gaa gga tta cct cct gaa aca aaa gtt act att caa gtg tca ctg			974
Leu Glu Gly Leu Pro Pro Glu Thr Lys Val Thr Ile Gln Val Ser Leu			
285	290		295
gaa cct ctt cag cca gga tca gtg gat gta gca tcc ata act gtg agc			1022
Glu Pro Leu Gln Pro Gly Ser Val Asp Val Ala Ser Ile Thr Val Ser			
300	305		310
aca tct gac tct gaa cca tca ctc ccc agg tct aaa agc aaa att tca			1070
Thr Ser Asp Ser Glu Pro Ser Leu Pro Arg Ser Lys Ser Lys Ile Ser			
315	320		325
aaa aag tcc cat taa ttctagtttc agtaaatcta aagcaagtat ttcaaacc			1125
Lys Lys Ser His *			
330			
attaaaaaac ctcataaaac aaaaaataca aaccatacat tattcagtag caccaaaaat			1185
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aaaaaa			1251
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	Met Pro Ser		
	1		
gca tcc tgt gat aca cta ctg gat gac atc gaa gat atc gtg tct cag			162
Ala Ser Cys Asp Thr Leu Leu Asp Asp Ile Glu Asp Ile Val Ser Gln			
5	10	15	
gaa gat tca aaa cca caa gat agg cat ttt gta aga aag gat gtt gtc			210
Glu Asp Ser Lys Pro Gln Asp Arg His Phe Val Arg Lys Asp Val Val			

20	25	30	35	
ccg aag gta cga agg cga aat acc caa aaa tat ttg caa gag gaa gaa				258
Pro Lys Val Arg Arg Asn Thr Gln Lys Tyr Leu Gln Glu Glu	40	45	50	
aac agt cca cca agt gac agc act att cca ggc ata cag aaa att tgg				306
Asn Ser Pro Pro Ser Asp Ser Thr Ile Pro Gly Ile Gln Lys Ile Trp	55	60	65	
ata cga aca tgg ggt tgt tct cat aat aat tca gat gga gaa tat atg				354
Ile Arg Thr Trp Gly Cys Ser His Asn Asn Ser Asp Gly Glu Tyr Met	70	75	80	
gct gga cag cta gct gct tat ggc tat aaa att aca gaa aat gca tcc				402
Ala Gly Gln Leu Ala Ala Tyr Gly Tyr Lys Ile Thr Glu Asn Ala Ser	85	90	95	
gat gca gat tta tgg ctc ctg aac agt tgc act gta aaa aac cca gct				450
Asp Ala Asp Leu Trp Leu Leu Asn Ser Cys Thr Val Lys Asn Pro Ala	100	105	110	115
gaa gac cac ttt aga aac tca att aaa aaa gct caa gag gag aac aag				498
Glu Asp His Phe Arg Asn Ser Ile Lys Lys Ala Gln Glu Glu Asn Lys	120	125	130	
aaa atc gta ctg gct gga tgc gtt cct caa gcc cag cct cgc cag gac				546
Lys Ile Val Leu Ala Gly Cys Val Pro Gln Ala Gln Pro Arg Gln Asp	135	140	145	
tac ctt aag gga ctg agt atc att ggg gtt cag cag ata gat cgt gtg				594
Tyr Leu Lys Gly Leu Ser Ile Ile Gly Val Gln Gln Ile Asp Arg Val	150	155	160	
gta gaa gtt gtg gag gag aca att aaa ggt cac tct gtg aga ctg ctg				642
Val Glu Val Val Glu Glu Thr Ile Lys Gly His Ser Val Arg Leu Leu	165	170	175	
ggg cag aaa aag gat aat gga agg cgg ctt ggg gga gca cga ttg gat				690
Gly Gln Lys Lys Asp Asn Gly Arg Arg Leu Gly Gly Ala Arg Leu Asp	180	185	190	195
ttg ccg aag att agg aag aat cca ctg ata gaa atc att tcc atc aat				738
Leu Pro Lys Ile Arg Lys Asn Pro Leu Ile Glu Ile Ile Ser Ile Asn	200	205	210	
acc ggg tgt ctc aat gct tgt acc tac tgc aaa act aaa cac gcc aga				786
Thr Gly Cys Leu Asn Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg	215	220	225	
gga aat ttg gcc agt tat cca att gat gaa cta gta gat aga gcc aaa				834
Gly Asn Leu Ala Ser Tyr Pro Ile Asp Glu Leu Val Asp Arg Ala Lys	230	235	240	
caa tct ttt caa gag ggt gtt tgt gag ata tgg ttg acc agt gaa gac				882
Gln Ser Phe Gln Glu Gly Val Cys Glu Ile Trp Leu Thr Ser Glu Asp	245	250	255	

acg ggg gct tat ggc aga gat att ggc acc aat ctc ccc aca ctc ctg	930
Thr Gly Ala Tyr Gly Arg Asp Ile Gly Thr Asn Leu Pro Thr Leu Leu	
260 265 270 275	
tgg aaa ctg gtt gaa gtg att cct gag gga gca atg ctg agg ctt ggc	978
Trp Lys Leu Val Glu Val Ile Pro Glu Gly Ala Met Leu Arg Leu Gly	
280 285 290	
atg aca aat ccg ccc tat att tta gag cat ctg gag gaa atg gca aaa	1026
Met Thr Asn Pro Pro Tyr Ile Leu Glu His Leu Glu Glu Met Ala Lys	
295 300 305	
atc ctt aat cac ccc aga gtc tac gct ttt ctg cac ata cca gtc cag	1074
Ile Leu Asn His Pro Arg Val Tyr Ala Phe Leu His Ile Pro Val Gln	
310 315 320	
tct gcc tcc gac agc gta ctc atg gaa atg aaa aga gaa tac tgt gtg	1122
Ser Ala Ser Asp Ser Val Leu Met Glu Met Lys Arg Glu Tyr Cys Val	
325 330 335	
gct gac ttc aaa aga gta gtg gat ttt ctg aaa gag aaa gtt cct gga	1170
Ala Asp Phe Lys Arg Val Val Asp Phe Leu Lys Glu Lys Val Pro Gly	
340 345 350 355	
ata act att gct aca gat att atc tgt ggt ttt cct gga gaa aca gat	1218
Ile Thr Ile Ala Thr Asp Ile Ile Cys Gly Phe Pro Gly Glu Thr Asp	
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cag gat ttt caa gaa aca gtg aaa ctt gtt gaa gag tac aaa ttc cca	1266
Gln Asp Phe Gln Glu Thr Val Lys Leu Val Glu Glu Tyr Lys Phe Pro	
375 380 385	
agc ctg ttt att aac caa ttt tac cca aga cca gga act cct gct gca	1314
Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly Thr Pro Ala Ala	
390 395 400	
aaa atg gaa caa gtt cca gca caa gtg aaa aag caa agg aca aaa gat	1362
Lys Met Glu Gln Val Pro Ala Gln Val Lys Lys Gln Arg Thr Lys Asp	
405 410 415	
ctt tct cgg gtg ttt cat tct tac agt cca tat gat cac aag att ggt	1410
Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr Asp His Lys Ile Gly	
420 425 430 435	
gaa aga caa caa gtg tta gta aca gaa gaa tct ttt gat tcc aag ttt	1458
Glu Arg Gln Gln Val Leu Val Thr Glu Glu Ser Phe Asp Ser Lys Phe	
440 445 450	
tat gtt gca cac aat caa ttc tat gag cag gtt tta gtg cca aag aac	1506
Tyr Val Ala His Asn Gln Phe Tyr Glu Gln Val Leu Val Pro Lys Asn	
455 460 465	
cct gcg ttc atg ggg aag atg gtt gaa gtg gac atc tat gaa tca ggc	1554
Pro Ala Phe Met Gly Lys Met Val Glu Val Asp Ile Tyr Glu Ser Gly	
470 475 480	

aaa cat ttt atg aaa ggg cag cca gta tct gat gcc aaa gtg tac acg	1602
Lys His Phe Met Lys Gly Gln Pro Val Ser Asp Ala Lys Val Tyr Thr	
485 490 495	
ccc tcc atc agc aaa ccg cta gca aag gga gaa gtc tca ggt ttg aca	1650
Pro Ser Ile Ser Lys Pro Leu Ala Lys Gly Glu Val Ser Gly Leu Thr	
500 505 510 515	
aag gac ttc aga aat ggg ctt ggg aac cag ctg agt tca gga tcc cac	1698
Lys Asp Phe Arg Asn Gly Leu Gly Asn Gln Leu Ser Ser Gly Ser His	
520 525 530	
acc tct gct gca tct cag tgt gac tca gcg agt tcc aga atg gtg ctg	1746
Thr Ser Ala Ala Ser Gln Cys Asp Ser Ala Ser Ser Arg Met Val Leu	
535 540 545	
ccc atg cca agg cta cat caa gac tgt gcg ctg agg atg tcc gtg ggc	1794
Pro Met Pro Arg Leu His Gln Asp Cys Ala Leu Arg Met Ser Val Gly	
550 555 560	
ttg gct ctg ctg ggt ctt ctt ttt gct ttt ttt gtc aag gtc tat aat	1842
Leu Ala Leu Leu Gly Leu Leu Phe Ala Phe Phe Val Lys Val Tyr Asn	
565 570 575	
tag aata caactaatgg aaacatctat aaagaagaat acatttctaa ttaaaatctt	1899
* 580	
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catcattggt ctttactaag tgaagtgact tctttcttta acaataaatg gaattggtat	2619
actaagcaaa aaaaaaaaaa	2638

agc cag gac ggg atc cag agg ccg ccc ttc cgc ttc ccc aag ggc ggg Ser Gln Asp Gly Ile Gln Arg Pro Pro Phe Arg Phe Pro Lys Gly Gly 160 165 170	768
cac ctc ctg cag ttc ctc tcg tgc ctg gag aat ggg ctg ctc cca cat His Leu Leu Gln Phe Leu Ser Cys Leu Glu Asn Gly Leu Leu Pro His 175 180 185	816
ggg cag ttg gac ccg cca ctg tgg tcc cag agg ggt aag ggc aaa gtg Gly Gln Leu Asp Pro Pro Leu Trp Ser Gln Arg Gly Lys Gly Lys Val 190 195 200 205	864
ttt cct aaa ctg cgc aag cga agc cct cag ggt tct gcc gag tcc aca Phe Pro Lys Leu Arg Lys Arg Ser Pro Gln Gly Ser Ala Glu Ser Thr 210 215 220	912
tct tca gac aaa gat gat gat gag gcc acg gat tat gtg ttc agg atc Ser Ser Asp Lys Asp Asp Asp Glu Ala Thr Asp Tyr Val Phe Arg Ile 225 230 235	960
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agc act tcc tcc gtc tct gtg ggc cct gcc tgg atg atg gtt cct gca Ser Thr Ser Ser Val Ser Val Gly Pro Ala Trp Met Met Val Pro Ala 255 260 265	1056
ggc cgg tcc atg ctg gtg gtg gcc aga ggg agt cag tgg gag cca gcc Gly Arg Ser Met Leu Val Val Ala Arg Gly Ser Gln Trp Glu Pro Ala 270 275 280 285	1104
aga tgg gac act act ctc ccc acg cca agc ccg aag gag cag ccc ccc Arg Trp Asp Thr Thr Leu Pro Thr Pro Ser Pro Lys Glu Gln Pro Pro 290 295 300	1152
agt aat gtc tgg gat ctc ccc gtc ccc agg ggc tgg gtg cca gcc acc Ser Asn Val Trp Asp Leu Pro Val Pro Arg Gly Trp Val Pro Ala Thr 305 310 315	1200
tct gcc atg ttg tca att gag ttc tgg tcc caa ggg aga tgg agg cag Ser Ala Met Leu Ser Ile Glu Phe Trp Ser Gln Gly Arg Trp Arg Gln 320 325 330	1248
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<213> Homo sapiens

<220>

<221> CDS

<222> (101)..(637)

<400> 341

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                                         Met Thr Lys Phe Leu
                                         1           5

att gtt tca gat aca cat ggt gat cgt gag atc att gct gat att ttt      163
Ile Val Ser Asp Thr His Gly Asp Arg Glu Ile Ile Ala Asp Ile Phe
                        10                        15                        20

gac aaa tgg cgg gat agc gtt gcc ggc att ttt tac aat ggg gat tct      211
Asp Lys Trp Arg Asp Ser Val Ala Gly Ile Phe Tyr Asn Gly Asp Ser
                        25                        30                        35

gaa tta gcg gct gat gac aca gta ttt gat ggc gta tcc act gtg att      259
Glu Leu Ala Ala Asp Asp Thr Val Phe Asp Gly Val Ser Thr Val Ile
                        40                        45                        50

ggc aat atg gat gat gat cct gat ttc gtg gcc gca agg gcg aca acg      307
Gly Asn Met Asp Asp Asp Pro Asp Phe Val Ala Ala Arg Ala Thr Thr
                        55                        60                        65

att gat ggg att act ttt ttc caa acg cac gga cat ctc tat gac gcg      355
Ile Asp Gly Ile Thr Phe Phe Gln Thr His Gly His Leu Tyr Asp Ala
                        70                        75                        80                        85

acc caa ttt aac gct tgg gcg aac cta aaa tta atg gcc gtg gca gca      403
Thr Gln Phe Asn Ala Trp Ala Asn Leu Lys Leu Met Ala Val Ala Ala
                        90                        95                        100

cag gaa gct aac gca cag gtc gcc ctc ttt ggg cat acc cat ctg gaa      451
Gln Glu Ala Asn Ala Gln Val Ala Leu Phe Gly His Thr His Leu Glu
                        105                        110                        115

ggg gcg gtt gtg ttt gat gat atc ttg ttt att aat cca ggt tca atc      499
Gly Ala Val Val Phe Asp Asp Ile Leu Phe Ile Asn Pro Gly Ser Ile
                        120                        125                        130

cgg ctg cct aaa ggg cca cat gcc aac tta ggt ggt act tat gct gtg      547
Arg Leu Pro Lys Gly Pro His Ala Asn Leu Gly Gly Thr Tyr Ala Val
                        135                        140                        145

ttg gat gtg acg gag acg agc tat gac gtg aga ttt tat aat cgt cag      595
Leu Asp Val Thr Glu Thr Ser Tyr Asp Val Arg Phe Tyr Asn Arg Gln
                        150                        155                        160                        165

cat caa cca ttg cca caa ctc acg gta cag gtc gca cgt taa gtgaccc      644
His Gln Pro Leu Pro Gln Leu Thr Val Gln Val Ala Arg *
                        170                        175
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caatttaatc aatggtatg 723

<210> 342
<211> 637
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<213> Homo sapiens

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tcctgggacc aagaccagga aatctaacca ataagcaatg gtaacagtga ctcaagtgtc 180
agtccgccct cagtggcccg agtccgaggt gggcatcatg gcaccagttt acatctcgga 240
aagggagggt cagagagggtc aagtcacttg cctaagggtca cccagggact gcttagctgg 300
ctaggatgag aaccagcctg ctccaacgcc ccctcgtgga acagttgcga gcttaggaat 360
taa atg ttc cct ccc cca ggc tat gcc aat gag gtg ggc gag gct ttc 408
Met Phe Pro Pro Pro Gly Tyr Ala Asn Glu Val Gly Glu Ala Phe
1 5 10 15
cgc tct ctt gtg cca gcg gcg gtg gtg tgg ctg agc tat ggc gtg gcc 456
Arg Ser Leu Val Pro Ala Ala Val Val Trp Leu Ser Tyr Gly Val Ala
20 25 30
agc tcc tac gtg ctg gcg gat gcc att gac aaa ggc aag aag gct gga 504
Ser Ser Tyr Val Leu Ala Asp Ala Ile Asp Lys Gly Lys Lys Ala Gly
35 40 45
gag gtg agt gtt agc cta ttt tcc aac ccc caa ccc tag ctctcctctt 553
Glu Val Ser Val Ser Leu Phe Ser Asn Pro Gln Pro *
50 55 60
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caacttgcct agtgcagtcc ataa 637

<210> 343
<211> 998
<212> DNA
<213> Homo sapiens

<220>
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 <222> (7)..(399)

<400> 343

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	1 5 10	
aag ttc atg cct att ctg ggg ttt ggc acc tct gtt gct agg aag gtt	96	
Lys Phe Met Pro Ile Leu Gly Phe Gly Thr Ser Val Ala Arg Lys Val		
15 20 25 30		
gct atg agt aat gta gaa gaa gcc gtc cag gta gca att gat gta ggc	144	
Ala Met Ser Asn Val Glu Glu Ala Val Gln Val Ala Ile Asp Val Gly		
35 40 45		
tac cgc cat att gac tca gct tat aca cac ctg aat gaa gaa ggc atc	192	
Tyr Arg His Ile Asp Ser Ala Tyr Thr His Leu Asn Glu Glu Gly Ile		
50 55 60		
ggg cag gcc atc cga aag aag att gcc aac ggc act gtg aag aga aaa	240	
Gly Gln Ala Ile Arg Lys Lys Ile Ala Asn Gly Thr Val Lys Arg Lys		
65 70 75		
gat ata ttc tat acc aca aag gtg tgg ggc acc ttt tcc cgc cca gaa	288	
Asp Ile Phe Tyr Thr Thr Lys Val Trp Gly Thr Phe Ser Arg Pro Glu		
80 85 90		
ttg gtc caa aga ggc ctt gaa atg tca ctg aag aaa ctt cag ctg agc	336	
Leu Val Gln Arg Gly Leu Glu Met Ser Leu Lys Lys Leu Gln Leu Ser		
95 100 105 110		
tac atg gat ctt tac ctt ttt cat ttc cca gta cct ttg cag cct ggg	384	
Tyr Met Asp Leu Tyr Leu Phe His Phe Pro Val Pro Leu Gln Pro Gly		
115 120 125		
agg agc ttt tgc tga cggatgcaca gggaaagatc atgtttgaca cagtgggtct	439	
Arg Ser Phe Cys *		
130		
ctgcagcaca tgggagagtt ttactcctgt tgccaaggct ggagtacagt ggcacgatct	499	
cggctcactg caacctccgc ctcccagggt caagcatgta cctctgcctc ccacatagct	559	
gggaatacag gtggaatata acccttacct caaccaaagc aaactcctgg agtactgtaa	619	
gtccaaggac attgtcatga ctgcatattc tgccttgggg tctgactcag acaaagactg	679	
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agtcaggatc ttcctccta gacctcctaa gtagctggga ctacaggagt gcaccaccat	859	
gcctggctaa ttgtttatct tcatttttgt agagacaggg tctcactacg ttaccaagc	919	

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tagaggtgta agccacggt 998

<210> 344
<211> 478
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)..(376)

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actgctgctg tggagctcag catcaagtac ttccaggaga agcttcagca ggacctagag 180
gcagagc atg gta gag gta gag gat aca gcc ctc ata cca ccg tgc tgt 229
Met Val Glu Val Glu Asp Thr Ala Leu Ile Pro Pro Cys Cys
1 5 10
atg tcc atc ttt caa gtc ctg gtg gtg ccc gca gag ttt gaa ggg aag 277
Met Ser Ile Phe Gln Val Leu Val Val Pro Ala Glu Phe Glu Gly Lys
15 20 25 30
cca ctg ctt cag aga tac cag gtg gta aat gca tgc cta gtg gaa gtg 325
Pro Leu Leu Gln Arg Tyr Gln Val Val Asn Ala Cys Leu Val Glu Val
35 40 45
tgc tcc tct gca tct atg cct ttg agc aga aag cct ttg agt ccc aat 373
Cys Ser Ser Ala Ser Met Pro Leu Ser Arg Lys Pro Leu Ser Pro Asn
50 55 60
tag tggg cccatgagtg gccaaaatga gggactggga cctgtatagc cgttaaacta 430
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taaatcaggg ccaaaaagga aagataaatt ataagtttaa agaaaatg 478

<210> 345
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201)..(368)

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tctcctgtgt cacctctctt gtgtccacag tctaaccat ctcttcattt ccctcaacct 180
caggtggagc ctccaccaaa atg cag att ttt cca aaa atc ctt aca ggg 230
Met Gln Ile Phe Pro Lys Ile Leu Thr Gly
1 5 10
acg atc atc acc cta gag gtt gaa ccc ttg gat aca aca gaa aaa tgt 278
Thr Ile Ile Thr Leu Glu Val Glu Pro Leu Asp Thr Thr Glu Lys Cys
15 20 25
aaa ggc caa tat cag gat aag gaa cga att cct cct gat cag caa aga 326
Lys Gly Gln Tyr Gln Asp Lys Glu Arg Ile Pro Pro Asp Gln Gln Arg
30 35 40
caa gtg act gga agc tgg caa gta act gga aga tgg aca taa ctttctc 375
Gln Val Thr Gly Ser Trp Gln Val Thr Gly Arg Trp Thr *
45 50 55
tgactacaac attcaaaagg aatttactct ttttatgttg tgttgagact tcatggtagt 435
gctaaaacta ggaagaaatc ttac 459

<210> 346
<211> 1867
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (9) .. (1835)

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Met Leu Thr Tyr Leu Asn Ile Ser Arg Asn Leu Leu Ser Thr
1 5 10
ttg cca aaa tac cta ttt gat ctt ccc ctt aaa gtt ttg gtc gtc agt 98
Leu Pro Lys Tyr Leu Phe Asp Leu Pro Leu Lys Val Leu Val Val Ser
15 20 25 30
aat aat aaa ctg gta tcc att cca gaa gaa att ggg aag tta aaa gat 146
Asn Asn Lys Leu Val Ser Ile Pro Glu Glu Ile Gly Lys Leu Lys Asp
35 40 45
tta atg gaa ttg gat att agc tgc aat gag att caa gtc ctt ccc caa 194
Leu Met Glu Leu Asp Ile Ser Cys Asn Glu Ile Gln Val Leu Pro Gln
50 55 60
caa atg gga aaa tta cat tca ctt aga gag cta aat ata aga aga aat 242

Gln Met Gly Lys Leu His Ser Leu Arg Glu Leu Asn Ile Arg Arg Asn	
65 70 75	
aat ctt cat gtt ttg cca gat gaa tta gga gac ctt ccc tta gtc aag	290
Asn Leu His Val Leu Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Lys	
80 85 90	
ctg gat ttc tct tgt aat aaa gtg acc gaa att cca gtt tgt tac aga	338
Leu Asp Phe Ser Cys Asn Lys Val Thr Glu Ile Pro Val Cys Tyr Arg	
95 100 105 110	
aag ctg cat cat tta caa gta ata att ttg gat aac aat cca ttg caa	386
Lys Leu His His Leu Gln Val Ile Ile Leu Asp Asn Asn Pro Leu Gln	
115 120 125	
gta cca cca gca cag ata tgt tta aag ggt aag gtg cac ata ttt aag	434
Val Pro Pro Ala Gln Ile Cys Leu Lys Gly Lys Val His Ile Phe Lys	
130 135 140	
tac tta aat att caa gca tgt tgc aga atg gat aag aaa cca gat tcc	482
Tyr Leu Asn Ile Gln Ala Cys Cys Arg Met Asp Lys Lys Pro Asp Ser	
145 150 155	
ctg gat ctt cca tca ttg agt aaa cga atg ccc tca cag cct ctc aca	530
Leu Asp Leu Pro Ser Leu Ser Lys Arg Met Pro Ser Gln Pro Leu Thr	
160 165 170	
gac agt atg gaa gat ttt tat cca aat aaa aat cat ggc cct gac tct	578
Asp Ser Met Glu Asp Phe Tyr Pro Asn Lys Asn His Gly Pro Asp Ser	
175 180 185 190	
gga att gga agt gat aat gga gag aaa cga tta tcc aca aca gaa cca	626
Gly Ile Gly Ser Asp Asn Gly Glu Lys Arg Leu Ser Thr Thr Glu Pro	
195 200 205	
tca gat gat gac aca gtc agc ctt cat tct caa gtc tca gaa tca aat	674
Ser Asp Asp Asp Thr Val Ser Leu His Ser Gln Val Ser Glu Ser Asn	
210 215 220	
aga gag cag aca tca aga aat gac agt cac ata ata gga agt aag act	722
Arg Glu Gln Thr Ser Arg Asn Asp Ser His Ile Ile Gly Ser Lys Thr	
225 230 235	
gat tct cag aaa gac cag gag gta tat gat ttt gtt gac ccc aac aca	770
Asp Ser Gln Lys Asp Gln Glu Val Tyr Asp Phe Val Asp Pro Asn Thr	
240 245 250	
gaa gat gta gca gtt cct gaa cag gga aat gca cat att gga tca ttt	818
Glu Asp Val Ala Val Pro Glu Gln Gly Asn Ala His Ile Gly Ser Phe	
255 260 265 270	
gta tca ttc ttt aag gga aaa gaa aaa tgt tct gaa aaa tct cgg aaa	866
Val Ser Phe Phe Lys Gly Lys Glu Lys Cys Ser Glu Lys Ser Arg Lys	
275 280 285	
aat gaa gaa tta gga gat gaa aaa aga ctt gag aaa gaa cag tta ctg	914
Asn Glu Glu Leu Gly Asp Glu Lys Arg Leu Glu Lys Glu Gln Leu Leu	

290	295	300	
gca gag gaa gag gat gat gat ttg aag gaa gta act gat ttg agg aaa			962
Ala Glu Glu Glu Asp Asp Asp Leu Lys Glu Val Thr Asp Leu Arg Lys			
305	310	315	
ata gct gct cag tta ttg cag caa gaa cag aag aac agg att ctt aat			1010
Ile Ala Ala Gln Leu Leu Gln Gln Glu Gln Lys Asn Arg Ile Leu Asn			
320	325	330	
cat tca act tct gtg atg aga aac aag cca aaa caa act gtg gaa tgt			1058
His Ser Thr Ser Val Met Arg Asn Lys Pro Lys Gln Thr Val Glu Cys			
335	340	345	350
gaa aag agt gtc tca gca gat gaa gtt aat tca cca tta tca ccc ctc			1106
Glu Lys Ser Val Ser Ala Asp Glu Val Asn Ser Pro Leu Ser Pro Leu			
355	360	365	
acc tgg cag ccc tta gaa aat cag aag gat caa ata gat gaa caa ccg			1154
Thr Trp Gln Pro Leu Glu Asn Gln Lys Asp Gln Ile Asp Glu Gln Pro			
370	375	380	
tgg cca gaa tct cac cct ata atc tgg cag agt gaa gaa agg agg cgg			1202
Trp Pro Glu Ser His Pro Ile Ile Trp Gln Ser Glu Glu Arg Arg Arg			
385	390	395	
agc aaa cag att aga aaa gaa tat ttc aag tat aaa tca atg agg aag			1250
Ser Lys Gln Ile Arg Lys Glu Tyr Phe Lys Tyr Lys Ser Met Arg Lys			
400	405	410	
agt tca agt ggc aat gaa aat gat gag caa gac agt gat aat gct aat			1298
Ser Ser Ser Gly Asn Glu Asn Asp Glu Gln Asp Ser Asp Asn Ala Asn			
415	420	425	430
atg tca aca caa tct cca gta tca tct gag gaa tat gac aga act gat			1346
Met Ser Thr Gln Ser Pro Val Ser Ser Glu Glu Tyr Asp Arg Thr Asp			
435	440	445	
ggt ttt tca cac agt ccc ttt ggc ttg aag cct aga tca gct ttt agc			1394
Gly Phe Ser His Ser Pro Phe Gly Leu Lys Pro Arg Ser Ala Phe Ser			
450	455	460	
cgc tca tct cgc caa gaa tat ggg gca gca gat cca gga ttt aca atg			1442
Arg Ser Ser Arg Gln Glu Tyr Gly Ala Ala Asp Pro Gly Phe Thr Met			
465	470	475	
aga aga aag atg gaa cat tta cgg gaa gag cga gag caa ata cga caa			1490
Arg Arg Lys Met Glu His Leu Arg Glu Glu Arg Glu Gln Ile Arg Gln			
480	485	490	
ctt cgc aac aat ctt gaa tcc agg tta aaa gta att ttg cct gat gac			1538
Leu Arg Asn Asn Leu Glu Ser Arg Leu Lys Val Ile Leu Pro Asp Asp			
495	500	505	510
att gga gct gca ctg atg gat ggg gtt gtt ctt tgc cat tta gcc aat			1586
Ile Gly Ala Ala Leu Met Asp Gly Val Val Leu Cys His Leu Ala Asn			
515	520	525	

cat ata agg cca cgt tct gtt gct agt att cat gta cca tca cca gca	1634
His Ile Arg Pro Arg Ser Val Ala Ser Ile His Val Pro Ser Pro Ala	
530 535 540	
gtg ccc aaa ctg agc atg gca aaa tgt cga aga aat gta gaa aat ttt	1682
Val Pro Lys Leu Ser Met Ala Lys Cys Arg Arg Asn Val Glu Asn Phe	
545 550 555	
ctt gat gct tgt aaa aag ttg ggt gtc tca cag gaa aga ctt tgt ttg	1730
Leu Asp Ala Cys Lys Lys Leu Gly Val Ser Gln Glu Arg Leu Cys Leu	
560 565 570	
cct cat cat att ttg gaa gaa cga gga ctt gtg aaa gtt ggt gtc aca	1778
Pro His His Ile Leu Glu Glu Arg Gly Leu Val Lys Val Gly Val Thr	
575 580 585 590	
gtt cag gcg ctc ctt gaa tta cca aca acc aag gca tct cag ctt tct	1826
Val Gln Ala Leu Leu Glu Leu Pro Thr Thr Lys Ala Ser Gln Leu Ser	
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gtg gct taa tataacattt taaaattcta aaaaaaaaaa aa	1867
Val Ala *	

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tacataactc ttttatctgc agttttgggg gagtccaatt ccaccatttt ttatgtctgt	120
tactgtcatt ca atg tgg att gct tcc tta tgt ttc att att ttg gat	168
Met Trp Ile Ala Ser Leu Cys Phe Ile Ile Leu Asp	
1 5 10	
tgt gag ctc atc ttt tgt agg gtg tta gct aca gaa atc cta tgc tgc	216
Cys Glu Leu Ile Phe Cys Arg Val Leu Ala Thr Glu Ile Leu Cys Cys	
15 20 25	
agg gtt gag att tgt ccc tat ttg ctt ctg tat tac tgc cta agg acc	264
Arg Val Glu Ile Cys Pro Tyr Leu Leu Leu Tyr Tyr Cys Leu Arg Thr	
30 35 40	
aac ttt gct cat tta aaa tat att tat ata agc tca aag att aaa gct	312
Asn Phe Ala His Leu Lys Tyr Ile Tyr Ile Ser Ser Lys Ile Lys Ala	

45	50	55	60	
gac tgt ggg gag gtc tat ggc taa aaattttcaa gggagatttc ttccccctaa				366
Asp Cys Gly Glu Val Tyr Gly *				
65				
tctggctaag atgggcagat toccattgtc ttcctgtgcc agtgtgcaga tatcatctag				426
tatactcttt cactgcaagc atgggtcttc gagggctctg gctctatgac gaagtcttca				486
gttccaaatc ttcattctgt gccagcctaa cgcctttgtt t				527

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ttttctgcta aaaccagatt ttgaggaatc agagaccccc aacactactc actcagtagc	180
tagcagcccc ttcctttcaa ctgggagtgt tattagaatg aaaagtaatt agttagaagg	240
gcatacatct cagtggcatg agcattgtgg aatatccttt cctaggcaca tttgtccact	300
aagggaacag cctcagaaac tgggtacagca atgggtgaga tgagatcctg gagagagaac	360
acagccatcc cctatagaaa ggcacagctt ttgggcttct ctggcctga	415
	atg cct Met Pro 1
tct ggg gta ttt cca tat gca aca gcc cag agt cat agc ctt ggg caa	463
Ser Gly Val Phe Pro Tyr Ala Thr Ala Gln Ser His Ser Leu Gly Gln	
5 10 15	
cca cac ata gag gtt tcc ttc tca ctt cag aca cat aca tca ctt tca	511
Pro His Ile Glu Val Ser Phe Ser Leu Gln Thr His Thr Ser Leu Ser	
20 25 30	
cac cac ttg ggg atg gaa ata cct aca aga gtg aag gtc aag ggc cct	559
His His Leu Gly Met Glu Ile Pro Thr Arg Val Lys Val Lys Gly Pro	
35 40 45 50	
ccc cag gca tct cat tca tta ctc agc ttc ctt cct gac caa gtc tgc	607
Pro Gln Ala Ser His Ser Leu Leu Ser Phe Leu Pro Asp Gln Val Cys	
55 60 65	

caa cca atg gcc agc tat gcg cct cat cct cat tgc ttc tgc ctc cac	655
Gln Pro Met Ala Ser Tyr Ala Pro His Pro His Cys Phe Cys Leu His	
70 75 80	
gta aat gaa acc aaa ggc ctc agc ata tcc tgg gag gac tgg ggg ctg	703
Val Asn Glu Thr Lys Gly Leu Ser Ile Ser Trp Glu Asp Trp Gly Leu	
85 90 95	
tta cct aat ggt cct ctc tgt ccc att ata ggt gca agg cac ccc atc	751
Leu Pro Asn Gly Pro Leu Cys Pro Ile Ile Gly Ala Arg His Pro Ile	
100 105 110	
cac aca ttt gca cca cta ctc caa gat agt att ttt ctt ttc aca caa	799
His Thr Phe Ala Pro Leu Leu Gln Asp Ser Ile Phe Leu Phe Thr Gln	
115 120 125 130	
tct ctt tac agc aga atc cag agt tgg gtt gta gtt tac ctt cct gga	847
Ser Leu Tyr Ser Arg Ile Gln Ser Trp Val Val Val Tyr Leu Pro Gly	
135 140 145	
aag ctc att atc ttt gtt tga at taacatttca gcatggaact aactgggcgg	900
Lys Leu Ile Ile Phe Val *	
150	
aggaaggatc gttatacgtc ttcagaaagt tctcattgcc ccagctgcct agtactatac	960
aagaagctct accttgatgg cagatctaag aaggctatag gcctttgttt gtaggaagca	1020
gtgtcattac attcaagctt cacttctctg attggcttcc aacctgagg attcaaagag	1080
aatccaaggt tctgcctatg tctgatgaca taaggaaaac ttggcttcct ctgctcaagg	1140
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caatcccaat aaattctgac atgtccttgg caatggaagc ctgggttgga gatcctgagg	1380
cagctgtgcc tactgttccc cacctcagaa gcttcctgcc cagagagcca gcagccttgg	1440
gatactaatag aggatgcaac tggcttattg gtatgaaata gaaggtggct ttgtaggggc	1500
aagcaggcaa agagtactat ccacatggca ggcagggtgc tttgtgtctg gaaagctttg	1560
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tcttttccag gataaagaag gaaattaaaa taccatgaaa aaatggacat ggcagtagaa	1800
aggaaacatt ctgatcagac cttgggaaaa gctggtgccg agagagggag aggccagggtg	1860
tccccccacc caactggcac tgattctcag ccccttctc ttacttctgt tggcttcaag	1920

110	115	120	
ggc tgg tat cat tcc cat cct cat ata act gtt tgg cct tca cat gtt			435
Gly Trp Tyr His Ser His Pro His Ile Thr Val Trp Pro Ser His Val			
125	130	135	
gat gtt cgc aca caa gcc atg tac cag atg atg gat caa ggc ttt gta			483
Asp Val Arg Thr Gln Ala Met Tyr Gln Met Met Asp Gln Gly Phe Val			
140	145	150	155
gga ctt att ttt tcc tgt ttc ata gaa gat aag aac acg aag act ggc			531
Gly Leu Ile Phe Ser Cys Phe Ile Glu Asp Lys Asn Thr Lys Thr Gly			
	160	165	170
cgg gta ctc tac act tgc ttc caa tcc ata cag gcc caa aag agt tca			579
Arg Val Leu Tyr Thr Cys Phe Gln Ser Ile Gln Ala Gln Lys Ser Ser			
	175	180	185
gag tcc ctt cat ggt cca cga gac ttc tgg agc tcc agc cag cac atc			627
Glu Ser Leu His Gly Pro Arg Asp Phe Trp Ser Ser Ser Gln His Ile			
	190	195	200
tcc att gag ggc cag aag gaa gag gaa agg tat gag aga atc gaa atc			675
Ser Ile Glu Gly Gln Lys Glu Glu Glu Arg Tyr Glu Arg Ile Glu Ile			
	205	210	215
cca atc cat att gta cct cat gtc act atc tgg aaa gtg tgc ctt gaa			723
Pro Ile His Ile Val Pro His Val Thr Ile Trp Lys Val Cys Leu Glu			
	220	225	230
tca gca gta gag ctg ccc aag atc ctg tgc cag gag gag cag gat gcg			771
Ser Ala Val Glu Leu Pro Lys Ile Leu Cys Gln Glu Glu Gln Asp Ala			
	240	245	250
tat agg agg atc cac agc ctt aca cat ctg gac tca gta acc aag atc			819
Tyr Arg Arg Ile His Ser Leu Thr His Leu Asp Ser Val Thr Lys Ile			
	255	260	265
cat aat ggc tca gtg ttt acc aag aat ctg tgc agt cag atg tcg gca			867
His Asn Gly Ser Val Phe Thr Lys Asn Leu Cys Ser Gln Met Ser Ala			
	270	275	280
gtc agc ggg cct ctc cta cag tgg ttg gag gac aga ctg gag caa aac			915
Val Ser Gly Pro Leu Leu Gln Trp Leu Glu Asp Arg Leu Glu Gln Asn			
	285	290	295
caa cag cat ttg cag gaa tta caa caa gaa aag gaa gag ctt atg caa			963
Gln Gln His Leu Gln Glu Leu Gln Gln Glu Lys Glu Glu Leu Met Gln			
	300	305	310
gaa ctt tct tct cta gaa taa at caggagacaa aatgggggaaa gatgaaaata			1016
Glu Leu Ser Ser Leu Glu *			
	320		
tccagtgtaa agttacttaa gctaaatcaa tttcaaagaa gaaaaacttg gaggactcat			1076
tttacctgac ttcaagactt actataaagc tatagtaatc aagatagatg gtattggcag			1136

aggaacagac acatacgtca atggaacaga tgagagaacc cagaaataaa cccatataaa 1196
 tatgctcagc tgattttgaa aaagtgaaaa agcaattcaa tggaggaaga atagcctttc 1256
 tgacaaatta tgctagagca attagacacc catggcgagg agaaaaaaga acctctactt 1316
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 tctgagccga tgtaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct 172
 Met Phe Ala Pro Ala Val Met Arg Ala
 1 5
 ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg atg gat 220
 Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Met Asp
 10 15 20 25
 cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct tta gag tcg 268
 Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser
 30 35 40
 gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg aag aat att 316
 Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile
 45 50 55
 cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa gga aga aat 364
 Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn
 60 65 70
 cca gaa agc ctt aag act aag aca act tga c tctgctgatt cttttttcct 415
 Pro Glu Ser Leu Lys Thr Lys Thr Thr *
 75 80
 tttttttttt ttaaaaaaaaa aa 437

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 <213> Homo sapiens

<220>
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 <222> (25)..(1239)

<400> 351

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                                   Met Ala Ala Gly Thr Ala Val Gly Ala
                                   1                      5

tgg gtg ctg gtc ctc agt ctg tgg ggg gca gta gta ggt gct caa aac      99
Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10                      15                      20                      25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc      147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
                30                      35                      40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg      195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
                45                      50                      55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac      243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
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agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc      291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
 75                      80                      85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat      339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
 90                      95                      100                      105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct      387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
                110                      115                      120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt      435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
                125                      130                      135

ccc aat aag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg      483
Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly
                140                      145                      150

act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag      531
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys
                155                      160                      165

gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc      579
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu
 170                      175                      180                      185

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ttc aca ctg cag tcg gag cta atg gtg acc cca gcc cgg gga gga gat	627
Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp	
190 195 200	
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac	675
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His	
205 210 215	
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg	723
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val	
220 225 230	
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta	771
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val	
235 240 245	
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc	819
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro	
250 255 260 265	
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc	867
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro	
270 275 280	
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga	915
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly	
285 290 295	
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc	963
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser	
300 305 310	
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act	1011
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr	
315 320 325	
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg	1059
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu	
330 335 340 345	
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc	1107
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile	
350 355 360	
ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa	1155
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
365 370 375	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1203
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
380 385 390	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1253
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
395 400 405	

gatcccatcc atcagctccc tttttttttt cccttgaact gttctggcct cagaccaact 1313
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Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
10 15 20 25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc 147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
30 35 40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg 195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
45 50 55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac 243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
60 65 70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc 291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
75 80 85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat 339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
90 95 100 105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct 387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
110 115 120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt 435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
125 130 135

ccc aat aag gta gtg gaa gaa agc agg aga agt aga aaa cgg ccc tgt 483
Pro Asn Lys Val Val Glu Glu Ser Arg Arg Ser Arg Lys Arg Pro Cys

140	145	150	
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act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys 170 175 180 185			579
gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu 190 195 200			627
ttc aca ctg cag tgc gag cta atg gtg acc cca gcc cgg gga gga gat Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp 205 210 215			675
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His 220 225 230			723
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val 235 240 245			771
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val 250 255 260 265			819
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro 270 275 280			867
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro 285 290 295			915
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly 300 305 310			963
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser 315 320 325			1011
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr 330 335 340 345			1059
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu 350 355 360			1107
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile 365 370 375			1155

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Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
380 385 390	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa	1251
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
395 400 405	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1301
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
410 415 420	
gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact	1361
ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca	1421
gagcccccca caatgatgat taaacacctg acacatcttg ca	1463

<210> 353
 <211> 926
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)..(600)

<400> 353	
tttcgtggt atg gtc ccc ggg tcc gag ggc ccg gcc cgc gcc ggg agc	48
Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser	
1 5 10	
gtg gtg gcc gac gtg gtg ttt gtg att gag ggt acg gcc aac ctg gga	96
Val Val Ala Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly	
15 20 25	
ccc tac ttc gag ggg ctc cgc aag cac tac ctg ctc ccg gcc atc gag	144
Pro Tyr Phe Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu	
30 35 40 45	
tat ttt aat ggt ggt cct cct gct gag acg gac ttc ggg gga gac tat	192
Tyr Phe Asn Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr	
50 55 60	
ggg ggg acc cag tac agc ctc gtg gtg ttc aac aca gtg gac tgc gct	240
Gly Gly Thr Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala	
65 70 75	
ccc gag tcc tac gta caa tgt cac gct ccc acc agc agc gcc tat gag	288
Pro Glu Ser Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu	
80 85 90	
ttt gtc acc tgg ctc gat ggc att aag ttc atg ggc ggg ggt ggt gag	336

Phe Val Thr Trp Leu Asp Gly Ile Lys Phe Met Gly Gly Gly Gly Glu	
95 100 105	
agc tgc agc ctc atc gcg gaa gga ctc agc aca gcc ttg cag ctg ttt	384
Ser Cys Ser Leu Ile Ala Glu Gly Leu Ser Thr Ala Leu Gln Leu Phe	
110 115 120 125	
gat gac ttc aag aag atg cgc gag cag att ggc cag acg cac cgg gtc	432
Asp Asp Phe Lys Lys Met Arg Glu Gln Ile Gly Gln Thr His Arg Val	
130 135 140	
tgc ctc ctc atc tgc aac tca ccc cca tac ttg ttg cct gct gtt gag	480
Cys Leu Leu Ile Cys Asn Ser Pro Pro Tyr Leu Leu Pro Ala Val Glu	
145 150 155	
agc acc acg tac tct gga tgc aca act gag aat ctt gtg cag cca gat	528
Ser Thr Thr Tyr Ser Gly Cys Thr Thr Glu Asn Leu Val Gln Pro Asp	
160 165 170	
tgg gga agc ggg gga tcc act tct cca ttg gtg tct ccc cgg aag ctg	576
Trp Gly Ser Gly Gly Ser Thr Ser Pro Leu Val Ser Pro Arg Lys Leu	
175 180 185	
cct gcg ctt cgg ctt cct ggt tga agaaaggcag cccccggcc tgggtggagc	630
Pro Ala Leu Arg Leu Pro Gly *	
190 195	
cgctgaggcc tccgacagat gttgaggcac tgaccgaggg acatggtggt gggttcgggga	690
ctcgtgctgc tgggggggggt ggtcagccca gggccttcaa taaagaagca gggcctgcca	750
acagagcgag cagagacgga accgcaccac cgcagagaac caaagaaagg cgcaaaaaga	810
aagcaacaga ggcaaaaaag cacacaaacg cacacgacac agccgcgcga caacacgacg	870
agccaacaca aaagacgacg cacaaggcac gccagaaaag aggcgagaga acacaa	926

<210> 354
 <211> 510
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (149)..(493)

<400> 354	
gataccagct tccttcagca gcgcaggcgg tgggtccctga ggcccgtgga aggagtcaaa	60
cttgcgaggaa ttttgcagaa gtcattgtat tcaaagaaga ataagcaaga aagaaaagaa	120
ggaaggaaga gaggtagaca gatacaag atg aaa tcc tgt caa aaa atg gaa	172
Met Lys Ser Cys Gln Lys Met Glu	
1 5	

gga aaa cca gaa aat gag agt gaa cca aag cat gag gaa gag cca aag	220
Gly Lys Pro Glu Asn Glu Ser Glu Pro Lys His Glu Glu Glu Pro Lys	
10 15 20	
cct gag gaa aag cca gaa gag gag gag aag cta gag gag gag gcc aaa	268
Pro Glu Glu Lys Pro Glu Glu Glu Glu Lys Leu Glu Glu Glu Ala Lys	
25 30 35 40	
gca aaa gga act ttt aga gaa agg ctg att caa tct ctc cag gag ttt	316
Ala Lys Gly Thr Phe Arg Glu Arg Leu Ile Gln Ser Leu Gln Glu Phe	
45 50 55	
aaa gaa gat ata cac aac agg cat tta agc aat gaa gat atg ttt aga	364
Lys Glu Asp Ile His Asn Arg His Leu Ser Asn Glu Asp Met Phe Arg	
60 65 70	
gaa gtg gat gaa ata gat gag ata agg aga gtc aga aac aaa ctt ata	412
Glu Val Asp Glu Ile Asp Glu Ile Arg Arg Val Arg Asn Lys Leu Ile	
75 80 85	
gtg atg cgt tgg aag gta acg aac cct cct acc cca ttt aaa tta gag	460
Val Met Arg Trp Lys Val Thr Asn Pro Pro Thr Pro Phe Lys Leu Glu	
90 95 100	
tac ccg gat ttc tct cat att aca tac cca tag cgctcttata gcagcac	510
Tyr Pro Asp Phe Ser His Ile Thr Tyr Pro *	
105 110 115	

<210> 355
 <211> 1045
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (95)..(1045)

<400> 355	
tagaggagta gattaccgag aaaaatatcc catcagtgag gagattttcg gtatcaccag	60
aaagaccaaa gatcagggct gcttaattgc tgac atg atg gga ctc acc gag	112
Met Met Gly Leu Thr Glu	
1 5	
ggg gtg ttc ctg att ctg tct ggc act cag ttc aca ctg gga att ctg	160
Gly Val Phe Leu Ile Leu Ser Gly Thr Gln Phe Thr Leu Gly Ile Leu	
10 15 20	
gtc aat tgt ttc att gag ttg gtc aat ggt agc agc tgg ttc aag acc	208
Val Asn Cys Phe Ile Glu Leu Val Asn Gly Ser Ser Trp Phe Lys Thr	
25 30 35	

aag aga atg tct ttg tct gac ttc atc atc acc acc ctg gca ctc ttg	256
Lys Arg Met Ser Leu Ser Asp Phe Ile Ile Thr Thr Leu Ala Leu Leu	
40 45 50	
agg atc att ctg ctg tgt att atc ttg act gat agt ttt tta ata gaa	304
Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr Asp Ser Phe Leu Ile Glu	
55 60 65 70	
ttc tct ccc aac aca cat gat tca ggg ata ata atg caa att att gat	352
Phe Ser Pro Asn Thr His Asp Ser Gly Ile Ile Met Gln Ile Ile Asp	
75 80 85	
gtt tcc tgg aca ttt aca aac cat ctg agc att tgg ctt gcc acc tgt	400
Val Ser Trp Thr Phe Thr Asn His Leu Ser Ile Trp Leu Ala Thr Cys	
90 95 100	
ctt ggt gtc ctc tac tgc ctg aaa atc gcc agt ttc tct cac ccc aca	448
Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala Ser Phe Ser His Pro Thr	
105 110 115	
ttc ctc tgg ctc aag tgg aga gtt tct agg gtg atg gta tgg atg ctg	496
Phe Leu Trp Leu Lys Trp Arg Val Ser Arg Val Met Val Trp Met Leu	
120 125 130	
ttg ggt gca ctg ctc tta tcc tgt ggt agt acc gca tct ctg atc aat	544
Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser Thr Ala Ser Leu Ile Asn	
135 140 145 150	
gag ttt aag ctc tat tct gtc ttt agg gga att gag gcc acc agg aat	592
Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly Ile Glu Ala Thr Arg Asn	
155 160 165	
gtg act gaa cac ttc aga aag aag agg agt gag tat tat ctg atc cat	640
Val Thr Glu His Phe Arg Lys Lys Arg Ser Glu Tyr Tyr Leu Ile His	
170 175 180	
gtt ctt ggg act ctg tgg tac ctg cct ccc tta att gtg tcc ctg gcc	688
Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro Leu Ile Val Ser Leu Ala	
185 190 195	
tcc tac tct ttg ctc atc ttc tcc ctg ggg agg cac aca cgg cag atg	736
Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met	
200 205 210	
ctg caa aat ggg aca agc tcc aga gat cca acc act gag gcc cac aag	784
Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro Thr Thr Glu Ala His Lys	
215 220 225 230	
agg gcc atc aga atc atc ctt tcc ttc ttc ttt ctc ttc tta ctt tac	832
Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe Phe Leu Phe Leu Leu Tyr	
235 240 245	
ttt ctt gct ttc tta att gca tca ttt ggt aat ttc cta cca aaa acc	880
Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly Asn Phe Leu Pro Lys Thr	
250 255 260	
aag atg gct aag atg att ggc gaa gta atg aca atg ttt tat cct gct	928

Lys Met Ala Lys Met Ile Gly Glu Val Met Thr Met Phe Tyr Pro Ala
 265 270 275

ggc cac tca ttt att ctc att ctg ggg aac agt aag ctg aag cag aca 976
 Gly His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr
 280 285 290

ttt gta gtg atg ctc cgg tgt gag tct ggt cat ctg aag cct gga tcc 1024
 Phe Val Val Met Leu Arg Cys Glu Ser Gly His Leu Lys Pro Gly Ser
 295 300 305 310

aag gga ccc att ttc tct tag 1045
 Lys Gly Pro Ile Phe Ser *
 315

<210> 356
 <211> 790
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (86)..(310)

<220>
 <221> misc_feature
 <222> (1)...(790)
 <223> n = a,t,c or g

<400> 356

agacaaacct catctgccct gttgtttttt gttctcacct tcttattcag tatgagtgtc 60

gtttggtgct tctaattgggc ttcta atg gtc ctc ctg gaa ccc aag ccc tgg 112
 Met Val Leu Leu Glu Pro Lys Pro Trp
 1 5

ctg gaa ctg atg ctg ctg tgg tgg tca ggg ttc agt gag cag gag gaa 160
 Leu Glu Leu Met Leu Leu Trp Trp Ser Gly Phe Ser Glu Gln Glu Glu
 10 15 20 25

gga ctt ggt gtt tac ccc ttg ttt acc cct ttc ctt ggc ttc ctt cca 208
 Gly Leu Gly Val Tyr Pro Leu Phe Thr Pro Phe Leu Gly Phe Leu Pro
 30 35 40

tgc agg cca ccc tgt gac ccc gtg gtg gcc ccc tct gga acc aag agc 256
 Cys Arg Pro Pro Cys Asp Pro Val Val Ala Pro Ser Gly Thr Lys Ser
 45 50 55

tgc cga ctt cca gca gca cac aca gga tca gtg ctg ggg cca tct gtg 304
 Cys Arg Leu Pro Ala Ala His Thr Gly Ser Val Leu Gly Pro Ser Val
 60 65 70

cac tga ccaaagcctc tgctggcctc accagaccaa ggccagtgtg tgcttcaggg 360

His *
75

agccttggat cctccaggct gccaacagaa acaccggccc tctcggcagc agcccatcc 420
ttccacccct gcaactgggtc ctgaaaagcc cattttgggg ccgttgctat ttagccaacc 480
tgccctccct tgctctcctg tgattttctca ctattccggc tgcagctcgc tgggagaaac 540
acttgagagt cttttgtgct ccacacccat gtacttaaaa taccaggcct ataggtcatt 600
tcaatgaggg aatttggctc ataacacgtg tgccccgagg cnagnatcct acttctgcag 660
atgctggcca agaagggctg tgtcccagcc gccatggggg ggggccacag agagggcagg 720
gccacgtgga gggcagagca tgtggctcct gtcaggtgcg ccattgctt nacttcagcc 780
cagtatcaag 790

<210> 357
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(246)

<400> 357
ggcatatttc aggtttcagt gacatagatc aagtaatttt aaaccaatth gggtatttcta 60
tctaag atg agg gac atg gct att aag gtc aag cca aac tat act aaa 108
Met Arg Asp Met Ala Ile Lys Val Lys Pro Asn Tyr Thr Lys
1 5 10
agt agt ata ggg cag cag tta aaa tta tct ttt gaa aat caa gta tta 156
Ser Ser Ile Gly Gln Gln Leu Lys Leu Ser Phe Glu Asn Gln Val Leu
15 20 25 30
cct ggt ttc ttc tgt cac aac aga ata gct ggt tac cta gtc agt cac 204
Pro Gly Phe Phe Cys His Asn Arg Ile Ala Gly Tyr Leu Val Ser His
35 40 45
agt tgc cct tgc ctt ccc ttg tta gtc cct gga ggt act tga gtggaac 253
Ser Cys Pro Cys Leu Pro Leu Leu Val Pro Gly Gly Thr *
50 55 60
agaaggtaga attagcaaca gctcaatcac tttaggtagc atttctcctg aattctgctg 313
ccaaatcctc aggtgtctatg gattgggttga aatagtaaaa tcacacatag tgatttcttg 373
cacagcgtaa aggcgtttta ttttagtgta tagtgaacaa agaaggaaaa ctgggtcata 433

<210> 358
 <211> 1483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (117)..(911)

<400> 358

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agttgattgc aggtcctcct ggggccagaa gggcgcctgg gaggccaggt tctggggatc      60

ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggacc      116
atg ggg gct ggg gcc agt gct gag gag aag cac tcc agg gag ctg gaa      164
Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
  1             5             10             15

aag aag ctg aaa gag gac gct gag aag gat gct cga acc gtg aag ctg      212
Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
          20             25             30

ctg ctt ctg ggt gcc ggt gag tcc ggg aag agc acc atc gtc aag cag      260
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
          35             40             45

atg aag att atc cac cag gac ggg tac tcg ctg gaa gag tgc ctc gag      308
Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
          50             55             60

ttt atc gcc atc atc tac ggc aac acg ttg cag tcc atc ctg gcc atc      356
Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
          65             70             75             80

gta cgc gcc atg acc aca ctc aac atc cag tac gga gac tct gca cgc      404
Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
          85             90             95

cag gac gac gcc cgg aag ctg atg cac atg gca gac act atc gag gag      452
Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
          100            105            110

ggc acg atg ccc aag gag atg tcg gac atc atc cag cgg ctg tgg aag      500
Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
          115            120            125

gac tcc ggt atc cag gcc tgt ttt gag cgc gcc tcg gag tac cag ctc      548
Asp Ser Gly Ile Gln Ala Cys Phe Glu Arg Ala Ser Glu Tyr Gln Leu
          130            135            140

aac gac tcg gcg ggc tac tac ctc tcc gac ctg gag cgc ctg gta acc      596
Asn Asp Ser Ala Gly Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
          145            150            155            160

ccg ggc tac gtg ccc acc gag cag gac gtg ctg cgc tcg cga gtc aag      644
Pro Gly Tyr Val Pro Thr Glu Gln Asp Val Leu Arg Ser Arg Val Lys

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165	170	175	
acc act ggc atc atc gag acg cag ttc tcc ttc aag gat ctc aac ttc			692
Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe			
180	185	190	
cgg atg ttc gat gtg ggc ggg cag cgc tgc gag cgc aag aag tgg atc			740
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile			
195	200	205	
cac tgc ttc gag ggc gtg acc tgc atc atc ttc atc gcg gcg ctg agc			788
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser			
210	215	220	
gcc cta cga cat ggt gct agt gga gga cga cga agt gaa ccg cat gca			836
Ala Leu Arg His Gly Ala Ser Gly Gly Arg Arg Ser Glu Pro His Ala			
225	230	235	240
cga gag cct gca cct gtt caa cag cat ctg caa cca ccg cta ctt cgc			884
Arg Glu Pro Ala Pro Val Gln Gln His Leu Gln Pro Pro Leu Leu Arg			
245	250	255	
cac gac gtc cat cgt gct ctt cct taa caaga aggacgtctt cttcgagaag			936
His Asp Val His Arg Ala Leu Pro *			
260	265		
atcaagaagg cgcacctcag catctgtttc ccggactacg atggacccaa cacctacgag			996
gacgccggca actacatcaa ggtgcagttc ctcgagctca acatgcggcg cgacgtgaag			1056
gagatctatt cccacatgac gtgcgccacc gacacgcaga acgtcaaatt tgtcttcgac			1116
gctgtcaccg acatcatcat caaggagaac ctcaaagact gtggcctctt ctgagcacca			1176
aatctttgct tatagatcca cagccagggc ctgtgctgca gtcgggggaca aggagcttcc			1236
gtctggcaag ggaagctgag agccatggct gaactatcag ggacaaaggc ccatgtcccc			1296
acatccctgc tccctccttc ctcatccagc accaaatctt tgcttatgct ccacagccag			1356
ggcctgtgct gcagtcgggg acaaggagct tccgtactgg caaggccggg gcacaatttg			1416
cactccctc agctagacgc acagactcag caataaacct ttgcatcagg caaaaaaaaa			1476
aaaaaaaa			1483

<210> 359
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (441)

<400> 359

atg aag ccc acc ctc atc tca gtg ctt gtg ata ata ttt ata ctc aga 48
Met Lys Pro Thr Leu Ile Ser Val Leu Val Ile Ile Phe Ile Leu Arg
1 5 10 15

gga aca aga gcc cag aga gtg act cag ccc gag aag ctc ctc tct gtc 96
Gly Thr Arg Ala Gln Arg Val Thr Gln Pro Glu Lys Leu Leu Ser Val
20 25 30

ttt aaa ggg gcc cca gtg gag ctg aag tgc aac tat tcc tat tct ggg 144
Phe Lys Gly Ala Pro Val Glu Leu Lys Cys Asn Tyr Ser Tyr Ser Gly
35 40 45

agt cct gaa ctc ttc tgg tat gtc cag tac tcc aga caa cgc ctc cag 192
Ser Pro Glu Leu Phe Trp Tyr Val Gln Tyr Ser Arg Gln Arg Leu Gln
50 55 60

tta ctc ttg aga cac atc tct aga gag agc atc aaa ggc ttc act gct 240
Leu Leu Leu Arg His Ile Ser Arg Glu Ser Ile Lys Gly Phe Thr Ala
65 70 75 80

gac ctt aac aaa ggc gag aca tct ttc cac ctg aag aaa cca ttt gct 288
Asp Leu Asn Lys Gly Glu Thr Ser Phe His Leu Lys Lys Pro Phe Ala
85 90 95

caa gag gaa gac tca gcc atg tat tac tgt gct cta agt ggc aca gta 336
Gln Glu Glu Asp Ser Ala Met Tyr Tyr Cys Ala Leu Ser Gly Thr Val
100 105 110

gct ggt ttt gca agg aag cag aac aca aac cct tta aat aca gga aat 384
Ala Gly Phe Ala Arg Lys Gln Asn Thr Asn Pro Leu Asn Thr Gly Asn
115 120 125

att tct ttg caa act ctc tgt atg gcc aca gca ggg cat tct ttc tcc 432
Ile Ser Leu Gln Thr Leu Cys Met Ala Thr Ala Gly His Ser Phe Ser
130 135 140

aga aat taa tattgag tttatctcgt agatattata tcatactca tcagctagcc 488
Arg Asn *
145

atacacccac ctcacaattt tgtccaaaaa attctcatca tttaccctgc ctaaattaa 548

tttaaaaaata gtaaactgtat tcatttcgtc tagcagcact ggacacacac cttcgaaata 608

aaaactacct tgcactgcac aaaaaacaaa aacaaaaaca cattgccggc cgccccctta 668

ttcccctcag tcagggtctac cctaccttcc acctcatccg ctcatt 714

<210> 360

<211> 3154

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (278)..(1483)

<400> 360

tggtttcttg gaagaacgtg ctcagcgcggt tctcgatatga aggagttttc cgcctgcagc	60
aactgcttcg cctgggtcggc cgcgcacccg ccggtctagc gaactggttg atcatgacct	120
ggtgccgcag ctggtccatg ttcaccgaca tggcgcgggc gcgcgggggccc cggcgtctcc	180
ggccgggacgc agacgcgggg ctgctgctcgt agcggggggccc cggatccccg agtggcgggc	240
ggagcctcga aaagagattc tcagcgctga ttttgag atg atg ggc ttg gga aac	295
Met Met Gly Leu Gly Asn	
1 5	
ggg cgt cgc agc atg aag tcg ccg ccc ctc gtg ctg gcc gcc ctg gtg	343
Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu Val	
10 15 20	
gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc cgg	391
Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser Arg	
25 30 35	
agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc cgc	439
Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val Arg	
40 45 50	
agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag ttc	487
Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu Phe	
55 60 65 70	
cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag tcc	535
Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser	
75 80 85	
agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac gaa	583
Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu	
90 95 100	
aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc cga	631
Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg	
105 110 115	
gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg ctg	679
Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu	
120 125 130	
cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag agg	727
Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg	
135 140 145 150	
aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag gtg	775
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu Val	
155 160 165	

aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg aat	823
Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly Asn	
170 175 180	
gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga cag	871
Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg Gln	
185 190 195	
cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca ggc	919
Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala Gly	
200 205 210	
ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt aac	967
Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly Asn	
215 220 225 230	
agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat tca	1015
Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp Ser	
235 240 245	
aag aga caa gtt gag aaa gag gaa acc aat gag atc cag gtg gtg aat	1063
Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val Asn	
250 255 260	
gag gag cct cag agg gac agg ctg ccg cag gag cca ggc cgg gag cag	1111
Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu Gln	
265 270 275	
gtg gtg gaa gac aga cct gta ggt gga aga ggc ttc ggg gga gcc gga	1159
Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala Gly	
280 285 290	
gaa ctg ggc cag acc cca cag gtg cag gct gcc ctg tca gtg agc cag	1207
Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser Gln	
295 300 305 310	
gaa aat cca gag atg gag ggc cct gag cga gac cag ctt gtc atc ccc	1255
Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro	
315 320 325	
gac gga cag gag gag gag cag gaa gct gcc ggg gaa ggg aga aac cag	1303
Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln	
330 335 340	
cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa gca	1351
Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala	
345 350 355	
gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga aac	1399
Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn	
360 365 370	
ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat tta	1447
Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	
375 380 385 390	

ctt gat cag cgt gaa aag cgg aat cat aca ctc tga attg aactggaatc	1497
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *	
395 400	
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3154

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atgtcctc atg ata ttt gaa tta cac aga tat acc tta tat ctg ctt atg	170
Met Ile Phe Glu Leu His Arg Tyr Thr Leu Tyr Leu Leu Met	
1 5 10	
tac tgt ata tac atc tta gtt tta tat att aat cat aag att ttt tca	218
Tyr Cys Ile Tyr Ile Leu Val Leu Tyr Ile Asn His Lys Ile Phe Ser	
15 20 25 30	
ccc ttc ctc ctc caa gaa caa att ttt acc ccc ttc aaa gca ata tgg	266
Pro Phe Leu Leu Gln Glu Gln Ile Phe Thr Pro Phe Lys Ala Ile Trp	
35 40 45	
ccc cac tgt tcc att gct tta agg gaa ata cca tgt aag cct cta tta	314
Pro His Cys Ser Ile Ala Leu Arg Glu Ile Pro Cys Lys Pro Leu Leu	
50 55 60	
tct acc aag ctc tga gcaggctctt cacatagttt cattaactca tcaaaaccct	369
Ser Thr Lys Leu *	
65	
gcttcctgat ctctaattct tttcctcatt ttggtaccaa caaacatgac cttcagtgga	429
gatattttgtt tagcaaaaga gattacctat ttttttctcc aaccagttgt tgatgccatg	489
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ctaaaccaag aagttggaat cgttggtaaa tacaggaccc gctatggggg ctccctccag	360
aaa atg gtg aag aaa att gaa atc agc cag tac gcc aag tac att tgc	408
Met Val Lys Lys Ile Glu Ile Ser Gln Tyr Ala Lys Tyr Ile Cys	
1 5 10 15	
tct ttt ctg tgg caa aac caa gat gaa gag acg agc tgt ggg gat ctg	456
Ser Phe Leu Trp Gln Asn Gln Asp Glu Glu Thr Ser Cys Gly Asp Leu	
20 25 30	
gtg ctg tgg ttt tgc atg aag aca gta aag gtg tct tca tcc agg aac	504
Val Leu Trp Phe Cys Met Lys Thr Val Lys Val Ser Ser Ser Arg Asn	
35 40 45	
cac att gtc tgg acc tac aat acc act tca gct gtc acg gta aag tcc	552
His Ile Val Trp Thr Tyr Asn Thr Thr Ser Ala Val Thr Val Lys Ser	
50 55 60	
acc atc aga aga ctg aag caa ttg aaa gac cag tag acgc tcctctactc	602
Thr Ile Arg Arg Leu Lys Gln Leu Lys Asp Gln *	
65 70 75	
tttgagacat cactagccta taataaatgg gttaatttat gtaaccaaaa aaattaaaaa	662
ggtttgtgga aaaactgaaa aaaaaaaaaa	691